

S.N. 08/401, 881



In re the Application of:

**William A. HASELTINE, Craig A. ROSEN, Steven M. RUBIN, Patrick J. DILLON,
Haodong LI, and Julie EARLE-HUGHES**

Serial No.: Unassigned

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For: HUMAN GENES, SEQUENCES AND EXPRESSION PRODUCTS-17

SEQUENCE LISTING

**SECTION 1 of 2 SECTIONS,
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Haseltine, William
Rosen, Craig
Ruben, Steve
Dillon, Patrick
Li, Haodong
Earle-Hughes, Julie

(ii) TITLE OF INVENTION: Human Genes, Sequences, and Expression Products

(iii) NUMBER OF SEQUENCES: 1767

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, & Olstein

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(C) CITY: Roseland

(D) STATE: New Jersey

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 5.0

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/401,881

(B) FILING DATE: March 10, 1995

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Olstein, Elliot

(B) REGISTRATION NUMBER: 24,025

(C) REFERENCE/DOCKET NUMBER: 325800-306

(vi) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGNANAAAGG AGGAGCACGA GGTGGCTGTC CTGGGGCGC CCCAAACCC TGCTCCCCA	60
ANGTCCACCG TGAATCAAA TCCGCAGCGA GAACCTCCGT GCCCAACCAT GTGNTGCTGG	120
TCCCTGTTCA ANACCCTCTT AATGAACCCC TGNTGCCTGG GNCTTAANAG CATTGCGCTA	180
CTCCGTGAAA GTNTAGGGNC AGGAAAGATG GTTGGCGACG TGAACCGGGG CCCAGGNNTA	240
TGCTTCCACC GNCAAGTGCC TGAAAATTG GG	272

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGAANACCAG CTCTGGGGGC ACGGCCCANC TTCCCTAAAA ATGTCTACTG TTCCANAAAA	60
TCCTGTNCAA GCCCAGCTTG AGGGGTAATC ACTCTANACC CCCAAGTCCA TATGGNTCTT	120
TAAAAGCCTA TNCTAA	136

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCANAGNAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAANN	68

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCCCCAACG TGNCCGGCCG ACACCAAGCT CTCCAAGATC AAGACTCTGC GCCTAGCCAC	60
CAGCTNACAT CGCCTGACCT GAATGGACGT GCTGGGCCAA GGGATGCACA GTCTGGCGA	120
TNCCAAGGGC CTT	133

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACTCAATCA TGGNTTGTGG TCTGGTCGCC AGAACCTGT AATCTCAAAC CTGGAGAGTG	60
CCTTCGAGTG CNAGGCGAGG TGGCTCCTGC ACGCTAACAGAG CTTCGTGCCT GNAACCTGGG	120
CAAAGACAGC AACANCCTGT NCCTGNACTT ACAACCCTNG CTTCAACGTC NACGAGAACG	180
CCAACACCAT CGTGTGCAAC AGACAAAGGT ACGGCGGGGC CTGGGGGGAC CGAGCAGCGG	240
GAGGCTGTCT TTCCCTTCCC AGNCTGGAAG TTTTGAGG GTGTGCATCA CCTTTGGACC	300
AGGNCCAACC GCCCTA	316

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCAGAGCCT GTCGGCCACC AAGGTAGTGC ACNGACCCAT GGGNCACCCG CAAGCACCTG	60
GTGCCCAAGG NACCTGGATA TNCGGCCTGT GAAAGACTCG GAACTCGTCT ATCTGCAGAG	120
CTGCACCTGA ACTTCTGCAT GAAGNAATGA GAAAGGTGNG CTCCCACGGG ANCACAAGAC	180
AGGNCAAGTGC AACAAAGGACA TCCAACCGAA AGCGAACATT GCGAGACCTT GATGTGCCTG	240
CGGGCGTGGG TGACAACCCC TACACAGGAC CGCNTGGTCG AGCGGTGCCA TGTNAGTTAC	300

CATGGTGCTG TTACGTTCAA NNGCCGCAGT NTG

333

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCACGAGCC TATCGGCCAC CAAGGTAGTA CACNGACCCA TNGNCACCCG CAAGCACCCNN 60
GTGCCCAAGG ACCTGGATAT CCGG 84

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GNAGGCAAGG CCAGGGATAA GGNGTGGATG CCGTCACCAA GTTGGGCCGC TTNGTCAAGG 60
ACATGAAGAT CAAGTCCNGG AGGAGATCNT TCTCTTCTCC TGCCCATTAA GGGTTCAANG 120
ATCATTGATT TCTTCCTGGG GGCCCTCTCA NGGATGAGGT TTTGAAGATT ATGCCGTNCA 180
GAAGNAGACC CTGCCGGCCA GNGAACCGGT TNAAGGCTTT 220

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCCCCTTG GGCATGGCTA TGGGGAGGGG GCTGGAGANG GTATCGATGA TGCTGAGTGG 60
GTGGTGGCCA GGGACAAGCC CATGTACGAC GAGATCTTCT ACACCCGTGTC ACCGGTTGNT 120
GGCAAGATCA CAGGCCTAA TNCCAAGANG GAGATGGTGC GCTCCAAGCT GCCCAACAGT 180
GTGCTGGCA AGATCTGGAA GCTGGCCGAC ATTGAACAAG GATGGCATGC TGGTACGACG 240
AACGAGTTG GCACTGGNCC AACCACCTAC ATNCAAAGTT CAAGCTGGGA GGGGGCACGA 300

GCTNACCAA .CNAGCTGGCC TNACCCACCT 330

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCCAAGAAC GTCATGATGA TCCAGTCCTG CAAATGCAAC TACAAC TGCC CGCATGCCAA 60

TGANGCAGCG TTTCCCNCT ACAGNNNTGTT CAATGACATT CACAAATTNA GGG 113

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCANAGNAG AACGCAGAGT ACAAGCAATT GCTGGGACAT CAAGACACGC CTGGNGGTGG 60

AGATCNNGAC CTACCGCCGC CTGCTCGATG GAGAGGGAGG TGGTTCTAGT TTTGCAGAAT 120

TTGGTGGTAG AAAACTCAGGA TCTGTAAAAC ATGGGATCCA GGGATCTGGT NATCCNGGTG 180

ACTCAAGATC TGGAAAGCTGT TCTGGTCAAG GACGAGATTG AAGCAAGACT AGAGTGNACT 240

AAGAACTATN GTTAGAGGNG TTGGTGGATG GCAAGGTTGT CTCGTTCTCC AAGTCCAGCA 300

GTATTTCTGA GGGTNGAAAG TTTAAATAAG GGACCTTNCC AGTTCAACAA AAGTGTCTT 360

TTNCAAGGGN ANAAAAATTC CAGG 384

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCAGAGCCC AGAAGAACCA CATCCCTNTT TTTAGTCCCG CACTTACAGA CGGNTCGCTG 60

GGCGACATGA TCTTTTCCA TTCCTACAAG AACCCGGGCC TGGTCCTGGA CATCGTTGAG 120

GACCTGAAGG CTCATCAACA CACAGGCCAT CTTTNCCAAG TGCACTGGGN ATGATCATTC	180
TGGGCGGGGG CGTGGTCAAG CACCACATTG CCAATGCCAA CCTCATGCCG AANGGGCCG	240
ACTTACGCTG TTTACATCAA CACAGCCCAG GAGTTGATG GCTCTGAACt CAGGTGCCG	300
ACCAGACGAG GCTGTTNTCC TGGGGCAAGA TNCGGGTGA TGACACGNCC GTCAAGGTTT	360
ATGCTGGAGG CNTNCCTGGG TCTTTCCCCC TGGTT	395

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCACGAGGC CTTCAGCAGA GGTCAGATGC AGAACCCATT TGAAGACGCC TCGTTGCGC	60
TGCGGACGGG GGAGATGAGC GGGCCCGTGT TCACGGATTc CGGCATCCAC ATCATCCTCC	120
GCACGTGAGTG AGGGTGGGA GCCCAGGCt GGCCTGGGG CAGGGCAGGG CGGCTAGGCC	180
NNCCAGCTCC CCCTTGCCCG CCAGCCAGTG GCCGAACCCC CCACCTCCCTG CCACCGTTCA	240
CACAGTGATT TTATTGTTCC CACAATGGCT GGGAAAGGGGG CCCTTTCCAG ATTGGGGGCC	300
CTGGGGTCCC CACTCCCTGT NCCATNCCCC AGTTGGGGCT GNGAACCGCC AATTTTCCT	360
TTAAGTATTG NATTCAGNA NGGGTGGGAG GTTCCAAAC CCAGGCATNT GGTGGGAGGG	420
GTGTTCCAA AGAGAAAGG	439

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCAGAGNAC AAGGGCCGTG GCCGCTTCGC CCTCATCATC TATGAGAACa TCCTCAAGTA	60
TGTCAACCTG GACGCCTGGN AACCGGGAGC TGCTGGGACA AGTACTGTGT GGCCTACGGC	120
GTGGGCATCA TTGGCTTCTT CAAGGCCAAT GAGGAACAGC CTGCTGAGTG CGCATTCAAG	180
GGCTTNNCC TGTTCCCTGC ACTCAAACCT GGGCCTGAAG GGACTGCAGC ATCAACCCCA	240
AGTCCCCGTT GGCTTCTACG TGGACGCGAA CCTNAGGNAG GGGTTGGNAG GAAAGGTTGT	300

TGCTTCNCC CGGGTNG

317

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCAGAGCCA ACATTGAGGC CAACGAGAGT AAGGNGGTCC GGCAGTTCCG GAGNACTCTT	60
TGCCAGCTG GCTGGAGGAT GACATGGAGG TCAGGCCAC AGAACTCATG AACATTCTTC	120
AATAAGGTTG TGAACACGNA CACCCTGATC TGAAAGACTG ATGGTTTG CATTGACACA	180
TGTCGAGCA TGGTGGCGT GAATGGGATA GCGNACACCA CAGGCAAGCT GGGCTTGGA	240
GGGAATTCA AGTNACTTGT GGAACAACC ATTCAAAAG GTGGNCAGGN CATATTACAA	300
ACAGTTCGA CAATGGNACC GATTCTGGGA CCATTT	336

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCAGAGCCA CAACCTCCCT GGCTCCTACC GCTGTGACTG CAAAGCCGGC TTTCAGCGGG	60
ATGCCTTCGG CCGGGGCTGC ATCGACGTGA ATNAGTGCTG GGCCTCGNCA GGCCGCCTGT	120
GCCAGCACAC GTGTGAGAAA CACACTNCGG CTCCTNACCG CTGTTCTGC GCCTCCGGT	180
TCCTGGCTAG CAGCGGNACG GCAAGCGCTG TGNAAGACGT GAATAAGTGT GAGGCCANC	240
GCTGTCAGCC AGGTAGTNTG CCAACATGNT TATGGGNTCC TACCCAGTGG TACTGCCGCC	300
AGGGGTTACC A	311

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCAGAGNAC AAGGGCCGTG GCGCTTCGCC CTCATCATCT ATGAGAACAT CCTCAAGTAT	60
GTNAACCTGG ACGCCTGGAA CCGGGAGCTG CTGGACAAGT ACTGTGTGGC CTACGGGTGG	120
GCATCATTGG CTTCTTCAAG GCCAATGNGA ACAGCCTGCT GAGTGCGCAT CAAGGGCTTT	180
NCCTGTTCCCT GCACTCAAAC CTGGGCCTGA AGGACTGCAG CATCAACCCC AAGTCCCCGC	240
TGCTCTACGT GACGCGACCT AGGGAGGTGG AGAAAGGTGT GCTTCCCCGG NGNAGGACTG	300
GGACGGTTTT TCCAGTTCAA ATCACTCCAN CTATGGAGCC CATNCTTGTN GGNCANGACG	360
GGGTTGGTTT TGAAGTCCA TGCCCACAAAC TGGGG	395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCAGAGCCA CAACCTCCCT GGCTCCTACC GCTGTGACTG CAAAGCCGGC TTTNAGCGGG	60
AATGCCTTCG GCCGGGGCTG CATCGACGTG AATGAAGTGC TGGGCCTCGC CAGGCCGNCC	120
TGTGCCAGC ACACGTNTGA AGAAACACAC TTCGGCTCCT ACCGCTGTTCTGAGACCTC	180
CGGGTTCCCTG CTNAGCAGCG GACGGCAAGC GCTGTGNAAG ACGTGNAATG AAGTGTGAAG	240
GCCCAGCGNT TGCAGCCAGG NGTNTGGCCA ACATCTTATG NGCTTCCTAA CCCAGTGGNT	300
ACTNNCCGNC CAGGGNTNAC CAGCTTGGCT TGAAGGGATT GGGGCACAAAC TGCAACAGAC	360
ATTGGACGA GTTNTGCTTC AAAGGGNGGC CGGAATCCTT TTGNAACTTT CCGTTGTTNT	420
TNAAAGTTG	429

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCACTGCCA GTTCGTGCTT GAGCATCGTT CTGTGCAGGA GGAAGCCGGC TTTCACCGGC	60
AGGCGTGGTG TCAAATGCCG GTTAATTGTT AGCGGACACG AAAACCAGGC CATTACTCAC	120

AGTATAACG

129

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTTNAGCATC GTTCTGNCCA GGAGGAAGCC GGCTTCACC GGCAGGCGTN NTGTCAAATG	60
CCCGATAATT GTTAGCGATA CACGACAAAC CAGNCGCATT CACTCNACAG TATAACGNCA	120
GGCCAGTCGT CATAAACCGT TCAGGGGAGG AGCCCGGTCA CCCAATTGCG CCCCTGATAA	180
GTGCNGTNCG ATATTACAAA TTNCACTTGN TCC	213

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCANAGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AANANAANAA AAAAAAAAAA AAAAANAAAA AAANG	115

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCACGAGCC CCCCTTTTT TTTTTTTTT TTTTTTTTT TTTAAANGNT TNANNTTTT	60
	60

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCACGAGCG CATGGGNNGTC ATCCTCTGGG GTGACGCTNG GGTACACCAC AAGCACGGAG	60
ACCTGCCAGT ACCNCAAAGA TTACCTGACA CGGCTGCTGG TCCCCTACGT GGTCAATTG	120
TCCTGGGCCA CCGNGTATTG CAGCCNGGCC GAGTGCCATG GCCGTNGNCG GCTGTGTGCN	180
	180

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TNCCATGNCA CGATATTTCG GCCAAGGACA TCGACGGGCA CATGGTTAAC CTGGNACAAG	60
NACCGGGGCT TCATGTGCAT CGTCACCAAC GTGTGNCTCC CAGTGAAGGN AAGAACCGAN	120
GTAAAACT	128

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CACCGCCTAT GGTNCTGACG CCAGGCCTGG GCAGAGCCCCG GGCCTCTGGA GGCGCTTNGN	60
NGCCGTNCTT GGGCTGCGGA AAGGCTCAGG ACCCAAGAAG GAGCGGAGAC GCACTGAGAG	120
CATTAACAGC GCATTCGGNT AGTGCGCGA GTGCATCCCC AACGTGCCGG CCGACACCAA	180
GCTCTCCAAG ATCAAGACTC TGCGCTAAC CACCAGCTTA CATCGTCTAC CTNATGGGAC	240
GTNNCTGGCC AAGGTGCACA GTCTGGCGAT CCCGAGGGCT TTCANGCTTG GAACTCAAGN	300
	300

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGNGTGAGGT GGCCCTGGGC AGAGAGCACC NTATCANCTT GGACAACCCC AGCTTGAAGA	60
GCCCCACCTCC TGGCTTCGAC AGTNTCATTG CCCGAGGCCA CACCGAGNCT GATCCGACCC	120
AGGACACTGA GTTGGAGCTG GATGGGCCAG CAAGTGGTGG TNCCCCAGGG CCAGCCTGTN	180
CCNTGN	186

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGNCCNTG TCATCGNAGA CTTCANGGTC TTAGCAGGGG ACAAGAACTT CATCACAGCT	60
GAGGAGCTGC GGAGAGAGCT GCCCCCCGNC CAGACCGAGT ACTGCATCGC CCGCATGGGG	120
NCCATACCAAG GGCCCTGACG CCGTGNCCGG NGCCCTCGAA CTTACAAGTC CTTCTTCACG	180
GGCTTTGTAT GGCGAGAGGG NNCTGTGAGG	210

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCAGAGGNC AAGCCGAAGA AGCCCCACTA ACCCAATCGN AAGTNCTGT CAAGTNCGGC	60
TNAGCATGGC CGNAAGCNNN TGCCTTNANC CCTGGGGAGG GCCACACCC GCAGGAGCAC	120
CAAATTGTCC TTGTGGAGGG TGGCCGCACC CAGGAACCTG CAAGGCGTNA AGCTTCACCG	180
TTNTGCGTGG NAAGTTANGA CTNTGGGCCA CGTGCCAGAA GAAAGTGAAC GGCTNGGGC	240
ACAGTGGGCT GGGNGCCCCT NCAGAACATG AAACCTTTCC GNNTCTGGGT TGCNAAAGGG	300
TTCCTCC	307

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCACGAGAG GGCTGGTGC	C GGGANTCCAC GACAGACGAG CAGCTATTCA GGTGTGAAGC	60
TGTCAGTGG	A GAAGTCCACA GTGCCTGCAG TCTGAGCTGG GAATCCTGTG AAGAGGCTGG	120
CAGGAGCTGG	G AGCCTGAGA AATGAAATGG TGCCTGCTTA CCATCATCCT GCTGGATGCC	180
GGGCACTGGG	ACCCCCCTGCT GTNATGAGAA AGGAAGACCC TGGCAGTGAC TTTGGGGACC	240
CTCAAGGCCG	T GGGACCCCA TGCGGGCAAC GTGATCTGGG TTGGACCTGC GCAAAGNTTN	300
CTTGCTGGG	AGGTTTAGCG TGGTTCAAGA TGGGAGTNAT GCCCGAGGTT GCGTGTGCTT	360
GGCANCTGGG	TTCACAAAGG TTCTTNAANA ATGCTTTGN CCATTTGGGG AACAAATTGCT	420
T		421

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCAGAGCNA ANCCCAGACA CAAGTTTCA CTCCCTCCTG CGAGCCCTGA GGAAGCCTTA	60
CTGGGCAGCC CCGGGCTCAT TGAAATGCC CGGNATGACT TGGCTAGTGC AGAGGGAATT	120
GAATGGTAAA CCACCGGGGT GAGAAGGGAA GGCTCCCCAT CTNCAGCCAG CCACATCCAC	180
AAGGTGTGTG TAAGGGTGCA GGCGCCGGCC GGTTAGGCA AGGCTCTACT GTCTGTTGCC	240
CCTCCAGGAG AACTTCCAAG GGAGCTTCC CCAGACATGG CCAACAAGGG TCCTTCCTAT	300
GGGCATGAGC CCCGNAGTGC AGTTCCAAA TTCGGGAAGA AGTTNTGACG AGGTAGTTG	360
NGGNGCGGTT TGTNGGAGTG GTTCATA	387

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGCAGAGGGA ACACCCAAGG GTTGATATTG GTGGTCGACA GCAATGATCG GGAAGCAAGT	60
AAATAAGGCC CGGGTAGAGC TGATGNGAAA TGCTGGCGGN GGAACGNAGC TCCGGGAATG	120
GCTGTGACTC CTTGTCTTG CCAAACAAAC AGGTNTCTGC CTGAATGCTC ATGAANCNC	180
TGCTGAGAAT GCACAGACAA GCTGGGCCTG NCATTCCCTT TCGTNACCCG TTAACTGGTT	240
ACATTGCAGG CCACCTGTGC CCACCAGCGG GGNACGGGC TGTNACGAGG GCCTGGTATG	300
GCTGGCCAT TCAGCTTCAA AANCAAGAAG TGNAAGCCA GACAGCCCTA ACAAAAGTACC	360
N	361

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCAGANAAC GGGATCCACT TCCGCAAGNC CCTTTGGNAA GGCCGGGTGG GCCANGCCTC	60
AAACTATGGC ATGAAACTCC CAATCCTGCG TTCCAACCCT GAAGGACCAAG ATCCTGTATC	120
AAACTGAAGC GGTACAATGA AGGAGACCTT TGGCTACGAA NTGCCCCATT CAAAGAAGGA	180
GGGGGGACTT ACGTGCTGGT CTTGAAATTG GCAGAGGTCT ACTTTGCACA GTCCCAGCAA	240
AAGGTATTTG AATGTTACGA TTGANTGGCC ACGTCTGGTG NAAGGGACTT GGGATATCTT	300
TGAATCGTGT TGGGGCANTA GCACAGTTCA CGGTTGAAAT TATTACCTAT GAAGCATTCA	360
GAAAGGGGGA AGCTGAGTTT TCCAGGGGGA GGTGTTCCAC CTTTCACAGG GGAACTTTAC	420
ATTGAGTTTT NTTAAGGGGT ACTTTGGACA TTCCCAGGTT TNTGCACTTT ACATCATGGT	480
TGGGACCATG GGNTGTTA	499

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGCACGAGGG TGAACGTCAT CGCNTCGAAA GCGTCGNAAT AAGACGCACA CGTTGTCCGC	60
NCGNTGCTGG GTCNAAGGCC TACCACCTTC AGAAGTCGAC CTGTGNAAA TGTGGGCTAC	120
CCTGTCA	127

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGGCCNTNC CANTTCNGGG CCCCAACCCG TTTNTCCTGG GGGACCGTGA GAAGGTTTGT	60
TGCCCCAAAA ACCCAGGAGA AGGCCAGGCC GTTTTGGACC GTTTAAAGGT NTTTNACGGT	120
ATCCCACCGN CTTNCGACAA GAAAAAGCGG GNTGGTGGTT TCCTGCTGCC CTAAAGGTCG	180
TGCGTTNTAN AGCCTAAAAG AAAAGTTTGC CTTTTTTGG GGGCGGCTTT GGTTTAAGGA	240
GACTGGTTGN AAGTTACCCA GGNAGTTGAC ANGCCANCTT GGNGGGGGGA	290

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCAGAGCTG TTCCCTNCCA CTGGNTGAGG NATCCTGCAC TGCNTACACC CTGAGNTGGA	60
AACATCGGGN TGTGANAGGT AGCACAGAGG NCTGTNCCCT TTTGTTTATG GTGGNTGTGG	120
AGGGAATGNC AACCGTTTG GNAANCCGTG AAGGNACTGA GAAGAGNCCG CTGACCCACC	180
CCGGGTGGTA ACAGAGACCA GGGGGACAGG TACTTCCCAG GAACTGAGGG NNCAGATTAT	240
TGNGNTGAGG TTCAGCATCC CCTGGAGGNG TCGGGGTTTC CGCAGAACCC CACTTT	296

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGCANAGGGA ACTTAAGCAA AAAATCAAAG ACATAAAATNA TCAGATGGAT GAGTCTTTCA	60
GAGAGTTGGA TATGGAATGT GCTCTTTGG ATGGAGAACAA GAAATCTGTA AACAACTGGAA	120
ACTTATGNAA GGAGNAAGGA GATTTGGAT CATCTAAACC GGNGAATAGC TGANCTGGGA	180
AAAGAAACAT TGTTGGTGAA AAGACCAAGG ATGCTGACCT GTTTGATGTT GAAAGCAAAC	240
ACTTTGNAAG ACCTGGGAGT TCCAGCAGCT TGTAAACATGA GAGCCGTCTA GATGTAGAAA	300
AGGTGGAAC TNGACTNCAA CAGCTCCNGC GTGNAAGTTG CTTGNATATT CT	352

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCAGAGCCC CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNNNTTTN AAGGGGGG	58
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(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGCACGAGGT AAATNTGGTG TTTCTCCTAG CTGTAAACTG TGTCTTAATC AGGATGGAAT	60
TTNNAAAGGAG ACAGATGCTG GAAGATGGGT TCATATTGTT TGTCCCCGT ATGTNCCTGG	120
AGTAGCCTTT GGAGATATTG ACAAAATTACG ACCAGTAACA CTAACGGAAA TNAACTATTC	180
CAAATATGGT GCCAAGGAGT GTAGCTTTN TAAAGACCCT CGCTTGCTA GANCTGGGGT	240
TTGCATTAGC TGTGAATGCA GGGATGTNCA GAGCCTATT CCATGTGAAC CTGTGCTCAA	300
AAGGAAGGTC TGCTTCAGA GGCAGCGGGC GGAAGAGGNT ATTAGCAGNT CCATTCTTTG	360
CTTATTGTAA GCAACTNGCA GNTAGGTTAG TNAGAAAGTG GGA	403

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGGGCGNGGA TTGGCCCGGG CCTGGCGGCC CGCGGGANCC TCAAGCCCCAC GGN CAGCAAG	60
CTNNGCGCTC CGCTGAGNTC CTGCAGGGGC TGCCCGAGTG CACGC GTTGN GCCACGGTCA	120
TCGGGNCACC ATCGTCAAGG CACGGGGCAA GCTCNNNCAT CCCGAGTGCT TCATGTGCAG	180
TGACTGGGG	189

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAAACCGCA TCANCTTTCC GGTGGTCAGC GACAACGTGT GGCCCTGGCC CGAACGC TTG	60
CGAAGGCCCG AAACATTAC TGCTCGATGA GCCGATGGGC GCGCTGGATA AAAAGCTGCG	120
TGACAGGATG CAGCTTGAAG TGGTGGATAT TCTGGAGCGC GTCGGTGTGA CTTGTGTNAT	180
GGTCACCCAC GATCAGGAAG AGGCGATGAC CATGGCGGGG CGCATCGCCA TTATGAATCG	240
TGGGAAATTT GTCCAGATTG GCGAACCGGA AGAGATCTAC GAGCATCCGA CTACCCGCTT	300
ATAGCGCTTG ACGCNACCGT GGGAAATCAA GACCAAANTC AATCTGATTN CCAAAAGCTT	360
CACGGATTN TGCCACGGTG TTAACCGCCG CATCTACCGN GCGGNAGTTA TTCAATTAG	420
NCCCAGTTCT TCAAAAACCG TTCANTTTG AAAGTATTG AAGNCGATTN TGGNTAGTGT	480
TTTTAAAT	488

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGCACGAGCC AACCCAGCTA TGGCCTATGC CAACGAGGTG AAACGTGTGG TCAGCAGTGC	60
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ACAGGAGAAG GGCAGGAAGA TTGCAGCCTT CTTCGCTGAG TCTCTGCCCA GTGTGGGAGG	120
GCAGATCATT CCCCTGCTG GCTACTTCTC CCAAGTGGCA GAGCACATNC GCAAGGCCGG	180
AGGGGTCTTT NTTGCAGATG AGATCCAGGT TGGCTTGCG CGGGTAGGCA AGCACTTCTG	240
GGCCTTCCAG CTCCAGGGAA AAGACTTCGT CCCTGACATC GTCACCATGG GCAAGTCCAT	300
TGGCAACGGC CACCCNTTGC CCTGCNTGGC CGCAACCCAG CCTGTGGCGA GGGCATTNA	360
AGCCACCGGC GTTGAGTAC TTCANCACGG TTGGGGGCA GCCCAGTGTC CTGCGCTGTG	420
GGGCTGGCCG TCCTGAATGT NTTNGGAGGA AGGNGCAGCT TCAGGATCAT GNCACCAATT	480
TAGGCAGTTT CTGA	494

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGCAGANCTG TGGACTGTTT CACCAACAAC CCCTCCNAGG CTAAGCTGCG GCGNGACTCG	60
ACGAATCCNT CCAGGTCGCT GAGAAGGTTG ACCAGGAAGT ACAACGAAGC TGCTAAAGTC	120
CTACCANTGG GAAGATGCTC AANACCTCCT CCTTGGCTGG AGCAGCTGGA ACGAGCAGTT	180
TGAACGGGG TGTGCCCGGC TGGCAAACCT NCACGCANGC GAAGACCAGT ACTGATCTGA	240
GGGTNACCAC GGTGGGCTTT CCNACACTTT CTGAACCTCG GAACGTTNCC TTCCGGTGT	300
CACTGANGGT GGTCGTGAA AGCTCTNTG AACTTCTGAA TTCCCATCCA CTGTGAACGG	360
TTCCCTTGTT AGGAANTTT TNCAGGNAAG NAACCCCTAA AATTTTATGG GAGGACCGTG	420
GG	422

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACGCCTGCNA TTGGTCAGGC TGACCTGGCC TCCCCGTGGGG CCACTCGCTG CCTTAGGTGC	60
CTTCTGCTCT CTGGAACCAAG AGGGACTAGC TGACTTTGC CAAGGAAGCA GTGCCAAGAG	120

GCATGGTCNT GGTNNCCTGC CTGCCCCGG GAGNNCACCT CTGTACACTT CCCTGAANAC	180
CTTCCCAGGT GTGGGTCACT GCCACCTGTG CCCATGGCA CCCCAGAAGC ACCCACTGTG	240
AACCACTGNC AGTTTTCTG CATGGCCAC AGGCAGTGGG CCTGTAANCC TTTCGCAAGG	300
GGTCCCAGGT CCCTTCCAA NNAATTAG CCTTTNTAA NGGTTGGCAA CCAAAG	356

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGACCTACC GAGAAGAAAA TCTTCACCTA CTTCATGGTG GGCGCCTCCG CCGTCTGCAT	60
CGTACTCACC ATCTGTNANN CTCTGCTACC TCATCTGCCA CAGGGTCCTG CGAAGGCCTG	120
CACAAGGACA AGCCTCGAGG GGGTTGCAGC CCCTCGTNCC TCCGCCAGCC GAGCTTCCAC	180
CTGCCGCTGC CACCACAAGC TGGTGGAGGC TGGGGAGGTG GATCCAGACC CAGGCAATAA	240
CAAGCTGCAG GTTCAGCACC CAACCTGACC CCCATCTGAC CACAGGGCAG GGTGGGGCAA	300
CATGCGGGCT GCCATGGGAC ATGCAGGGCG GTNTGGCAAG TGGAGAGGTN CTACAGGGNT	360
GAGTGACCCA TTTGGAGTTC ATAAGTATGC AATTGGTTT TGGCAGTATT TTTGACATG	420
GGACTNGGNT GTTGNCAGGG TTTAGTAACC CCAGGCCATG GCANCCTNAA GGGCATGGTT	480
TTGAAAAAGG ATTAA	495

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCAGAGGGGA AACTTTCTT TTGTCCATCG AGGTGTTCA TAAGTTTTT GGTGTGTTTT	60
CTGGGTCGTC TATGTGTCAT ATGGTTTNAC TTTTCTCTCC TTTTCGTTT TCAGAACATN	120
NTTCTGTCTG TTTTGGATTC ACTGCTTCCA TTTNACAGAA TGTGNACTCT TTGACTCTC	180
AGTCCATCATT GCCATCGGGT ACTCTTGTG CAGTGTAATT TTAATNACAT GCGGTTATTT	240
CCCTAACGAA TGTGCTATTC ACAGTCCATC TTNCAAACTC CATTTCCTA TCCAGCCAGN	300

GTCTACAATT TAGTGCCNT GGCTCCNATT TCGGTCTCC TCCCCGGGC TTTNCCCTGG	360
CTGCGGTGCT GGGCCAAAAG CAGGGGTTT ANT C	394

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGCANAGGAG GGCTGGTGC C GGGANTCCAC GACAGACGAG CAGCTATTCA GGTGTAANCT	60
GTCAGTGGAG AAGTCCACAG TNCTGCAGTC TGANCTGGGA ATCCTGTAAG AGGCTGCAGG	120
AGCTGGAGCC TGAAAATAAA TGGTGCCTGC TTACCATCAT CCTGCTGATG CGGGCACTGG	180
ACCCCTGCT GTATGAGAAA GGNAGACCCT GCAGTACTTC CAGACCCTCA AGGCCGTGGG	240
ACCCCATGCG GGGCAACGTA TCTGGGATGG ACCTGCGCA AAGTTTCCTT TGCTGGGAGG	300
AATAAGCGTG CTTCAAGAAT GGGAGTNATG CCCGAGGTTG CCGTGTNCTT GCACTGGGT	360
TCACAAGGAT CTGAACAGTG GTTCTGCCAT TTGGGAACAA CTTGTTCTTT GGTCAACCAT	420
TTTGATTNG TTNACANATC GGCTTCGNAA CCTNG	455

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGCANAGCAA GAAATGGCAC CAGGAACAAAC ATTAAACCCG GTCATTGGTG ATTCACTNT	60
GGATCCAAAA AAGGTTAAGA CCCTCGTTT CTGCTCCGGC AAACATTCT ACTCCCTGGT	120
GAACAAAGAG AATCTNTGGG GGCCAAGAAG CATGACTTTG CCATCATCCG AGTAGAGGAA	180
CTCTGGCCCC TTCCCGTTGG ATTCTTACA GGAAGAGAAT GAGCAAATAC AAACATGTTA	240
AAGATCATAT TTGGAGTNCA GGAGGAACCT CAGAACATG GGTCCGTGG TCGTTGTTT	300
CTNCCAAGGT TTGAAAAGCA GCTGGNCCTG CAAGCTTCCG TTCTGGTTGG GCCGGNCCCC	360
TTTGNCATG ACCCGNTGTT	380

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGTGACCGG TTCTNCAGCA CCCGGTGCTN GAGNTTNGC AATGTCCCGC ACCGGGACGN	60
TCATCCTGGG GACCTGGTAC ATGGTAGTAA AACCTATTGA AGAGCAATT GCCTAACTGT	120
GGGAGTGAAC TCATCCAAAC TCCATGCCAG TNNNNAGCNT C	161

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCACGAGGG TGCGCTGAGT CGGAGCCAGA GGCGCGGGG ACACCGGGCC ATGCACGNCC	60
CCAACTNAAG CTGCATCTCA AAGCCGAAGA TTCCAGCAGC CCAGGGGATT TCAAAGAGCT	120
CAGACTCAGA GGAACATCTN CGGAGAGACC CCCGAAGCCC TCTCCAGGGC AGTCCTCATC	180
CAGACGNNTCC GCTAGTNCA GACAGGAGCG CGCATGGGCC CCCGNNTCGG	230

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTGGGCCAC CTCACCAAGT GCAGCCATGC NTTCCACCTG CTGTGCCTCC TNGCCATGTA	60
CTGCAACGGC AATAAGGATG GAAGTTGCA GTGTCCCTCC TGCAAAACCA TCTATGGAGA	120
GAAGACGGGG ACCCAGCCCC AGGGAAAGAT GGAGGTATTA CGGTTCCAGA TGTCGCTCCC	180
CGGCCACGAG GACTGCGGGA CCATCCTCAT AGTTACAGC ATTCCCCATG GGCATCCAGG	240
GGCCCTGAGC ACCCCAATCC CGGAAAGCCG TTCACTGCCA GAGGGTTTTC CCCGCCAGTG	300
GTTACCTTTC CAGACAACGG CCAGGGCCGN AAGTTCTTAG NAGCTTCCTG GAAAGTGGGG	360

CNTNGTAAGA GGNGGGTTCA T

381

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGCTTGTGT TTACTTCTGC CATTGCCAAC ATGTTCACCT GTAACCACAC CCCCATACGG	60
AGCTGTGCAG CCCGGATGCT GAATTTAACCA CCTGCTGACA TCACTGCCTG CCACCTGCAG	120
CAGCTCAATT ACTCTCTGGG TCCTGGGATG CTCCCCGTG TGAGGGNACC ATGCCACCT	180
GNCAGCTTTC CTGAGGGCTT CTTCCAATGA GACCTTGAT GGGCTGGGAC TGTCCAGCTG	240
CAGGGGAGGG TGGCCCTCAA TNTGTANGNA CCCCTGTGAA TNTCTNCTGG TGGTTTGCG	299

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCAGAGCAC CATCCTATCC AGCCTAACNT TTAATTGAAA GCAACAAAGC ACCTACACCT	60
TCCAGCTGAA GGNAGTGGAA TNAGTGGCGTC CCACCTGCAC TCAGCTTACG TTGGTGTAC	120
CATCAATGTG CCTGGNACGA GAAATGAACA ACGNACCCTA TATTCACTGN CCCCTTCCTT	180
AACACCTCTT NANAAGCTGC TG	202

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTAAAANTNA TCCAGCTCTT NCTCAGTGAA AGAGGAAAAT CCCTCCATGG NAGAGGTCAA	60
CGCCTCGNTG GCATACAGAC TGGGGACCTT GGACATGCCGG GNNTTTTCC GNAACACCCA	120

AGNGGAANAT ATCGATTCTN CCTCGGGAAA GCCCCATCCA ACANTGGATG GTCCATCTGG	180
GAGTTCCAGT ACCGCCCTNG GGGCCCGGTN ATTNATTCC TGAACAACCA G	231

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGCACGAGGA GAAGTGGCCT TAACTGTNCC AGGTACACAG TGAAATAAG TACAAAAGTA	60
ATGACTAAAA TAGGCCAAGT TGTCCGAGCA CTTTGTACAT AGGGGTATTA TACGACTGCA	120
AATTGTGTGA TGTTAATTG TCACAGANAG AGATACTCGT TTTAACACT TTTAGCCTAA	180
TGTNCTGGAA AATTNCTTAA TGGATTTNA TACTCTATTG GAAACATTTC CATATTGGTG	240
NAAATGCCAC TNCATTCCTT TTNCCTGAGG GGGCAAATCT TGAGTAGGCA ATGGGAAGG	300
AAAGCCTGGG CAACAGCCAC CATTGTCTT GTGGGACCTG ACATGGTTA TTCCACCTNG	360
GAAAAGGAGG AATTGCTTAA ATGGCACATT GGTTACCCTT TAGGTTAAC NCAGGTTTNC	420
ANTTTGTGCT GGAATTNTTT AGG	443

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGCAAGTTG GGNATNCTGA CCCTAAAGTA CCCCATTAAG CATGGGATCG TNACCANTTG	60
GAAGGCATGG AGNAGTTCTG GGAACAAAAC TTTTTAAAAA GNAGTTNGG GTTGGGCC	120
G	121

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCTTTGGGC AGCTTGGAAAG TAACCAANAA TAATGGGCAC TACCGTGAAG ATCCCAACTG	60
GTTTATAAAG AAAGCCCATG AGCATAAAAG GGAATTNANA GAGGGCCAGC TGCAGGNGGG	120
AAAAGCNTGT N	131

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGCANAGGTT TGTTTCCATT CAGTTCCATT CNNGCTTATG TTNGTCAGAG TTAGTATCTG	60
TGGGTTACAA CAAAGAACTC TGATAAACCC AGCAATAATC AATTAAAAGT GCAATAAGAA	120
GAAGCTGATA TACGTTATCC ATCAGAACCA TCAAGTATCT GGGAAATAAAC TTACAAGCAA	180
GCATGGTAGA CCTTTAGGAA GAAAATATA AATCTTGCT GAGGCCATAG GGAAAAAAAC	240
CTGANTGGAA GTGGNNCATA ATATTTCCC TAGTNGGAA ACACTGGGTG GTNTGAAGGT	300
GTTGAATT	308

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCANAGCTA CAACAAACACA TCCTAATGNG CANTAATTNT CCTTGCAATA CTCCTATTCT	60
GCCGGTANGA AAAGCCTCTG GGAACCTTACC GTCTAGTACA AGATCTTCGC CTCATCAACG	120
NGGCAGTCAT CCCTACAGTC CCGGTAGTTC CTAATCCATA CACACTCCTC TCTCGCATCC	180
CCCCAACAG GTCTCACTTC ACTGTTCTGG ACCTTAAAGA TGGNNNTTTC TCTATCCCAC	240
TAGACCCCGC TTGTTAACTT CCTCTTGCT TTCCACATGG GNAGGACCCA GAACACCGGC	300
GTNTTTAAA CAATTCACCT GGGACGGTTC TGNTTACANG GGNTTTAGAG ACAG	354

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCATGCCATA CTATGTTGG CAAAATGTNA NTGGNAAAAC TGTATAATAA ACTTTTCATC	60
TTAAATTGG GAAACTATCA GTAATACAGT AGATAAAAAT AAACAAATAC CNTTGGAGGT	120
AGTCTCAGAT CCTGGNATAC TCTCTCTGAT CTAGTTCTT CCAGCGNATC CATTAGTTG	180
ATTACCATAG GTGTGATTAA AATCCACCAG CTGGNGTCCA GTAACATTGG NTCCACCATG	240
TATGAAACCT CTGAAGGGGA AATNTCCTNG GATTCTTCT GANAAATTAA TTACCA	296

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGCACGAGCG GTCTGGCTTC ACAGGTCAATT TCGCTCCCC CGTTTCAGGT TGATCTCTCT	60
CGCCGTGAAT TATCTATTAA TGACGAAGTG ATCAAACGTGA CCGCNNTCGA ATACACCATT	120
ATGGAAACGT TGATACGCAA TAATGGCAAA GTGGTCAGCA AAGATTGTT AATGCTCCAA	180
CTCTATCCGG ATGCAGGAGCT GCGGGAAAGC CATAACATTG ATGTACTGAT GGGACGTCTG	240
CGCAAAAAAA TTCAGGCACA ATATCCCCAA GAAGTGATTA CCACCGTTCG CGGCCAGGGC	300
TATCTGTTCG AATTGCGCTG ATGGAAAAAT TTACTGNGC TTTTTTCCC CGTTTTCTG	360
TGCGGGTACG TTTNCTGTTG GCAACGGCAA CGTAGTACCN GTGCTTTNN	409

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTAATGCCCT CACCCCTTAA AACCAGAAAG CGCGCACAG TTTTTTAANA GGAGACGACG	60
AGGAAGGGAA AGCTGGAAAT CCAGGTGTAA ATTAATGGTC TTCTGGCTTT CCAGGGNCAG	120

CCCTCCCCTC CTTCCCGGAT CATAAATCTT NAGCATTTNA AAAATAACTG CANNCTNGGT	180
GTGGTGGNTT GT	192

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGCTCCGTN NAGTAACGAG CAGGAAAGAG GTGGATGTCC GAAGAGAAAG ACCTTGTGGA	60
GGAAATCAAA AGGAGAACAG GCCAGCCCCT CTGCCATCTN CTGAACGTGAA ACAAACTATC	120
AAAGGAAAGG AAGTGGGGAC TGGGCACCTTA TTTAAGGTTA AGAACAAACT GCATATGTNC	180
TTANAATTGC TTTGCACCTTT TCCCGTTTTN AGCGGAAGGA CCTGAAGAGT GGTNAGNAAC	240
AGAGGCCCTT GAATTTAAA TTATGGGTTA NTTTNATTGG TTATTAACGT GGCAAAACG	300
GGCCNGTTAC CAACACCTTT TTTCNATTAC AGGGCCCCCG GGGGNTTTAG TNCCCGTCTG	360
TGCTTCCGGG GTTAAAAGGN CCCCGCNTGA NATGGTCCCC TTTTN	405

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGAATGCATA TGCAGGGAGA ATCCAAAAAC CATGCAGGAA GCTCCGAAGT ATGACGATGT	60
CTTTCCAGAA GTGAAATCGC TACTTTATTG AGCAAATAGC ACGTTGCGAG NCAGGCGGGT	120
ATCCAAAAAA GAAATTGTTG CTCGACCCCG GATTGGTTT CGGTAAAAAT CTCTCCATA	180
AACTATTCCAT TACTGGCGCG CCTGGGCTGG AATTGNACC ATTTCAACC TGCCGTTGT	240
TGGTGGGTAT GTCACGGAAA ATCGGTGGTT GGGCCANCTT GCTGAACGTG GGGGCCNTTC	300
CGAGCGNNNTN AGCGGTTNGT TCTGGGCCTG TGCCGGTTTC ATTNGCCG	348

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CNAGTGGAAAT CCCCCGGCCT GCAGGANCAT NATCCCACGC NAAATGCGGT GAAATATTAT	60
CNCNATCGTA ACCCATGCCG TTAAAGANAT GACGATGCCG CANTTTATCG CNATCGGCCA	120
GATCGTTAAC TAATGANNTT AATGANCCCT CCTTTTTGT TTCNAGAAAG TNTAGCCAGA	180
AACCCTCAGG GGGANTTTG GTTATTGGNA AAAAANTGTT TNACCCTGTC CCGGGNGGTT	240
AACCGT	246

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GGAANACCTG TTTGGAAGTA ACAATAAGGA GGAGGACAAG GAGGCAGCAC AGCTGCAGGA	60
AGGAGCGGCT ANNGNAGTAC CGCGAAGNAA GNAAGGCCAA GAAGCCTGC	109

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGAAGACCNC TATTGGNCTA CCGAAAGAAT GGTGTAACCC CATATATAAT TTCNTTTAAG	60
GNTGGTTTAG AAANTGGAAA ANTGTAAACA AATGTGGCAA TTTTTTNGGN TGTATGCACC	120
TGTGNATGCA TA	132

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGAAGACCNC TGGCGCCGTT TTTNGNACAA NAAGGTGCTG CTGTCCTTG GAAAGGCCTT	60
CAAGTGTAAA GAGCCTGGTT GGTTTCCCTT TGTTTCTAA AACCAGGTCC ACCGGTTTG	120
CCTGGNTGAA GCCAGNCTGC TTTTNCNAGC CCAGTNCC TT AACTG	165

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAGNTNAACA TGGNCANNNC CAGCCAGACC NTGGCCACCT TCCTAGNTNN NCTGGCGCAG	60
AAGCTAAAGC CCCTGGGGNA GCAGGAGANT CGCGGTGATT NTGGAGCTNA TTNCNTGCGG	120
AGTGCAGGCC CCGGGGCCTG CCCTTCNACG GCCGCATCCT TGCCTGGAAC ATGCGCTACT	180
ACATGAACCA GGTGGAGGAG ACGCGCTACT GCTTGGACCA NAACCTNCTC AAGGAGTACT	240
TCCCCTTNCA GGTGGTCACG NACGGGCTTC TTGGGATCTA CCAGGAGCTC CTGGGGTTG	300
GCTTCCACCA CGAGGANGGT GCANTNCCTT	330

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGCACGAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANNNN	58
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(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AACANANCTN GAACTCCCAC CCGATCAGAC GCCTCCTAAA NCTAGTGAA TCCCCCGGCC	60
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TGGTTAACG ATGAACGAAT TNACCGAATC GCCTCGTAA ATTTCGCCGT AATATGGCA	120
ACGTTAAGAA ATTGGAGCTT TTCCCCTACN AAGAGCTGGG NAAACANAAA TGGG	174

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGGCGCCGNT TTTNGGACAA CAAGGTGCTG CTGTCCTTG GNAAGGCCTT CAAGTGTAAA	60
GAGCCTGGTT GGT	75

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGCAGAGNCA ATTAATAAAC AAGCTAGATA CCCAGTCTAT TTTCTTTGA GGATATTTTC	60
CTGTAGGTCA TTTTAATTGA TTTGTTTGAC ATGACTACAT TTATAATAAT CTANTATGGT	120
AAACCTAACGC ATCCTACATC TTGTCTTAG CTTATAAAGA ATTTCCCTTT CTTGGAAGCA	180
TTAAGTGACT TCTGGTCCCT TAAAATATTC AAATGTGTTG TTTTGCCAA AATTNCCATA	240
GGCAAAGAAG AATGGAGAAA AGAAATTGTA AAATGGTTCT CGGAGCTTCT TTGGGTTAAA	300
GGGTCTAATG CCAGGGACCA GCATACAAGT TNCGAGTTGG TGCTGTGGGG GGACCCCGGT	360
TTGTGAGTTC CAGAGGGTGT GTTTGNGNAC AGGCCAGTG GAGGCTCACA CCACACNGTT	420
CTGGGTTCCG CTCAGGTNG NGGCCGCCAG TG	452

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCAGAGCAG GTCTCAACTT CCAGCGAGAG AATGANAGCC CTGTGGTGC GGCCANGGT	60
GCCANCCTTG ACCCTGGGTG AAGCAAGAAC GCCGACGNNG CCCTGCAAAA CCTCCGGGTG	120
GGTCATGAAC AGTGCACAGG NTTCCATCAA GCAANTGGTT TCCGGAGCTT GAGGACANTG	180
AATTTGTTN CCGAAATCCT TAAATCTTTA GGCAGAATT TTNAAGTTAA AGACGGGGGA	240
GGAAGGCTTT TNAGGGACCC CTGGGTGTTC TTAAGCATNA AGNTTCGNGT TNTACCCTGA	300
GGTTAACAC GGTCGATCT TAA	323

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GATACGCCCT TTGGCAAAGA ACCTGGNGTN TAGANATGTG GTGTTCGNT CCATAATTNT	60
GGAGATCAA AAAGGAAGAG GCTGTGGCCC TAAAAAAAAT CACGTTTACC TGCCAGCTGC	120
ACCACCTACN TCCAAANCAG CTGGCACGN GCCTTGCCTT GGGAAATTNA AAANACAGCN	180
ATGAATCTTG GCTGGCNTGG ACGTNACGAN GAGCCGATCC TTGTCCTCCC CACCGTGCCA	240
TTATAAACAT GGGCGGNATT TCCNACCAAC TTACAAGGGG CAGGTTCTNG AGGGCACGTG	300
AATTGGNCCA GGNTTCAAAT T	321

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGCAGAGGTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GNAATTNTT TTTTTTTTNN	60
GGGN	64

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCACGNGAA CGGGCTGGGC CGAGCCCGCA CTNTCGCGGN TCCGAGAGGA CNNGCGTCGC	60
ATCGTGCTGC CAGCCATCGA CAANATCAAG TACAGCACGT TTAAGGTGCA GCAGTATGCG	120
AGACGNNGCC CATGGCTACA ACTGGGGCCT CTGGTGCATN TACATNATAT CCCCCGCAGT	180
ACTGGANTGG ACC	193

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCANAGGGA GGAAATGTGT TACAAAGATA TATGTACAAG TGTATTTCATC ATTTTCCTGT	60
TTATAATTAA TAAAATGAAA ATGAGNGGGN ATGTTGGGTT NTANGTTTG N	111

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCAGAGCAA ACTTCAGGGN AAGCCATGCN CATTGGAGCA GAGGTTTACC ACAACCTGAA	60
GNAATGTCAT CAAGGAGAAA TATTTTTTTT TNGGGGTGNG	100

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AACAATTAGC TCCAGGAAAT AACAGTTATT TNATCATAAA ACAGTCCCTT CAAACACACC	60
CCNNCCGTTT GTNT	74

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTACCATTTG TCTGACCTCT NTAAAAAATG TGATCCTACA GAAGTGGAGC TGGNATAATC	60
NGNTAGTTAC TGCTACCCAN AGCAATATCT GTGAATGAAG ACAGTGCTAC AGAGGACCTG	120
GCTACACTTA TNNAACAGAAA CAAGTGCTAC ACAGCTGTGG ANCCCACTCG NGATATGGTG	180
GTGNAGAACC ANAATGGTGG TAAACAGCCT TTAACCCCAG AATGCCTGGC TNATCCTGGA	240
CTGANTTTGA AGTCATTGCT GGACTGCNTA GCGCTTTTC CTTNGAGAGG	290

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

NGTAGNGGNT CAGACCCAAA GNCTATGAAG TTAATGCTAC TCTGAAGTCT CTCAACA	57
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(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGCAGAGGNA GACCCGGTN TNACGGAGTT AACGTACATG ACCTACGTAA GGGAAAGACCT	60
GCGNGTGCTG CAACTGTNAN AAGCGCTGTG GNCNCTGGAA CGTGGTCTTC GTAATCAANA	120
GCTCCAAAAG CATTGGGTAC ACCAACTTNA CACTGGNGAA GAAACTTCGT GAATCAACGT	180
GGTCAACAGG CTGGGTGCCA TCGCTAAAGG ACCCCAAGTC CGNGAACAGG GACGCGTGTG	240
GGCGTGGTGC CAGTACAGCC ACGAGGGCAC CNTTGAGANN CATNCCA	287

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGCANAGCAA CCCCATAGGC GGGATCAGCA AGACGGACCT CAGGGCCTTC GTCCAGTTCT	60
GCATCCAGCG CTTCCAGCTT CCTGCCCTGC AAGCATCCTG TTGGCGCCGG CCACCGCAGA	120
AGCTGGTAGC CCTTGGCTGG ATGGACAGGT GTNCAAACC GACGAGGAAG ATATGGGGAT	180
GACATATGCG GAGTCTCGG TCTATGGAA ACTCAGGAAG GTGGCCAAGA TGGGCCCTA	240
CAGCATGTTA CTGCAAACTC CTCGGCATGT GGGAGACACA TCTGNCACCC CGAGACAGGT	300
CGCTGACAAA TGAAGGGTT TTTTTTCCAA GTACTCCATG AACAGACACA NGATGACCAC	360
GTTCACAAACC GNGTTACCAAG TCGAGGAACt ACAGCCCTGA GGNCANCAGT TTNATTG	418

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGCAGAGCTG ACTGAGTGGG ATTGAAGGGG AGGTAGGGTG GGTGTGCCCT ATGAATGTAG	60
GGCCTGCTGC ACCCTGGGGA GGGGACCCGG ATGCAGTNNA TGCCCAAGTT CCAGCGTTCA	120
GAATGCCTGG GAAGCCCTGA GAACTCCCTG NACCCAGCAG GACGCCCAT CCTTGGTTT	180
NNGGGGTAG A	191

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGCANAGGTA TCATCAAGAG CCACCAGGGC CTGGACCGNC AGTAGCTGAG CTTTGGANCC	60
CGGTCCCTCT ACTACAAGCT GCGTGCCGCT GAAGCAGTAC ACACCCANGG NCAAGTACCA	120

TGGCAACGTG ATGCTACTGC GCGCCAAGAA CGGGTGGCGN CTACGGCAGG GNNCCTGGC	180
GCGGACTACA ACCTTNCCA GGTATGCAAC GGGAAAGTAT NCGT	224

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGCANAGCGG GATCCCGGGG ACCTCTGGCG ATCCACAGAT GCTGGAGACT TAGATCTACT	60
TGGAAGAACCC ACGTTTCTGG CTCTTCTCAG GCACGGGAGA CCTACTAACAA GAACGGGACT	120
TGCTCCGGCT CCGGCTCCTG CTCCTGCTTC TTGACCGGCT GTANGATTG CGACTACGGG	180
AACGGGNATC GGCTACGAGA CCTGAGAGGA ACTTCTGGTC CGGGATCGAG ACCTGNCTTC	240
TTGNACCTAC TGTGNNCTTT TGCTGCCTT	269

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CGNGCACAGG ACCAGGNCT TGGTGAGAAA TTCCCAACCT GGGCNAACAA CCAAACCAGA	60
ATTAGAACTN CTGGGGCACA ACCCGAGGAG AAGANGAACAC ACCTCCAGCT TTACGATCGG	120
TTTAAGAGGA CTCATCAATC TTGGCAACAC GTGCTTTATG AACTGCATTG TCCAGGCCCT	180
CACCCACACG NCGNTACTGA GAGATTCTT TCTCTCTGAC AGGCACCGGT GTGAGATGCC	240
GAGTCCCGAG TTGTTGTCTG GTTCTGTGAG ATGTCGTCGC TGTTTCGGG GAGTTGTTAT	300
TCTNGGAAAC CCGTNTTCTT GATGTGGCCC TATAAGGTNA CTGGCAACTG GTGGTGGGAT	360
ACANGGCCNG GCATTTT	377

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGCANAGGNA	AAAAAAGGAA	ACACCGCAAA	CGGTCCGGG	ATCGAAAAGAA	AAAGTCTGAT	60
GCCAATGCAA	GTTACTTAAG	AGCAGCTCGA	GCTGGTACAC	CTTGAAAAGG	CCCTCGACTA	120
CATAAAAAAT	GGAGTTGACA	TCAACATTG	CAATCAGAAT	GGGTTGAACG	CTCTCCACCT	180
TGCTTCCAAA	GAAGGCCATG	TAGAGGTTGT	TTCTGAGCTG	CTGCAGAGAG	AAGCCAATGT	240
GGATGCAGCT	ACAAAGAAAG	GAAACACAGC	ATTGCACATT	CGNATCTTG	GCTGGGCAAG	300
CAGAGGTNGG	TAAAGTCTTT	GNTTACAATG	GGGGCCATGT	TCATGGANCA	TTTN	354

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AAAGCTGGCA	TCCCTNACCT	CCTGATCTGA	AAAGAAAAGC	TTTCAGGNAT	TCATCACTAA	60
GCATTTNGTC	CACTGTNTGT	TTGTCTTAAG	ATTGCCTTTA	TCAGATTAAG	GAATGTNCAT	120
TTNATTCCCTA	GTGCGCGAG	AATTTTATT	GTCATAGGAT	GTGAAATTG	GCCACATCTT	180
TTTCTGCATC	TGTTGGGAGT	AATCAAATTA	TTTAGCTTA	TAATCNCTTA	ATATGGTGGT	240
TTACATTNGG	TTTATAAAN	GTAAANCCAA	ACAGGGTGGT	CTGGTATATT	GCCANGTAA	300
						300

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GGCANACCCG	GATTGAATAG	TNTAACCAAG	CTTCNTGGC	TTGCTGAAC	GCATGAGGCT	60
CTNACGCAGT	TGTTAACCGG	CCCCTCCACC	AGCACCTTCT	GCTCCTNATA	GTAGTTCAAGC	120
AGGTGGTTCC	AAAGCGGCTG	CTTGAATAG	TGCCCTTCGG	GTTGCCACAA	ATGAATGACG	180
CCATACCTTG	CTCTGGTCAG	GGCCACGTTN	AGACGCCTGG	GGTCATTAA	AAAGCCAATG	240

CCTTGGTGCT CGTTGGCCCCG NACACAGGGN CAGGNTGNTG AAGTCCTTT GG 292

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCTCTCCA GTGTAAACTC TTTAATGTCT TGTAAGGCAC GNAAGTCGAC TAAATACCTT	60
GCCACAGTNA CTGCATTTGT AAGGTTCTC TCCAGTATGT ATTCTCTAAT GTNGTGCAAG	120
GTGTGAATTG TAACTNAAGA CTTTGCCACA TTCATTACAT TTGTNTTNNT TTGTTTGT	180
TTTTGTTTTT NTTTTT	197

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GACACGAGCT NGAGCCCACC CTGGAGGGAG GAAGAGGTNG TCACCCCTGA CTTCCAGGAG	60
CCTCNGGTGT CCAGTGGGT AAGAAGAAC CCTGNATTNTT GGTAGGTAGA AGCANGAGTC	120
TCAACANACC CTNCAGCCCT GACCCCTGGG GGANCCCATG ACTGGACCT	169

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CTTCCTGCAC AGGAAGGACG TCCTCGGTNN CTCGNAGGAG GAGGNCATGG GGCTCCNNGA	60
GGTCAGCGTT TCGNACATCA AGCCNCCAGC CCCANAGCTG GGCCCCATGC NANANGGCCT	120
NNGCCCTCAG NAGGTGGTCC GGAGGCATAT CCTGGGCTCC ATCGTGCAGA GCGAAGNCAG	180
CTACGTGGAG TCTCTNAAGN GGATACTCCA NGNCTACCGC AACCCCCCTAA T	231

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

NGTTTGAATT GANCCCTCAC TAAAGGGGCA AAAGCTGGAG CTCGCGGCC CAGAGCGAAG	60
NTGCGGACCG CGCCGCGACC TTGGNTTGAG CGCATTNGTT TGCTGGAACA CGCCAACCGT	120
CAGGCGAGTA ACCTGGCCTA TGGTGACCAAG CGCCGTCTTG AGATTGCCCG CTGCATGGTG	180
ACGCAGCCGG AGATTTAAT GCTCGACGAA CCTGCGGCAG GTCTTAACCC GAAAGAGACG	240
AAAGAGCTGG ATGAGCTGAT TGCCGAACTN CGCAATCATC ACAACACCCAC TATCTTGTG	300
ATTGAACACG ATATGAAGCT GGTGATNGGA ATTTCGGACC GAATTTACGT GGTCAATCAG	360
GGNACGCCGC TGGCAAACGG TACGCCGGAG CAGATCCGTG AATAACCCGG ACGTGATCCG	420
TGCCTATTAA GGTGAGGCAT TAANATGNGA AAAANTNCAT GTTTGTCCCTT TGGACAAAGT	480
CAGGCGTCCA CTTANGGTAN ANTNCCAAGG CGGTTGCATG AGGGTGAGCC TTCATATTCA	540
ATTCAAGGGC GNGATTAA	558

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGCACGAGGG AGCNCAAGCA GGATTCTTCC CGAGTCCCTG GCATCCTCAG AAGCTTCAAC	60
TCTGGAGGCA ATGGGTCGAA AGGGAGAAGA TGACTGCAGT NCCTGGAAGA AACAGACCAC	120
CAACATCCGG AAAACCTTCA TTTTATGGA AGTNCTGGGA TCAGGAGCTT TCTCAGAAGT	180
TTTCCTGGTG AAGCAAAGAC TGACTGGAA GCTCTTGCT CTGAAGTGCA TCAAGAACG	240
ACCTGCCTTC CGGGACAGCA GCCTGGAGAA TGAGAATTNC TGTGTTGAAA AAGTTCAAG	300
CATGAAAACA TTGTGAACCC TGGGAGGACA TCTNTGAGAA GCACCACCCA CTAATAACCT	360
GGTCATTNC AGCTTGTNT CTGNGTGGGG NAGCTTTG AACCGNNNTTC CTGGGAGCGG	420
GGTGTCTNCA CAGAGNAAGG ATTCCCAGTT TTTGTCANTN CCAGTAGGTT TTTGTCGGGC	480

AGTGNAATA CCTACATGGG GGATTGGGAT GTCC 514

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AGCAGGTATG GTGTTCCAGC AGTTTACCT CTNCCGCAT CTGNACAGCG CTGGNAAAC 60
GTCATGTTG GNCCGCTACG GTGTCGTNGC GCGAACAAAG AAGAGGCGGA AAAACTGGCA 120
CGTGAGCTGC TGGCGAAAGT CGGTCTNGCA GAACGTGCAC ATCACTACCC NTCCGAACCT 180
TCTGGTGGTC AACAGNAACG TGTGGCGATT NNCCCGCGCG TGGA 224

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGAACAAAAG CNTNAGCTCG TGCCGCCGGC AGGTCGACAC TAGTGGATCC AAAGAATTG 60
NGCANAGTCA CAGCTGATTC CTGGGNAGAG GCTGAGAGGC ACTCCTGGNA TCTCTGGAGA 120
GNGGCGTCTC CCAGCTGT 138

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGTAGNTN GTCAGANAGG TAGCGAGGAA CAAGAACGGA AATTAGTTGC CGTTCATTTA 60
ATCGCGGCAA ACCTGGCAGN GCATGNTTCA CATGGTATTT GGANCATCCC AAGNTATGTA 120
CGN 123

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GNGTAGCNNG GAAGNCACAG CGCATCTCCC CGCTGTAGGN TTCCTCCAC AGAACCGT	60
TCGGACCTTC AAAGCGTCTG GTGGAGATGC TGTTGCCGCT GCTGCTGCTG CTAACCCATG	120
TGCCTGGGCC GTTGNAGNTC AAGAAGGCC CNGGGCGTNN TCCCT	165

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AACCCTNCAC TGAAAGGGCA NCAAAAGCTG GGGCNCGGGC GCNCTGCAGG TTCTGTACACT	60
AGTGGATCCA AAGAATTCTGG CACAGTTGTG GTTTNTCTCA NCGCCTNGGT AGCCGGTAAC	120
AAACGNGGGT TCCCNGNGAT TGGACCGACG CAGCCANGCC NCTGTGGACT TGTTATCAA	180
AGAAAAGCTAA CTGCTAGATC TTTATCGAGT TAAGAGTGTG GATCTGCATC CTACAGAGCC	240
ATGGGATGTT GGCAAGTCTT NNACANNGGN	270

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGCCCNGGGA TGTGCCACTG AGCCTCGGGCC CCATCGTGGG GAGCTNTNCC CATCCNGCCT	60
GTAACCCACC TCTGGNCCCC ATCCATAGAT GATAGGGACC TCTCAACTNT AGG	113

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TGNCTTNGGC TTTGTCCAGC ATNAAAAGGC AGAGCGAACG TTTTCAGTC AGGCTGTTTC	60
CCNCCAGGGC AAGTGGGACA GGGCGAGTNC TGACGTCTGC AGGCATGGTG TGCATTTAGG	120
GGTGGGCGGC ACCGAGGGGG CATCATTGG CATAGGCGGG CCCGGGGGTC ACTGGGCTAG	180
ATGACTGGCT GGTTGCTGGG GGCAGGTGTC ACAGCCTTG CTGNGCACCC TTTAAGTNGA	240
GGACAGAACCA TTGTTGGGAG GAGTCCAGGC ATAAAGTNAC ATAAACAGCG NC GGNGAATG	300
GGACCAGCGC ACCTTNAGAG GTGGATTCA TAGCCTTNAG TCAACTGGGG T	351

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTGGNACACT TTCCACGGCC TCTTCAAGTC CACGCTGGTN TGCCCCGATT GTGGCAATGT	60
ATCTNTNACC TTCGACCCCT TCTGCTACCT CAGTGGTCCA CTGNCTATNA GCCACAAGAG	120
GGNCTTGGAG GTCTTCTTA TCCCCATGGA TCCGNGNCGC AAGNCAGAGC AGCACTGGGT	180
CGTGGTTCCC CAAGAAAGGC AAGATCTTCG GGTCTAATGT GTGGCTCTGN ACAAACACAC	240
GGGGNAT	247

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGGCAGGTGT CCAAATGGGC AATNCCTGCT GGGAAAGCNCT ATTGNTTGGG AACATGGGTT	60
TNACCCCTGNT GGGCAGATGC CAGTGAACAA GACCATTGGT GGAGGGGACG ACTCCTTCAC	120
CACCTTCTTC CTGTNAAANT GGTGCTGGAA AANACGTACC CCGGGCAGTT TTTGTGAGNT	180
CTGGAGCCTA CGGTCATTGA ATGAGAATCC GAAATGNGCC CANACCGACA GTCCTTNCCA	240

NCCAGAGCAG CTCC

254

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGCACGAGGT GGCGTGATGN CTCCCCGGGG CACGGTGGGG TGAAGGATGG CGAGCCGGAC	60
ATACCATTNT TGGATGTATT TTTTTTAAAA CAGCAATAAT TAGCCATTAA AAAGGGAGGGA	120
TGTACCTGTN TGTGTNCATG TCCACGTNTT TGAGCGTGTG TNTGTGTGTN CAAGTGGGTT	180
CTTGGATATG TGTAGTGTGA GCATGTGTGC ATGTNTGAGC CTGTGCACGT GCATGTTGTA	240
GGTGCATAAG CATGTACACG CGTGACATGC ATGTCCGTGT ACACGTNTAT AGGTGTACAT	300
GTNCATGAGT TGTGTACATG CGTGACACGT GTATAGGATG TACGTGTGTN TNCGCATGTG	360
TGCGNGTAAC ATGTNTTGT GNTCTGGGG TATGCATAAG CCATACACGT G	411

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GGGCACGNGC AGAACGTCAG GTCANTAAA TGAAAAGCCC TTACCTGAAG GTTGGGAAAT	60
GAGATTCAACA GTGGATGGAA TTCCATATTG TGTGGNCCAC AATAGAAGAA CTACCACCTA	120
TATAGATCCC CGNACAGGAA AATCTGCCCT AGNCAATGGA CCTCAGATAG CCTATGTTCG	180
GGACTTCAAN GCAAAGGTT AGTATTCCG GTTCTGGTGT CAGCAACTGG CCATNCCACA	240
GCACATTNAN GATTACAGTG NCAAGAAAAA CATTGTTT	278

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGGGGCAGGA CCAAAGGCAA GATCCATGCC AACGCTGCTG ACCAACCCCC AAAACCAAGC	60
TGGCTTTGGG TCTGTGTCTG GTGCCACTGG GCAATGTGGC CTAGATGGAA GGGTGAAGGG	120
GTCCTTCACTCT CAGTGTTCCTT CCTGTGTTCT TCCTCCTTCC ATCTTATCTC TATCTCTGGG	180
CTGGTTTGTN AGCTGAAAGA GTTCACACAT ACCTGGGTG GGCCTCTGTC TCCTCGACAG	240
AGTGGGACTG AGGAGCGAGG CCTGAAGCAT TACTGGTTCA CATCCTGGCC CGGACCAGAA	300
GACCCCAGAC CGGGCCCCCCC CACTCCTGTA CCTGGTGCAG GAGGTTNGAG GAGGCAGCCC	360
AGCAGGAGGG GNCCCACNT TGCCCCCATT CATCGTCCAC TGGCAGGTGG GGTNCTCCCA	420
GCCAGCCATG GN	432

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTGNCAAGGTN CGACACTAGT GGATCCAAAG AATTGGCAN AGCTGATNTG ATGCGTCACA	60
TGNTTATGGC CAACCCCCAG ATGCAGCAGT TGATGGAGCG GAACCCCTGNG ATCAGCCACA	120
TGNTCAATAA CCCTGAACTC ATGAGGCAGA CAATGGAGCT TGCTCGGGAA TCCAGCCATG	180
GATGCAAGAG AATGNTGCAG AACCAGGACC GGGNCCTGAG CAACCTTNTN GAGCATCGCT	240
GGGGGGTATA ATGCCCTCNG CCGTATGTAC ACGGGACATN CAGGAGCCCA TGTTTCAGTG	300
CTGCCCCGGGG AACAGTTTG GCAACANTCC NTNCT	335

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ACCTTCTTTA AATCCGTCAA TAGCCTGCCA GCCAGTAAGC TGTGCCAGTT TGTCAACAAT	60
CGCAGGCCGG GTACNGGNTG NATATAGACG ATTTTTTTC CCGGCGTGGC TTTCAGCTCA	120
AGCGGGGCCG CCCCAGCCAC CCGTTCCCTTC CTCATATCGA CTTTACCTAC ATTACCACTA	180

TTTCAATGCT GGTTTCGCG GTGGCGGAG CAGNAGNAAG ATTTCTCCCT ACGTAATCA-	240
AACCGCGAAC CCAGGAAAAG AATTCCAAA AGGGATGTTA TGCCTGGCGG TGGATGGTTG	300
CGGTTTGTGN CCATTCTGGG CTCGCTGGCG ATGGGGATG GATGTTTGA TTGNGTAAT	360
ATCCCAGATG GACTTTAATG GACCCAAGGT CANTTATTAA CGGCCTTCC ANAAGTTNGG	420
GNNG	424

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

NNNAGNGCCT NCAGGTCGAC ACTAGTGGAT CCAAAGAATT CGGCAGAGAA AAAAACAAAG	60
CCATTGACAA GTTACAGATT TCCAGGAAGA AGGCAAAAGA AAAAGGAGCT TAGACAGGGA	120
AGGAAGAGTC CCCTCTATCC TTAAGTTCTC CCATGTCCGT TGTAAAAGGG CTCCACAGCT	180
CCACAGAAGA AGAGGGNAGG AAGGACAAGC GCTGGTCAAG GTTATGCAAT CCCAACCTGC	240
CATCTTCACT GCACCATTAA GCTGGNTATT CTGAAATATG CTTCTTCTC GACTTCCGG	300
CANATTAA ATTNAACATT AGAATCCAAC CGGTCGACCT GNTNGTCATT G	351

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GGCACGAGGA ACTGTGGATC TCCTACAATT TTATTGAGAA GTTGAAAGGG ATCCACATAA	60
TGAAGAAATT GAAGATTCTC TACATGTCTA ATAACCTGGT AAAAGACTGG GCTGAGTTG	120
TGAAGCTGGC AGAACTGNCA TGCCTCGAAG ACCTGGTGT TGTAGGCAAT CCCTTGGAAAG	180
AGAAACATTC TGCTGAGAAT AACTGGATTG AAGAAGCAAC CAAGAGAGTG CCCAAACTGA	240
AAAAGCTGGA TGGTACTCCA GTAATTAAAG GGGATGAGGA AGAAGACAAC TAATGCCACG	300
CTTCCACTG TGTGTTAACT TATTGAAAT GTCCNTAGGA NCATTAGATA ATTTTATGTG	360
ATTGTNNNTT TTAAGATTCT GTATGGGGCA AAGTTTCNTA AGTTAAACCG TTCANNNCNTC	420

NCCANCTTT TTTCCCTTA ACCTATTCCG TGNTTNCCC CCAAACGTGGT ANGCCANCC	480
TNTATATCCC TTCCCCNTTT TAGGAACCCN CAATTTTC	518

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCGNAGNGN CTNCAGGTG ACAGCGCTTC CTGTCCACGA ATCATATCCG CTATTTCTC	60
GCCAATCATA ATTGTGCGTGG CGTTCAAATT CCCGGTGATA ATCTGCGGCT TAATCGACGC	120
ATCCACCACA CGCATGCCTT CTAACCCGTG TACGCCGCCT TCGCCGTCAA CCACGGACAT	180
CTCGTCGTAACCCATTGC AGGTACCGCA CGGATGGAA GGCGGTTTCG GCGTGGTTAC	240
GCACGAACTC ATCGAGCTGT TCATCCGTCT GGCATTCGAC ACCGGGGCTG ATTCGCGGC	300
AACGATACTN ATCCAGCGCG GGTTGATGCA TGATNTCGCG GGTGATGCGA ATTGCGTCGC	360
GGGAACTCCT GCCAGTGCCT GCTCGTGCAG CATGTGNTTG AACAGAATN CGCCGGATGG	420
TAGTGCGGGT AGCGGGGTTT NATGCCGNAC NGG	453

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGGCNAGCT NCACTGANGC TACCAAGGAGA TCTCCANGCG AAACTCAGCC TCCTCCCAAG	60
CTCCCTNTGG GATCCTAGCC ACAAGCTCTC CAACAATTAC TATTGCACTC GAGAATGCC	120
GCCGGGAAT CTNAGCCCN TTGCCATCAT GCATNTGCGT TCNACAGAAG NNGCTGGTGT	180
GCAGGCAAGA CAGCAGAGAG CTCTGCTGTG AGCTGACCAC TGAGCNGGNA GGCGNTGCNT	240
CCANNTCTT NTATTAAAGA GNTTGGGCT TNNCTTCGGG CCACCTTAN CTGTTTACAC	300
TGCAANCTT AGGGNCACCG GATGANNTNG CCNCCTTGG GATTTCNAC CAGGGGGTT	360
TTGGACNCAN TTTTNTGGNC AACTAGGGGG GNTTGGGTTT CNTTTGGTT TTTTTTGNA	420
AATTAAAAN AAGGGGGNGT TTTTAAAAAA AAA	453

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTTTTTCNCGC GGNCGGTGGC GCGGCAACCG CCAGANGATC CAGAAGAAAA GCAGATNGTT	60
GGCGAAGATG GAAATCGCCA GGCCAATCAN TCGCCACGTC GTTTCAGCC ACTCANTGCT	120
GTTCAGGTGC AGGGCGCTAA TAATCATTG CTGCCCGAA CGGCAACCG AGGTGATCGA	180
AAGCTTCACA ATCAGCGCAA TCAACAAACC AATCAGCGAA ATAAAATCTC GCAGATATT	240
TACCCAGAAC TTCTCCTGAT CTTGCCGCGA GCNTTCCCAG ACATCGCGCG NACTGGGCCA	300
CGATTCGTTT CACGCAGGTT AACCCATCCA NTTGATGCCG GNANTAAAGT GCCACCGCCA	360
GTCCGACAAG CCCTACAGTC GTTACGCTGC TGGNACGGTG GTGTTGNNGG TGTTTTTNCA	420
ACGTGGTGGC TNNGTGGG TNCNTGNNGT TTTGCAGAA TTTTTTCGNA GATTNTCCNG	480
TAGGCAACAT GGNTGGGAG GNCCAGCAAC AAGGCCCNNG NGGGCAAANG ACANCNTCAA	540
AATGGTNT	548

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CCATCAGAGA GGCTGGCTCC AGCATCTTAC GCATGTCCAC ATTGTGGTCA GTTGCAAGA	60
AGTCACCCGT GATATGTGGC AAAACAGCCG GACTCCGAC ATAAAGTGCT GGAAGGAAGA	120
CTGTGAGGGA CACAGTTGTA AAGGTTCTCG AATTGTATCT GTCTGATCAG AGAAACAATT	180
TAATGTCCA GATCAAAGTC GAGAGGCAGG CTCTGGAAC TGGGCTGTGA GCAGCCAGAG	240
AAAGGCGGCA GAACCAGTTT CTTCAAGGGCA GGTCTCTTT ATCTGCTTGT CTGGATTGCC	300
TAGTGGACAC TCCATTGGCT CCCAGAGGCC TTCCCTGGTNC ATNTCNTCCC TCTGGCTGGG	360
TCCTTGATCT TTGCAGATGG CTGCGTCCCT GGGGCCAGGA GCACCAATGT GTGCCGNTGC	420
TGGNCAGGTA NGGNGGTATN CNAGGTNATG TTNTTCCAGG TTCACCNGTG CTTGGTGTG	480

CGGTTTATTG AGTGAANTCN GT 502

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGCACGAGCC AAACACTCCA GAGACCGACG AGTCCCTGNT CGACCCCCAAC ATCTTGTCTC	60
TCAACATCCT CTCTTCGGGA TACATCCACC CAGCCCAAGA TGACCGGACC TTTTACCAAT	120
TTGAGGCTGC GTGGGACAGC TCCATGCACA ACTCTCTCCT GCTGAACCGG GTCACCCCTT	180
ATCGAGAGAA AATCTACATG AACACTCTCC GCTTATTATC GAGATGGAGA ACTGCACCCA	240
GCCGGCTGTT GTCACCAAGG AACTTCTGGC ATGGTCTTCT ATTCCCGTGA ATGCCAAGCT	300
GGCCAGCCTN CGNGGCTNCC ATNCCGCAAC CTNTTTGGN CAGTGGGGAG GCCTTTCGGG	360
CCTNCAGAGA GTGAACCTGT GNANTGGTGT GTTANNAGNT TCAGCNTGTG GCCACGTGGC	420
TGANGCGGGN CAGCCCAGGG NTGCAGCGNC GGNGCCGNAG NGTCNGGGA CACATTGTGG	480
GCTNTGTTCC GGGCGAGGAG AACTGGCAGN TG	512

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGCANGAGCG AAATACACAG AAATGGACTA CGCCCGACCT GGTAACAAAG CAGCTTCAC	60
TGTAAGCCTG GATCCAGGGC CCCTGGAGCA GTTCCNCAN TCCATGGAGC CACAGCTCAG	120
GCAGCTGGGC CTGCCAACCG CCCTCAAGAG AGGTGTGGTG ACTCTGCCTG TCTGACTACG	180
AAGGTGTGCA AGGNGGCGA TGTGCTGACC CCAGAGCAGG CTCGNNTCCT GAAGCTTTT	240
GGGTATGAGA ATGGCTGAAT TCAAGGTGAC CATCAAATAC ATGTGGGATT CACAGTTCGG	300
GAAGGTTTCC AGCAGATGGG NAGACGGATT TGNCCAAAGA AGCGCATTAA AAGTCCACA	360
GAAGNGTTCA GATTCCAGAA GGTTGNNTGA TTGAAAAGGG NNNTCGGGAC TTAAGGTNTT	420
CCTGGGAAGT TTTTGGGTTT TCATTGGGCC CTTCAGGATT TTTTCCGCC CTTTGGNGAG	480

GGCAGTTTT TATTNTTCT TAGNAA 506

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GGTCAACATG GNGCCGACC AGTACCANAT GGGGAGCACC AAGGTNTTT TCAAGAACCC 60
ANAGTCGCTT TTTCCCTCTG GTAGGTAGNT GCGAGAAGCA AAAAGTTCCG ATGGGTTTT 120
GCCCGTAAAC CCATNCCCAG GAAGGTTCTN GTCTGCGGN CACGTTGGGT CTGTTNCC 178

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGTGACCAT GTNTGGCCTG GGNTGTAAGA AGTACGTGGN GGCCAACATC TCCCATAAGT 60
AACGCACAAAC TGTNAAATAT ACAATNAAGA CTCTAGCCAG CTGTNCTGAG ACCGTAATCT 120
TNATGCTGCT TGGNATCTNA GCCGTGGACT CTTCTAAGTG GGCTGGGNT TCTGGGCTGG 180
TGCTGGGCAC CCTCATCTTC ATCCTGTNCT TCCGAGCCCT CGGTATTGCT GGCACCCCTCT 240
GCTTCCCAC TCTNCCTTCC TGTCCCGCCC CTCCCTGCAG CTCATCTCCC TATGTGAAGT 300
CCACATCTT GTNAATTCCCT AAAGCCTCCT CTTGTTGCTC ACCTGTCCA GCCCTGTAAA 360
GACCTCAGCC CAGATAATTG GGTCCCCATCG GGTCCCAAGT CCTTCAA 407

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 423 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGCAGAGCTT NGTGGGAGCC TCGAGCCTTC ATCATGCAGT GTATTTNTTT CTGTNGTAAT 60

CCAGCTGATC CATTGATCAG TGGGGTTGGG GACGCTTCTN TNCTGCTCAT TTATTGCTGT	120
GTACAAACCA CCTCTAACGTG AAGGGCTTTA AAACAAGATC GTTCATTCT TTTGCACATG	180
GGCATTGGGG TANCTGGCG CACTACGGCA CTTCTTACCT GGGGCTCAT CAGTNAGAT	240
GGGGCCAGGT TGGGTTAGCC CCAAGGCTTC TGGCATTGGN CTAAGAAGGC CTTCAGAACAA	300
ATGAGGGCTT TGGGCGGCTG GGGGCTCCCC ACCAACAAACC CTTNCACCTT CGTGGGGCCT	360
TCCAGGTTAG CCTGTTCCAC CTGNNCAGA ACACACACAN CCAGTCCCAC AGGTTCANCC	420
CTT	423

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGCAGAGGNC AAGATGGCCA CTGTNATCCC TGNNCCCTG AGCCTAGGCG AGGANTTCTA	60
CCCGCAGGCCA TCGAGCACTG CCGCAGTTAC AACGNGCGCC TGTNNCGTAG CGCAGCCTGN	120
NAACTGCCCT TCCTCGACTC GCAGACCGGC GTGGCCAGA ACAACTGCTA CATCTGGATG	180
GAGAAGACCC ACCGCGGGCC GGGTTTNGCC CCGGGNACAG ATTTACACGT ACCCCGCCCCG	240
CTGTTGGAGG AAGAAACGGA GNCTAACAT CCTGGAGGAC CCCAGACTTC AGGCCCTGCG	300
AAGTTACAAG ATCGACTGTG AAAGCACCCC TGGAAGAAGG AGGGTNGCCT TCCGGNAAGG	360
GCCGGTTNCT TCGAGGGTTT TATTGTTNTG CCANACTACG GGGGGAGAAA GAAAGGTTT	419

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AGTGGTATCC AAAGAATTNG GCANAGGNCG GAAGATCTNA AGACACAAAG GCCCAGTCCT	60
ATGGGAGAGG GAGCTGCAGG GNCGGGAGC TGGGACATCC CANGNTCAT GAAGTGGGGG	120
NGCAGCCCCC ACGCCTGGNA AGCTGAGGGA AGGGCTCATC TCCCCTNTAT GGGGGNCAG	180
GAAGGGANTA CCTGNCCCT GACTTNGTTG GGATTGGAA CTNAACCCTG GGNGGCCCT	240

CTGAGAGCCC ACCAGCCACA GGNCANTGAA TGCCAACAAA GAGCCCGTTG CTGGAAAGGT	300
CTGTAGCCTG NGACTCAGTG GNGCTGCCTC CTGN	334

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGCANAGGGN GAGGGCAGAG GAGGAGAGTC GCAGGGCGGCC GCTTGGGCCG ACTTNCCGGG	60
TCACCTTGTC CCGGAGGAGN AAATGGCTTC CCTGAGGCAA GTGTACCTAC ATTCCCAGCC	120
CACCAGCCTG ACAGCCCAGCC AGGGAAGAGA GTACCATGGA TGGCATCATT GGAACAGAAC	180
AGCATGCTGG TGCACAGTGA AAATCACTGA TGCTGGCAAG AGGAATGGTT TAATTGAACA	240
CCAGAAACTT GATGGCCGAG AGCAGAGATG GTCTGGTGTC TGTTTACCCA GCGCCCCAGT	300
ACCAGAGCCA CCGGGTNGGG GGCCAGCACA GTGNCGGNCA GTCTGGNACA GCAGCAGGAG	360
TTAACCCNTT TGTCAGCAGT TGGTT	385

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TGGCNNAGGA CCAGCCATCG GAGGTGACTG ANAGATATAA TTTGGGACAG GTCATCAAGA	60
CTGAGGAGTT TTGTAAAATC TTCCGGGCCA AGGACAAGAC GACAGGCAAG CTGCACACCT	120
NCAAGAAGTT CCAGAACCGG GACGGCCGCA AGTGTGGAA AGCTGCCAAG AACGAGATTA	180
GGTATCCTCA AGATGGTGAA GCATCCCAAC ATCCTACAGC TGGTGGATGT NTTNTGAAC	240
CCGCAAGAGT TACTTTAATN CTTCTGGGA GCTGCCACG GGGAGGGAGG TGTTTNACTG	300
GNATCCTGGG ACCAGGG	317

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCGCCTGCAG GTCGACACTA GTGGATCCAA AGAATTCTGC ACNAGGTNTT NTTGGTGTG	60
GGNNNGCTGGT CTGGGGACAG GTCATTGCCA CCATCCCCAC CAGCCAGCTC AAGTGCCTGT	120
NGGAAGCCGG GCACGGGCCN GGNAAGGGAC GAGATGACCG ACGTAGGGAG CTGGCCGAAG	180
GAGGTAAGAG AATCGACCAT GTCGAGCGGG AACTCCGCAG GGNCCAGA TCCTCTGGTT	240
CCGGGGCCTG AACCGNATTG AAACGCAGCC TGGGCCTCTN CCCACCACTT CCCCAGAAC	300
GGCGCTCGTC TNAGGNCCTG GGAAGGCTGC CTTTCCGGTT CGTGGGGTA CGGGGNTGTT	360
CCCNNGCAATG GGTTNCCTGG TCT	383

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACCTGCGCGG GGNCAATCCCG AATNCNTTN AGCACATCTN CACCCACATC TCCCGCTCCC	60
AGAACCAACA GTACCTGGTC CGGGCCTCCT ATTTGGAGAT CTACCAGGAA GAGATTCGAG	120
AACCTNCNCT CCAAGGAGCC GGGNCAAGAG NGCTAGAGCT GGAANGAGAA ACCCCGAGAA	180
CTGGCGTCTT ACATGCAAGG GACCTCTTCC TGCCTTGTT CACCAAGNAA TGNG	234

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAACATGNCG AGGCCATCGT AAGCNGGAAG CAGGAGGTGC TGCAGGNTTG GAAANAGCTG	60
CTGTAACCTG TNAAGGTTGC CCGCTTGCTT GTTAAGCTCC ACAGCCGNCG CCCTGGCCTT	120
CCACAGCCAA GTCCGCGAAC CTGNTCTCCT GGTTGGTTGG CATGCCGCN AGANTTGGGG	180
CAGCCGNCAA GCCCAGGTGC CCCTNAATCC CTCCTGGGGC TTCCNGCCTC CCCCTGGTGG	240

GCCTACCCCT GGCAACCCCC AGCCC

265

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCTGTNCG AGGCCGGNCC CCGGTGGCT GNNAACGCTG GGACCTGCAG AAGCACTCTT	60
TCCTAATTNT AATCGGCGAT ATCGGTACAG AGAGTCANCT GNGGGCCGTG CGGGCCAACC	120
TTAAACAAGG GAATTCTTTC CTGGTAACAT TGACCTGTNA TCCTTGANT TGAACCAACA	180
GTTGAAACTC TTCATTACCC GGACCTAGC TCACTTCTCC TCAAAGGTCA AAGGCCAGAG	240
GACCCTTTGC CACCAGAGTG AAGATCCTAG AGACCATCAT CCTGGTAAAT CCCAGTGNCA	300
GACAGCATCA GCTCTGAGGT TTCATCATCT TCTTTAGGCA GTTCNTCACT TTATAAACTA	360
TTATTTGAA TGGGGCAAAG TTTTNGGAGC CTNGGGGGGN GACCTNAT	408

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCGCNCTGC GGGAGNNNGG CTTCCCGTAC ATNACGCCGG TGCAGTCCGC AACCATCCCT	60
CTNTTCATGC GAAACAAAGA TGTGCGTGCA GAAGCGGTCA CAGGTAGTGG NAAAANACTC	120
GCTTTTNTNA TCCCCATCCT GGAAATTNTT CTNAGAAGAG AAGAGAAGTT AAAAAAGAGT	180
CAGGTTGGAG CCATAATCAT CACCCCCACT CGAGAGCTGG CCATTCAAAT AGACGAGGTC	240
CTGTCGCATT TNACGGAAGC ACTTCCCCGA GTTCAGGTGG AATTGGATGC AGTGTCCCTG	300
TTAACGTTCAT GGGGCTGTTT TNTCGAACTT NAATCAAAGG CTGTTTTCT TGTTGTAGNC	360
CAGTTTCTTT TTGGATTCGG AGGCAGGAAT TCTGGAGGAA NTTTTGAGA GGTTTAAGGC	420
AANAAGGTNG GGGACCACATCA TNTTGGGCCA TTCCAAGGCC GTTTGGNGG ACATTT	477

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCCAGCACCC	GAACATNATC	ACCCTCAAGG	ATGTCTATAN	TGGTGGCAGG	TTTGTGTACC	60
TGGTAATNGA	GCTGNATGCN	TGGTGGGAA	GCTCCTGGAC	CGCATCCTCC	GGCAGAGATC	120
ACTTCTCGGA	GGCGCCN					137

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GGCAGAGCAG	ACTGTCCCCG	TGTTGTCTGA	GGCAGACCCC	TCAGGTTGGT	GAGCAGGGTG	60
CTNTGTGGCC	GAGGGCTGGG	TGGGCTGGCC	TTTGCAGTCA	TCTCACCATC	TTCACGAGCT	120
TNTNTCTCTT	CAGTCACGCC	GATGATGGAG	CTGAAGCCCA	ACGCAGTNAG	CNACCGTGCG	180
CTGGGTCTGG	NAACACCCAC	GCTGGACTTC	GGCCGACGAG	TGCCCCAAGC	CAGAGCTGCT	240
GGCCATCCGT	TTTCCTNGAA	TGCTGAGAAG	TGAAGCCAAG	GCCCTGGGNG	ACCTGGCCTT	300
GACTTNGGGG	NTTCACCTGN					320

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GGCAGAGGTT	GGTCTTTGCC	ATGTCCTTG	TCCCGGNCAG	NTTCACTCTT	GTCCTCATLG	60
AGGAGCGAGT	CACCCGAGCC	AAGCACCTGC	AGCTCATGGG	GGGCCTGTCC	CCACCCCTCTA	120
CTGGCTTGGC	AACTTTNTCT	GGGAACATGG	TGCGGGGGCT	GCTTGGACGG	GTGGGGGCC	180
AGCCACTGCT	TGCCACTGCC	CTGTNTGGNC	CCTTGTNAGN	CAGGGGCTTG	TCCAAGATGG	240
CCTGGGTAAA	GTTCAGAGGG	ATTGTGGGAG	ACTTTNTGGC	CTTCCTAATT	AAAAAGCAA	300

GGNGGTTCAA GGTGGGAACA GGGCTNAGGG TGGGCAGTGC CCAACTNNTT TTAGGGTTGA	360
TAAAAGGT	368

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAGGGCCATT CAGTGNATGG GGAAAGGTGA ACATNCCATC GTGTACCTCA AGCCCAGCTA	60
TGGTTTTTGG TAAGTNTTGG GGANGGAAAA NTTCCAATC CCACCAAATG CTGGAGCTGG	120
NA	122

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTCAAACTCG CCTGGNAGCA CCCATCATCC CCNTGCCGGT CCTNACCTCT NCCTGGAGCN	60
GTCCCCCCGC TTCCTTCCCC ATCCAAGGAG GAGGAGGGAC TAAGGGCTCA GGTGCGGGAC	120
CTNGAGGAGA AACTAGAGAC CCTGAGCACT TNAACGGGCA GNAGACAANG CAAAGTTAAA	180
AGAAGCTGGA GAAACANAAA	200

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TGTGCTACAT CACCTACGTN AGCAATCAGA CCTACCAGGA GCGGACCTAT AAGCAGCTNC	60
TCCAGGAGAA GGCAGCTTTC CGGGAAGCTG ATCGCNCATA GGAGCTCGAC CCCAAGTGCA	120
GGGGGCTGCC CTTCTCCTCC TTCCTCATCC TGCCCTTCCA GAGGATCACA CGCCTCAAGC	180

TGTTGGTCCA GAACATCCTG AAGAGGGTAG AAGAAAGGTC TAAGCGGGAG TNCACTGTTT	240
TGGAATGCTC ANAAGGGNGC TGAAAATGG TGGTAAAGGC ATGNAACGAG GGCCTTCAGG	300
NAAAATGAGC CGCACGGAAC AGATGATCAG CNTTTCAG	338

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATGCGCTNCT GGTGTTCTNA GTGGCCAAAG TCTNTGCCA GCCAACNTG GCTGAAATGA	60
TTCAAAAAGG TGAGCAGNTA TTCCCTGGTAG CCAGAGCTGT GTTCATNG	108

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AAGCCCACAT NGCCACCCCCG GAGCAGCTCT ATCCNGNCTA CNTTGGGGGC TATAAGCAAT	60
GTAATGCTGG CTGGNTTTGG GATCAAACCG TAAGTTATCC CATCCAGACC CCACGAAAGG	120
CCTNNAACGG GGACATNGNT GG	142

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

AATNCANTCT TAAGGCCAG GGGAACACAA TGAACATATGN ATTGACTGAA TGCAGAACCT	60
GGTTGTGGNA GAGCNAGCTG AATGTTGGC CCAGAAGAAG CCTGTTCTGT TTTGGGAGCA	120
GTNANAACCA GNATATGACG TGAGAAA	147

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGCAGAGNCT GCAGTTGCA GNGCCCGGAT AACCGAGGCA GTGGCCCCTC CCGCGTCCCC	60
AGGTTTCAAG GACGCTAGGN CTCTCCGCGG CCCTGAGGCT TCGCACTGGG GAGTGGGGCC	120
GCCAGATGGG ACGTGTCAT GAAGGGCCTG TCCATGGCCA AGGAGGGCGT TGTGGCANCC	180
CGGGAGAAAA CCAAGCAGGG GGTCAACCGAN GGCGGCGGAG AAGNCCAAGG AGGGCGTCCT	240
CTACGTCGGA AGCAAGACCC CNGAAGGTGT TGTACAANGT NTTGGCTTTC AATGG	295

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

NANGNGCTCT GCCAGGTNCG NACACTAGTG GATCCAAAGT AATTCCGGCAG AGGATGGAGC	60
GGCAGGTCCT CCCAGACCCC GAGGTGCTGG AAGTGTGGGG GACAGGCAGG ATGGGCTAAG	120
GGAACAGCTG CAGGCCAG TGCCCTCCTGA CAGTNCCCC AGCCTGCAA ANATGGGTCT	180
TCTGCTGGAC AAGCTGGCCA AGGAGAACCA GGACATCCGG NTGCTGCAGG CCCAGCTGCA	240
NGCCAAAAG GGAAGAGCTT CANAGCCTNA TGCACCAGCC CAAAGGTTAG GAGGGAGGAG	300
AATGCCAGC TNCGGGGGGG GTTCTGNAGC A	331

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAGGCGCTGC GTCTTCCAG CGTTTCGCAT CCGGAATACA TTGGACGGGT CGGAAGTTCT	60
TTAGCGATAT CGGGGGGGGG GCGCTACTAA TGCATGGTAC TGAAGGTGAA GTGTATGCTA	120

ATCCGCAGCG CTGCCCGCAG ATCAAATCTCA TTGACCGTGA AAGGGATGCG GGTGCTGTAT	180
GAAAAACAGG ACAC TGCTGG TAGCGAGTTA CTGCCACAAG CAAAAGATCC GGAAACCACG	240
GCCCATGGGT TGAGCCGTTG CCTTGCTGGG AGCGGAACCG ATTCCCGAAT CGCTGAAAAT	300
CCAGATGGNT TNCTNGCCTG GTGGTTACGG GTTAAGCGGG CAACTTTCA GCGACGGNCT	360
TGGGGCGTT TAATCCGGGC ATTTNAATTTC TTTTCTCTA	400

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GGCAGAGCCC CACCGTGTAA AAAAACTACA CTGCAAGCTT TNAAATCGAN AAGCGCCGCA	60
TTGAGCTCAA CATGTGGAA CATTCAAGTT CCTCTNACTA TGAATAATNT CCGGCCTCTG	120
GCTNATNCCT GAATTCTGAA TGCTGTGCTC ATTCTGCTTC GAACATTAGN CGACCAGANA	180
CACTGGGACA GTGTTNCTTC AAGANAGNGG CCAAGNGGNG ATTTCAAGAG TTCCTGNCCC	240
CATGCCAAG GTTGTGCCCTG GTTGGCTGT TAAACTGGGA CATGNGGAC TTGAACCTGG	300
GCCCACACTG NNGGGAGCTG TTCCAGGCAG AGGGCTTATN CCCTGTTAAC ACATGNGCCA	360
AGGGCACTGT GCCTGGGCCA GCAGGTGGGG GGGTGGTGTGTC CNATGTTGNG TGGTNCT	417

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GGCAGAGTGG TGCTGGACAG TGACCAGCNG GTCAGTGCAG CTAGNCCACT NGCCCACGCC	60
TACTTNNGCC AGTACCAACGA CCCCGAGGAT GAGCCAGAGG	100

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TACCTGGATA TNCNCGTNTA ACGCCGTGGG GGTCTGGNCC TAAGTGTGTA AGCNTTGCAC	60
GCCGTGGAGA AAGACGTGTG GACCGCCTGT GCCAGATGGC ATCCCCCACA AACTCGCNCT	120
ATGGGCAGAA GGAGTCCTCG GAATCAAAAC TTCGACTACA TGTTCAAAAT TCTNAATCAT	180
CGGCAACAGC AGCGTGGCA AGACGTCCTT CCTCTCCGC TAATGCTGAC. GAACTTCGTT	240
TCAGGNCTGN TCTTCGTNAG CACCGTGGGG CATCGACTTT CAAAGGTTCA AGACCATCTA	300
TTCGCAACGT CCAAGAGGNT TCAAGTTGGC AGNTTTGGGG ACACAGCAAG GGCAAGAGCC	360
GGTTNCCGGN NCCTT	375

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GGCANANC GG CAGGAGGCTC NATACTACAA GCTGGGGAG ACCACCCTGG AGGAGTGGAA	60
GAGGCGTATC CAGGAGAAC CAGGGCCCTG GGGAGAGCTG GCCACGGACA ACATCATTNT	120
AACCGTGCCG ACTGCAAATT TTCGTACTCT GGAGAACCCCT GAGCCCGNTG CTCCGCCTCT	180
GGGAATGAGG TGATGCAGGC TGTGGCGCGA CTGGNAAGCT GAGCCCTTCC CTTTGCCT	240
GCTTCAAAGG ATTNTTGCCG ACGTGCAGAT CTTCAGTGGG NTGGGATGCA TNCAGGGTAC	300
CCCATCCATG TGCCATCTGG AGTTCAATGN CAGGAGCTTC ATTCAACGGG GAAGCTCCTT	360
CAGGAACCAA GGGGCTGTTG GGGGCCCGT TCCATGAGCT GGGGCCGCAA CCAGCAGTGG	420
CAGGAGTTGG GGAGTTCCA GGGACAATAC CAACGGGGC NACTTGAAN CTGTTGGTGG	480
TGTGTTATGT GCATGANAAC GTCTTTGGGG NNNTCTT	517

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

AGCTGGNTNN CGCGCGCCTG AATTGCCAG GAAGCAGGTA TGGNGTTCCA GCAGTTTAC	60
CTCTTCCCGC ATCTNACAGC GCTGGAAAAC GTCATGTTG GCCCGCTACG GTGCGTGGNG	120
CGAACAAAGA AGAGGCGGAA AAACCTGGCAC GTNAGCTGCT GGCGAAAGTN GGTCTGGCAG	180
AACGTGGCAC ATCACTACCC TTCCGAACCTT TCTGGTGGTG AACNGTCAGC GTGTGGCGAT	240
TNNCCGCGCN GTGGCGGTGG AAGCTGNGGG	270

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGCACAGTTT CATTCTGGT TTTAAGGAGT TCACGGCCA TGTGGATCGC ATCTTGAGG	60
ATGTCAAAGA GCTCACTGGA GGCAGGAGTGG CAGCCTACAT CCCTCAGCTG GCCAAGTCAA	120
ACCCAGACCT NTGGGGTGTG TCCCTGTGCA CTGTGGATGG TCAACGGCA CTGTGTGGGG	180
CCACACAGGG ATNCCCTTCT GCCTGGCAGT GCCTGGTNTG NNAGCCCCTN ACCTATGNCC	240
ATCTCCATGA AGGCACCCCTN AGGCACTGGA CTTACGTGTC ACAANGTTT NTGGGNCAAA	300
AGAGCCCAAG TGGGCCTGGC GCTTACGAAC A	331

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTGNAGGTGCG ACACTAGTGG ATCCAAAGAA TNTGGCNGAG CNAGGGGTGA AGTCCTTNAG	60
GCCCTGAATG GTCAGCTTGT CCACAGGGTG AATCTTGTG TAGTCAGCCG GGTCAANNAG	120
GTNAGAGGCA GCAGGACCTG TTTNTTCAGG TTGGTCTCTG GAAAGCAGGC GGCATTCGGT	180
CATCGGGGGC CTNACTAGCC TGGAGAGCTT CATTCTAA ACCCATCTGG GGCTCTGGGA	240
AGATGCCCT TAATCCTGNT GCCTGGGAAC AATNCCCGGG TCAGTGAAC TATGGGNGCC	300
CTGGGTGCTG CTTCCCTTTC AACTAGGGGT NCCCCTAGCA AGTNTGACGC TGGGTGCTGG	360
AGGTTTGCAA GGNCTTCCT NGTTGGCACA TTGCATGGAT N	401

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACTCACAAAGC TTGNNTTTGA NCACCAGCCA GGTGACATCT TTGGCTGTNT GGCGACATC	60
GGNTGGTTTA CAGGACACAG CTACGTGGTG TATGGGCCTC TCTNCAATGG TGCCACCAGC	120
GTCCTTTTG AGNAGCACCC CAGTTTATCC CAATGNCTGG TCGGTACTGG GAAGACANTA	180
GAGAGGTTGA AGATCAATCA GTTCTATGGC GCCCCAACGG GCTGTGCCGG CTGTTGCTGA	240
AATACGGTGN ATGGCCTGGG GTGGAAGAAA GTGATGGATC GGTCCNTGCC CTGNGGGACC	300
CTGGGGGTCA NTNGGG	316

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GATCATTATG CTAAGNTNGT NTGNGNCTCC AGGTCGACAC TAGTGGATCC AAAGAATTG	60
GCACGAGCAG TTGGTGGAGG ACAGAAGGTC CGGTGGTTAA AGAAGGAAAT GGAGAAATAC	120
GCTGACCGGG AGGATATGAT CATCATGTT GTGGATAGCT ACGACGTGAT TCTGGCCGGC	180
AGCCCCACAG AGCTGCTGAA GAAGTTCGTC CAGAGTGGCA GCCGNCTGCN CTTCTNTGCA	240
GAGAGCTTCT GCTGGCCCGA GTGGGGGCTG CGGGACAGTA CCCTGAGGTG GGCACGGGGA	300
AGCGCTTCCT CAATTCTGGT GGATTCATCG GTTTGCCAC CACCATCCAC CAAATCGTGC	360
GCCANTGGAA GTACAAGGAT GATNGACGAC GACCAGCTGT TCTACACACG GNTCTACCTG	420
GNCCCAGGAC TGAGGGAGAA ACTNAGCCTT AAATCTGGAT CATAAATTNT GGGATCTTTC	480
AGAACCTCAA CGGGGCTTT AGATGNAATG GGTTTAAAAA GTTTAATNG GGAACCGGGT	540
GCGTATNCGG AANGNGGCT AAGGACAAGG T	571

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGGAACATNG AGACTTGGGC CACCCAATTN GAGAGGATCT TGGACAGAAA CCCCTTCATA	60
AAACCTNAGC CTCAAAGGGC TTCNCTGACT GTGANAAAAA AAAAAAAAAA ANTCC	115

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGTCNTGATT AACCTCATGA AGGGGCCAAA GNTCGGGGNC NGCGCCTGCG GGTCGACACT	60
AGTGGATCCA AAGAATTCGG CAGAGCAGCT TTTTNATGCC TTTNAAGATG ATAGGTATCT	120
GTNCATGGTA ATGGAGTACA TGCCTGGTGG AGACCTTGTA AACCTTATGA GTAATTATGN	180
ATGTGCCTGA AAAATGGCC AAATTTACA CTGNTGAAGT TGTTCTTGCT CCTGGATGCA	240
ATACACTCCA TGGGNTTAAA TTACACAGNG GTGTGNAAGC CTGACAACAT GCTCTTGGGA	300
TNAANCATGG GACATCTAAA ATTTAGGCAG ATTTTGGGCA CGTGTATGAG GGTGGATGAA	360
ACAGGGCATG GTTACATTGT GNATACGGCA GTTGGGAAC ACCGGATTTA TATNNTCACC	420
TGAGGGTTNC TGAAAATCCA CAAGGGGGGT TGATGGTTT TCTTATGGGG CGGN	474

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 538 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TACAGCGATC TNCGAGTGGN ACATGNTGGG TCCAAAGANT CGGCANAGGG ACAATCTCTA	60
ACTAGTGTCA TGGCTCCATC TGGGGCTGGG CTGGGGTCAG GACTCCGTCT GAGGCTGTNT	120
TTTGACTGTN AGGTAGCCCA GGCTGGGCTG ACTCCTGATT GTGCAGTTT GCATCTTCTC	180
CCTGCTGAGA GTCCACCAAA GTNTTCTATG GTAGACCCAG TNTCTGGAAG TNATCATCAN	240

GCAGCAGCAA CAGGGNGTGT TGTAGGTCAG CAATGGGGAG ATAGGCAATG CAGAGGTGTC	300
TNTTCCAGNN CCCTGGAGAG CCATTTGTC GGNANTTGGA GCTGGTNAAT NAGAGGNTGC	360
TTGAGCAGTG TCGGAATAAT CCCGTCAGGA CAGCTGCTAG TTCAAGCTGG TTTGGTGAAT	420
GTATGGANTA CTGAGAGGTG AGTGCAGAAAG GTTGGCTGCT TCTAAGTTG GTGAGTCATT	480
GTTTTNTTGC TNATTGCATG TTGGGNAAGA TACCACCTCA NTGCTTACGT TATCAGCN	538

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GGCAGAGGTC ATGATGGAGG TCGAGTCCTC CTACTCGGAC TTCATCTCCT GTAACCGGAC	60
AGGCCGTCGG AATGCGGTCC CTGANATCCA GGGAGACTCA AAGGCTGTAA GCGTAAGGNA	120
AGCTGGCTGG AGACATGGGC GAGCTGGCAC TCGAGGGGGC AGAAGGACAG GTGGAGGGGA	180
AGCGCCCCAA ACAAGGAAAG CTGGGCAACC AGCCCCAGAG CAGCGATGGG NACCACCTTC	240
GTTTTGAAA TCTGAACCTT GTTCCAAGAA GGCTTGGACG AGAGACCCTT NTGTTCCCCT	300
TCCCANAGGG GGGGAACCCCT GGGCAATTGG GCCCANAAAN GCTTTTTTT TTN	353

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GGCAGAGCCC AGCAGGAAAT AAAATTITTN NAAACCCCTAG TGCCATATGN TGAAGGGGCC	60
CCTGCTTTTA AGGGAAGGGC TCCTGCCTTT NCTNACGCTT CTNTCCACCC CAGGTATGAT	120
CTCATGTACC AGTGCCTGGA GTGCTGACCC CAAGCAGCGC CCGANTTA CTTGTCTGCG	180
AAATGGGAAC TGGGAGAAC A TCTTGGGCCA GCTGTCTGTG CTNATCTGCC AGNCAGGACC	240
CCTTATGACA TCAACATCGA GAGAGCTGAG GAGCCCACTG CGGGGAGGCA GCCTGGAGCT	300
ANCTGGCAGG GGNTCAGCCC TACATGGGGG TTGGGGATGG CATTGGCNTN GGGGCATGGG	360
GTGGCACTNC CCAT	374

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCACGAGCA ACTGCTGGTT CTCCTAGAGG CCTCTCCTCA AACTCGCAGN CTGCCTGATC	60
ATTGCTACAG AATGAAC TCT AGCCCAGCTG GGAACCCAA GTCCACAGCC CTCCAGGGCC	120
AATGGGAAAC ATCAACCTGG GGCCTTCAGC CAACCCAAAT GCCCAGCCC CGGACTTCGA	180
CTTCCTCAA A GTCATCGGCA AAGGGAAC TA CGGGGAAGGT CCTACTGGCC AAGCGCAAGT	240
TTGGATGGGG CGTTCTATGC AGTGAAAGGT ACTACAGAAA AAGTCCATCT TTAAAGAAGN	300
AAGAGAGCCA CATT CATGGG CAGAGCGCCA TNTGGCTTTC TGAAAGAACG TGCGGGCACC	360
CCTTNCTTGT GGGGNCTGN GCTNATTCT TTCCAGAAC AC	402

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CAGACGCTGT CCAGCTGGNA GTAACAGTGG GGCTGGTGA ACGTCGGATC GGCCCAGGGG	60
AGCCCTTGGN AACTCCTGTG CAATGTGTCA GGGGCACCTTC CCCCAGCAGG CCGTCATGCT	120
GCATACTCTG TAGTTGGGA AGATGGCACC TGCGAGGGCA CCTGGGCCCT GGCGCCTGG	180
TAAGCCCAGC TGGACACAAA GGGTGTGGGN CAGCCTGGC CCTGGCTATG AAGGGCCGAC	240
ACATTGCCAT GGNCAAGGT GGCATCCAGA ACATACCGGN TTAGNGTTAG AGGCTGCCAG	300
GNCTGGGTGA TGCGGGCAAC TNACCGTTGT CTTG	334

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GGCAGAGTTT GTTTGAAGG AGACCGGNTG GCATTCTCG GGACAGAGAT ATCTTCAGA	60
TCCAATGGAG AAGCACTCCA GCAGCTATAA TCAAGGTGGT TACAACCANG ACAGCTATGG	120
ATCAAGCAGT GGGTACAGTC AGCAGGCGAG TTTGGGCCA NNCTCAGATG AGTTGGCCA	180
ACAGCCTACT GGCCCCACTT CCTTTACCAA TCAGATTAA CAGAGTAGCA TTTGCATTCT	240
TCTGCAGTGC GCCTCACCAT CTTCCATTTC AGTGGGCAGA AGAATTTTT AAGGGTTCA	300
ATCAATTATT ANTGCAGAGA GTATTGANTG TNAATGCAGA GCTCTCTAGT NTTNCATTAA	360
GGCAGCAAT	369

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGCAGAGCCA AGGCGNTGGC TNGAGGGAGT CAGCGGCCTC GGGCTTGGGG GCCTGTTGGA	60
GGAGGAAGGA GCCGGGGCAG GTGCTGCCAA GAAGGAGGTG CTGGAGCCTG GCAGGGAACT	120
CTCCACCCCTC NTGGAGGCCG CAGCCTGNAT GGTGAAGGCC AGCCAGACAG AAGACGTGGA	180
TGGNACCTGG GGCTCTTCAG CAGCCAGGTG GAGCGAATCA GGGGCCAGC ACAGACTTNT	240
CGGCGACCCCT CCCAAGGCC CCCTGCCAGA TCCCCCAGTT CAGGACTTTT TCCTTCATTG	300
AGGACACCGA GATCCTCGAA CANTNCCCAT GTTATCGGGA GCCGTGCCAA TTTGGGGCG	360
CAATTTTG GGGCAACGGG GCCCCGGTCC ATTGGNCTG GGGGGTTACT TTGGGNCTTT	420
NGGGGNAGC ANAATTCTGGA TG	442

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CGGCTTTATT TGTAGGGCAG ATCTTTGTNC GCNTCATATG GTCCACACGG GAGATCAGCC	60
CTATTATTGT NAGAGTGTGG GAGTGCTNCG ATAGGCCNCG TGTCTTGAN ACATCAGAGA	120

GNCCCCGTGG AGA

133

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GGCACGAGAA CACCTATGGN TTTCCAATGG ATCTAACTGG ACTAATTGNT GAAGAGAAGG	60
GCCTGGTGGT AGACATGGTT GGCTTTAAAG AGGAGAGGAA ACTGGCCAG CTGAAATCAC	120
AGGGGCAAGG GAAGCTGGTG GGGAAAGACCT CATTATGCTG GACATTTACG CTNATCGAAG	180
AGCTCCGGGG CACGGNGTCT GGAGGTCACA GATGATTCCC CAAAGTTACA ATTNACCATT	240
TGGNGCTCCA GTGGTAGCTA ATGTATTTNA AGANACACAG TGGGCTACGG GTGAATGGTT	300
TCTGCGNCAG GGGAGNAAGA TGTTCCGTGG GGAGAGGTGT TCCCACAGGT CCAGGAGTTG	360
TTGGGAGTTG GTTGCNTGGG ACAAGANCCN GTTTTT	396

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TGGCACGAGT GCGACGCGGT GGTCACCATG TGGATCTTGG GTCTGAGGAA AGAATTNAG	60
GAAGGCCAGGA AGTGGGTGTC GAAGAAGTTA CACTTGAAA AGGACGTGGA CGTCAACCTG	120
TTTNAGAACG ACGATCCGCA TCCTGGGGGG GCTCCTGANT GCCTACCACC TGTTGGGA	180
CAGCCTCTTC CTGAGGAAAG CTGAGGATTG TGGAAATCGG CTAATGCCTG CTTTCAGAA	240
CACCATCCAA GATTCCCTAA CTTCGGGATG TGAAACATCG GTNACTGGGA GTTGCCACC	300
CGTNCACGGT GGGAACCTCC GACAGCACTN TGGGCCGAGG TGACCAGCAT TTCAGCTGGN	360
AGTTTCCCGG GAGCTCTNCC CGTTTTTCAC AGGGGGATNA AGNAAGTTT TCAAGGGGG	419

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

NNANACTGAG TGGATCCAAA NAATTGGCA GAGCAGTGGA AGATCAAAGC AATCGGGCAT	60
GTAATAGAGG ANGGCGGTGT CAAAATAAAG CTAACCGTAA TCANCACCCC AGGCTTTGGA	120
GACCAAATCA ACAATGAAAA CTGCTGGAA GCCCATTAAG AAAGTACATC AATGAAGNCA	180
GTACGNAAA GTTCCTGAAA GGAGGNGGTT CAACATGCC AGGTAGGAAA CGCATCCCTG	240
AAAACTNCGT GTCCACTGNT GCCTTGACT TGCATCTCTC CCACAGGNCA CTCCTTGCGA	300
ACCTCTGGGA TCTTGAAGTT NCATGAAACA CCTTCGGCAA GGTTNTGANA CCTCATCCCT	360
GTTCATTGCT TANGGCNTGG ACACCCTGGA CCCTGGTGGG TGGAANGTCT GATTTCAAG	420
CCAAGGGTTT CGCCAAGG	438

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 554 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

NTNTGACTNC AGGTCGACAC TAGTGGATCC ANAGAATTG GCACGAGAGC CGGCTCGGGG	60
AGAACGAGCT CANCTGGAC ATAAGGTGAC ACAACTGGCA AGCTATTTA AGCCCTTNAN	120
CTTAGCCGCA GTTGGTGTGG CCTCCAAGAT TCTTGATCAT CAGCAGCAGA TGACGGTGCT	180
GGACCAGACC AAGACTCTCG CAGAGTCTGC CTTGCAGATG TTGTATGCAG CCAAAGAAGG	240
TGGCGAACAC CCCAAGGCAC AACACACCCA TGACGCCATC ACAGAGGCCG CCCAGTTGAT	300
GAAGGAAGCC GTGGATGACA TCATGGTGAC GCTGAACGAA GCTGCCAGTG AAGTGGGGCT	360
GGTTGGGGGC ATNGTGGACG CCATTNCAGA AGCCATGAGC AAGCTNGATT GAAGGCACTC	420
CTCCAGAACCC AAAGGGNAAC ATTTTTTCGA CTATCAGACG ANTGTGGTTT AAATACTCCA	480
AAGCCATTG CGGTTGANCA GCNTNAGGGA AATGATGACT AAGTCGGTTT ACTAACCCGG	540
AGGGNGTTG GGAG	554

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GGCACGAGGG CCCNCGGCAC TAAGTCATCT TGGAGTTATT AACCACTGGG CCCTAGGCAC	60
TAAGTNATTT GTGGAATGTA AAGGTTCCCTA GCGAGCATCT CACCCCAGGC TCCAGGGCCT	120
CCTGAGTGCA CTGAATTAT TTTGCACAAT ATCGTGCACA TGAGCTCATC TGNGAAGAGC	180
ATCCAGTCTT CATCAGTCTA CCAAACCTCA GGAACCACCG TTTCCCCCTC AGTTCCTTGC	240
AATCTGTTCA TTTAAGGATG AGGAACCAAA GTCCAGGAAA GAGGAAGGGG TTGCCAGGG	300
TACTGGATAG TNTTCTGCAG AGTGGGACAA GGGCTCTCTG GGTNTTTCTG ACTNCACCAN	360
ATCTNGTTCA CCCCTGNACC TGGACCTCCT TGGAACCTCA GTTTCTCCCT GAGGGGACCC	420
TGCACACCCA CAACTTCANA ACAACATTTC CTTANAANCT AGNGG	465

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ATNANTTAG AGTCAAGTAT GAAACANACC TGGCCATGCC CCANTTTGTG GAGAACGANA	60
TCCATGGGCC TCCGCAAGTC CATTGAATGA CACCAATATC ACACGACTGC GAGCTGGAGA	120
CAGAGAATCG AGGCTCTCAA GGAGGGAGCTG CTCTTNATGA AAGAAGAACC ACGAGGGAGGT	180
AAGTTAAAAG GCCTTACAAG CCCAGATTGC NAGCTCCTGG GTTGAACCGT GGAGGTTAGA	240
TGCCCCAAA TTTTNAGGGA CCTCGCCAAG NTCATGGNCA GACNTCCGGG CCCCAATATG	300
AACGAGCTGG CTCNGTAGGA	320

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGCACGAGAT GATCCTTNAG TNCCCTNAAAT TGATCGGATC TACAAAACAG ATAGAGAAAA	60
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TTACATCGCA TACTTCTGAA GTCCATTCCN GAGCTATTCT GTTGTGACTT TTNTCGNGAC	120
CGATTGGCA GGAAGACANC TGATNCCTGT CCCG	154

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGCACGAGAA GCCTGAGACT AGGGAGGAGA GGGTTGCTCC AAACTGGTTC CTACACAAACC	60
AGGAGGCAGC CCTAGGAACT TCAGATCAAA GCGGATGGAC TTTGGATTAC AGGAGAAATA	120
TTTAGTGGTA TCTGGAAAAG AAATACATTA AAAAGAATAA AATAACTTTG AAATTAAAAAA	180
ATCCAACAA TCTTTGTTT CACATTTAG CTGCGGATCA GCATTTAGGG TAAAGGTGTA	240
ACTTCCTCCT GAAGGTACAT CCTTGGCTAG AAATCTGAAA GGCCAGGTCA TTNCTTGTT	300
TCTCTGGAAC CGGATTAGG CATAGTTCC ATTCAAGTTT TTCTNGGTNC TTTGAAGTNA	360
ACCTTTCCA NTATTATTCC ANTGGTTA GGGCTTAGTT ATTATGAATG TNCCCTCAGA	420
TGGGCAACTC CGGTTTCAN CCNTCAGGTC TAGCCCTGGG GAAGGAAGNA GGAGGGCCAG	480
GTTCNNGTGG GTTCAAA	497

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GGCACGAGGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAANAAAAAA AANAANANAN	80

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGCACGAGCC ATGCCCGCT ACGCCGACGC GTCGNNAACGC AACACGCTTA GCGGCTTCTC	60
CTCAGNCCAC ATGGGCAGTN ACGTTCCCAG CCCCCANAGCC AGGGTCACCA CGCTGTNCAA	120
CCCCATNGTG GNCTCGGTCT CCAGACGGAC CGCACCCGA GGTAAGTGGG GCAGTGTCCG	180
GACCAGTGTG ANGNAGCAGT GGTCTTGGCA CCGATGTGGG CTCCCGGNTA GCTGGCAGAG	240
AACCGCGCTNG NCCCACCCCA GG	262

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

AGAGCGCGCC TAACCGTAAA GGTCGTTACC TGTATATGGA ACCCAAGCCC TACCTGGAAG	60
TCTNCCTGCA CTNGGAGCCC CGGNCCAATN TGAGNAACTG ATCGG	105

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CACGNNNCGG CACGNACCG TTCACCTTCC AGCCAGAAGG GGTCACGTGG CGGGAGCAGA	60
AGGAGCAGCG GGCGCCCTC ATGGTGGGCA TGNTCGTTGG CGTGTTCGNG CTCNGCTGGT	120
ATCCCCTTCT TTCTCACCGA GCTCATCAGT CCCCTGCGGC TCCTGNGACA TCCCCGGCCA	180
NCTGGAAAAG CANCT	195

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCACGAGCA CACACGNACC ANCATCTACA GGACGTGGAC ATTNAGCCCT ACGTCAGCAA	60
GATGCTAGGC ACTGGCAAGC TGGGTTTNTC CTTCGTACGC ATCACGGNCC TGCTTGTNGC	120
GGGCAGCCGG CTCTGGGTGG GCACCGGCAA CGAAGTGTG CATCTCCATC CCCCTGAACA	180
GAGACTGTGG TCCTGACACC GAGGCCAGCT CCTGGGGNTC CGAGCCAATT AAGAACATCC	240
CCCACCTCTG GGGAGGGCGC CCGTCCCCGGG GGCATCATCC ACGTGTATNN GCGATGACAG	300
CANTNAACAG GGGGGGNCAA CAG	323

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CCAACCCTGG TGTGGTACCA NCCCGATGGC ACTCGGGTGG TCAGTNAGGG ACACACTTG	60
GAGAACTGCT GCTACCAGGG AAGAGTGCAGG GGATATGCAG GCTCCTGGGT GTCCATCTGN	120
CACCTGCTCT GGGCTCAAAG GCTTNGTGGT CCTGAACCCC AGAGAGAAGC TATAACCCTGG	180
AGCAGGGGGC CTGGGGACCT TCNAGGGTNC TGNCCATTAA TTTNNGCGGA ATCCAAGATC	240
TCCACCTG	248

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGCACGAGCC AATGTGGCAG CCGCCCTGGG GGTGGCAGAG CTCCTNTTCC TGCTGGGAT	60
TCACAGGACC CACAATCAGN ACCTTCGNGT GGNTCTCGT GCAGGGGCTG CACCTNTACC	120
GCATGCAGGT TGAGGCCACGN AACGTGGACC GTGGGCCAT GGCTTGCTAC CATGCCCTGG	180
GCTNGGGCGT CCCTGGCTTT GCTGCTGGGC CTTGCTGTGG GGCCTGGACC NTNAGGGNCT	240
NT	242

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TGAAGGAGTN CTTNCTTNNA ACGAAACGCT CCAACGANTA CCACCTGATT AATTGTCCCC	60
AGTACTTCCT GGACAAAATC GACGTGAATC AAGCAGGCTG ACTATTTCCC GAGCAATCAG	120
GACCTGTTTC GNTGCCGTTT CCTGATTTCT GGAATNTTG AGANCCAAGT TCCAGGTGGA	180
NAANGTAAAC TTCCACAT	198

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGGGCCAGCG GGACAGGGCA GAGNTCATCN TNTGCAGAA TNTGGGGGT GGGGAGGCAG	60
GGCCACAGGA AATAATTGGG GTNCAGCTCC AGCCCCTCCA ACCAGCCCCA GAAGTAACCA	120
CGGTCCAGCT CCAGCCAGCG CANGAGGTGA CCACAGTCCA GCTCCAGCCA GCACAGGAAG	180
TAACCACGGT CCAGCTCCAN CCAGCACAGG AGGTGACCAC GGTCCAGCTC CAGCCCGTGG	240
CGGGCCAGNT NTCCAATTCC ANTGGGGAG CTNTGG	276

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GGCACGACCT CGTCCAGCGA CTCAAGTCTC ANCAGATTGC AAAGTTGCC TTTAACTATG	60
CCACCAAGAA GGGGCGGGGC AAGGTCACTG CTGTCCACAA GGCCAACATC ATGTGANGGG	120
GCATGGCTTT GTNTAGGGAT GGGTTCTGG GAAGGTAGCC CCTGTACTTT CTNGGGTAAT	180
TCTGTCCNCT TTGGGCNATG GGACAGGTAA ACTT	214

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GGCACGAGGC AGGATGAGCG CTGGCAAGAC CTCATGTGA TCAGCAGCCT GCTCAAGTCC	60
TTNTTCCGAA AGCTGCCGA GCCTNTTTN ACTGATGACA AATACAACGA CTTCATNGAG	120
GCCAACCGCA TTGAGGACGC GCGGGAGCAA TAAGGACGNT GCGGAAGTTG ATCCGGGGAT	180
CTCCCAGGAC ANTACTATGA AANGNTTCAA ATTCCATTGTG GGGCCATNTT TAAGACCATG	240
GGTGGACCAC TTTNAGTTCA CCCTTT	266

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

TTCCAGAGGG CCACANAGGT GCTCNGCGCC GCCCAAGGAG ACCATNTCCC TGGCCGAGCA	60
	60

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGCANNGGA AAGTGGGGNT TAAAAAGGGA GAAGCAGACC TCTGNATGNA TCTGCCGCTT	60
GAACATGTCA GCTTTNAGCT GAAACCTCCC GACGCGCCAT CTCCTCATTC AAAGGTCTGC	120
NTCTCCCTTT TCAACCCCAA CTTCCATTCT NNAAGGGTTT TCCTGNAGAC TGCATTCNT	180
GGGTTTTCCCT	190

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GGCANAGACA ACCGTGAGAA GCTCAGCGAG TCGGTGCTGA TGAAGGGGA GCGGGTNATC	60
GCNATCCTAA AGCTCATTGA GCACCCCCAC GTCCTAAAGC TGCACGACGT TTNATGAAAA	120
ACAAAAAAATA TTTGTNACCT GGGTGGCTCA GGAGACCAAN ANTGTN	166

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GGCAGAGGTG TGGACGGCAT AAATGTAATA NNATATGCTG TGTGGATAAG GAGCACAAAGT	60
NTCCTTGAT TTGTGGGAGG AAACTCCGTT GTGCCCTCA TAGGTGTGAA AGAACCTTG	120
TNCATCGTGG GAAACTGCC CCAAGANGCAA TGCGGTTTGN NTTTTTN	167

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GGCANAGCGG CANGAGCCAC AATGAAACCA AGGAGGTAGA AGATGACTGG AAATACGTGG	60
CCATGGTGGT GGACAGAGTA TTTCTTGGG TATTATAAT TGTNTGTNTA TTTGGNAACT	120
GCAGGGCTTA TTTCTACAGN CCCACTTACT TTGGGGGGGG GGN	163

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGCACAGCAA GCNTTCACAG GTGGTGGNAT TNTTGGGGC CCAGCTAACG CCAGCCGCC	60
GGCGGCAGCA CATGCAGGAG CGCAGAGCCA CCCAAACCTC TCCACTATT AATCAGGAAG	120
GGTCCCCCTA GCCCTAAGGC TTCTTTTGC TTCCAGGTGA AACACAGNAA GANTCAGCCT	180
TCCCAGCAGC CNGGGGGAG ACCCACAAGC CCCTAAAAGC NTGCACTCAA GAGGGGGCCC	240
AGTNTTCACC AGGAACCTTG GAGGAAGTTC CCACAGGGAG CGCAAAGTNC GGCAGGCATC	300
GNCCTTCCGG GGCTTCTTNT TNTGGCATT	329

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

AGCAAGGNAG CTCTGGCTGA NACCACCGGN NAGACGCACC TCCGGGACCA CACCCACCAA	60
GGCTCCTGCC CCTNTTGTTC CTGGGGTCCC CAGTTGTTCT TAGGGCCTNC TGTGGGGCCA	120
GGCCCGANTG NGCTGTGNGA GCACTTCATT ACCGAAAGG	159

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GGCACGAGGC GCTTTCTNCC NATTGTNTGG TTTTACTTTT GTNCTGGTAT GAATTCGATT	60
CCATTTTAAT NCATCCTGTT AAATNAAGTT AAATGAGGGG AAANAAAAC CAAAAGGNAA	120
AAAAGGCACA GAGTGAGAGA CAACCCAGCA CAGGACCCCC AGGAAGGCAA GCAGTAACGC	180
TCCAGCAGCC GGGTTGTGCT GCCTGGGCC AGGCTTCTGC NAGGTGGTTT ACAGGCGGGA	240
ACCATTGNTA CCACAACCAC CAAAGGNGGT GGGAGTNCTG TGTTGTGCC CTTTACAGAA	300
GAGGAGACCG NGNNCTCAGA GAAGATCCAG CAGTAAGATT TAGAGTCAAG GTT	353

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GGCACGAGGC CAGCNTTCGC CAATNNTTGG AGAGTGGGT TNTGGGTCA GGTGGGGAC	60
CCCCACGGGG TCTGGANTTC TNCCGGGAGG AGATCACCAC CTTCATCGAT GAGACACCTC	120
TCCTTTCTCC GACTGCTTCA CCAGGGCACT CTCCTCGTCG GCCCCGGCCA CTGGGNCTNT	180
AACCCGCCG ACTCTCCCT TGGNTCCCCT GAGAACAGA GCCGTTGGAC TTCCCTTGGG	240
AACTGAAGCG CAGGGAGACG CTGCTCCCTG ACGGGGGTG AAGAAAGTNC CAAGGGCTTG	300
GGGAGGATCC TGGGGCCCAG GCAACCCCAT NTTTCCCCA GNTGACCTGT NAAGCCCAAG	360
CAGGNTGTTG NAACHTCAGA GGAGAAAGTT GA	392

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GGCACGAGCT GGGCTCATTC CCAGCCAGCT GCTGGAGGAG AAGCGGAAAG CATTNTNA	60
GAGGGACCTG GAGCTGACAC CAAACTCNGG GACCCTATGC GGCACCTTT AGGAAAGAAA	120
AAGAACGAA TGAATGTATT TNACCACCAA GNAATGCAGC CTGGTGAGCA GCGCNATCTC	180
CCTGTNTCCA GAGTTTGACC GTNATGAGCT GCTCATTAT GAGGAGGTGG CCCGCATGCC	240
CCCGTTCCGC CGGAAAACCC TGGTACTGAT TGGGGCTCA GGGCGTGGGA ACGGCGCACT	300
GGATAGGAAC AAGCTCCTTC ATGTGGGAT TCCAGATTG NTATGNGCAC CAAGGGTGCC	360
CTAAAAACTT CCCGNGGNC CGNAAAATT CAGAGCGGGG AAGGTTCAAGG GTTAAACAGT	420
TTTTNTTCC CCTTGGGGGA AGATGGNAGG	450

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GGGCAGGGAC	GCCCTGGCGC	CTCTNTAGGC	CGACTNCTCG	AGCTGCTTAC	CAAGCTGGC	60
CGCGACGACG	TGCTGCTGGA	GCTGGGACCC	AGCATTGAGG	AGGATTGCCA	AAAGTATATC	120
TTGAAGCAGC	AGCAGGAGGA	GGCTGAGAAG	CTTTTACAGG	TGGCCGCTGT	AGACAGCAGT	180
NTCCCACGGA	CAGCCAGAGC	TGGCGGGGGC	ATCACCAACAC	TTGAATGACC	CCCTGGGGCA	240
TATGCCTGAG	CCGTTTCGA	TGCCTTCATC	TGCTNATTGC	CCCAGCGAAC	ATCCAGTTG	300
TGGTAGGAGA	ATGATNCCGG	GNAACTGGAA	CAGACAAACT	ATCGACTGAA	ATTGTGTGTG	360
NTTTNGACCG	GATGTTCCCTG	CCTGGNA				387

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TCACCGATTG	GGATTNNNGAC	ATTGGAAAAT	TCCGACGTTT	TCTTGTTGG	TGTGGTTCTG	60
GGAATCCACG	CCAANGGGAA	GCGCATAANG	NACTGGTTTG	ACTGC		105

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GGCACGAGGN	AGAGCTCAGC	ATCACCCCTCA	CGCTGCGGAT	GCTGATGCAC	GGGNAGGAAG	60
TGGGCAGCAT	CATCGGGAAG	AAGGGCGAGA	NTGTAAAGCG	AATCCGGGAG	CAGAGCAGTG	120
CCCGGNTCAC	CATCTCCAAG	GGCTCCTGCC	TGCAACGCAT	CACCACCATC	ACCGGGTCTA	180
CAGCAGCTGT	TTTCCATGCA	GTCTCCATGA	TTGCTTCAA	ACTGGATGAG	GACCTTTTG	240
CCTGCTCCTG	CAAATGGTGG	AAATNTCTCC	AGGCCTCCAG	TGAACCCTGN	GGCCTTGTGN	300
ATCCCTGGCC	AGTCNTTTN	GGCTCACTGG	TTTGGGG			336

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GGCAGAGGTA AGCCATATGT NTTCGACAGA GTGCTACCTC CCAACACGAC CCAAGAGCAG	60
GTTTACAATG CATGTCCGAN AAATTGTCAA AGATGTCTT GAAGGTTATA ACGGGACGAT	120
TTTGCGTAT GGGCAGACTT CATCAGGAAA AACCCACACC ATGGAGGGGA AGCTGCATGA	180
CCCCCAGCTC ATGGGGATCA TCCCACGANT TGCCCATGAT ATCTTTGACC ATATCTACTC	240
CATGGGATGA GAAACCTGGG AGTTCACAT AAAGGTTCC TATTTGAGN ATCTTACTTG	300
GGACAAAATA AGGGACTTTA CTTGATTGTT TTCCAAGACC AACTTGGGCT GTTCCNTGAA.	360
GGTAAAAAAC AGGTNCCTN TGTAAAAGGG GTTNCATNGG GCGG	404

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GGCANAGGGT GGAGAACGTC NACTACAAGA TGGAGCTCTN CAAGGAGATC CGNGAGGNAC	60
ACCTGGCCGC ACTGGCGAGG GGCTGCGCGA GNAAGGAGCT GCACGNGGNC GAGGTGCGCA	120
NGAACAAAGGA GCAGCGAGAA GAGATGTCGG GCTAAGGGCC CGNNACGNNG TCGCCCATGC	180
CTGACGAACG TNAACACGTT CGGGTTTTG GTTTGTTTC GTTCACCTCT GTTTAGATGC	240
AACTTTGTT CCTCCTCCCN CANCCNGGNC CCCAGGTTCA TG	282

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GGCACGAGCT TTCTTGGGCG GGTCTGTAAG AGAGAGGCCA CGGTCTGAG CTACGATGGC	60
TCCATGTACA TGAAGATCAT GCTGCCTAAC GCCATGCACA CGGAGGCAGA GGATGTNTCC	120

CTGCNTTNA TGTCCCAGCG GGCTTACGGA CTCATGAATG GCCANCACCTT CCAGGGAGTC	180
TGCCGACACC CTACGCCTGG AGCTGGATGG GGGGCAGATG AAGCTTNACT GTCAACCTCG	240
ACTGCCTGCG CGTNGGCTGC GCACCNAGTN AAAGGNCCCG AAACGNTGTT TGCGGGGTAC	300
AAGTTCATTG ACATGAGTGG NCACAGGNTT GAGGGTGGTC CGGCCGTGGG CAAGAGNCTT	360
GCAATTGTTT TTGGGACAAC GTGGACTTTN GGAGGGGACA ATTNG	405

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGCAGAGCAG ATAACAGCCA TGGTGTGAC TAAGCTGAAG GAAACTCCTG AAAACAGCCT	60
CAAGAAACCA GTAACAGATT GTTTTATTC AGTCCCTCC TTCTTTACAG ATGCTGAGAG	120
GCGATCTGTG TTAGATGCTG CACAGATTGT TGGCCTAACAC TGTTTAAGAA CTTATGAAAT	180
GNCATGACAG CTGTTGCTTT GNAATTACGG AATTATAAG CAGGATCTCC CAAGCCTGGA	240
TGAGAAANCN TCGGATAGTG GGTTTTNGT TTGGTTAGGG GGCCATTCCA GCTTTCCAA	300
GTGGTCNNNGC TTTGTGCTTT TTTAACCAAG GGGGAAA	337

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CTTCNAGGTG AGCCAGCTCT ATNACTGNAN ACTGGATCGT GGTCAACTGC TCCACACCGG	60
CCAACTACTT CCACGTNCTG CGCCGGCAA TCCTGCTGCC CTTCCGCAAG CGCGCTGAAT	120
TATNTTCACA CCTGAAATCT CTGCTGAGGC ACCCAGAGGC CAAGTCCAGC TTTGAACCAA	180
ATGGTATCCG GGACCAGNTT CCAGGGGGTG AATTCTGAA GATGGGGCCG AAGNACGGGC	240
CCTTGANCNA GGTGAAGGGG TTAATTTTT GAAAGGGNAA GGTTTAT	287

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GGCAGAGCTT CTNCAAAGCT GCCCTCTNCC ACTTCATAGT AGNCAGTTG AATGCCAAGC	60
TTGCNCTTNA GAAATATGAG GAAATGTTTC CAGCATTNNN NGNTCAAGA GNNTGTAAAT	120
NNTTGAAAAA ACTCCTAGAA GCTCATGGAA GAACAGNNCA GTGNAAGCTT ACACTGAAGC	180
AGTGTAAAGGA ATTTGAACTC AATATCTCGC TTGGNTCAAGT GGCTGNCCAC CATGTTGCTT	240
CGCATCAAAA AGTCCATCCA AGGGGNTGGA GAAGGAGATG GAGACCTAAA ATGNNTGTTT	300
TTGGNCTTTG TGGGCATGCA GCTAACTCCT CTTTAGTTT GTTCTTAGGG TCCAAGTGAT	360
CTTTTATGGG GATGCCNCTT TTAATGGGTT TAATTTGTT TGGNATATGA GGCCCAACGG	420
GCCNGTGNNA AT	432

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GGCACGAGTA CGAGTCCCTT CAAACCGCCA AAAAGAAGGA TGAAGNAAA ATTGCCAAGC	60
CTGTTTCGCT GCTTGAGAAA AGNCGCCCC CAGTGGTGCC AAGGCAAACG GCAGGCTCAT	120
CTCGTAGNTC AAACTAACCT GCTCCGAAAT CAGGCCGAGG AGGAGNTCAN CAAAGCCCAG	180
AAGGTGTTTG AGGAGATGAA TGTGGATCTG CAGGAGGAGC TGCCGTCCCT GTGGAACAAC	240
CGCGTAGGTT TCTATGTCAA CACGTTCCAG TGGCATCGGG NGCCTGGTGG AAAAACTTNC	300
ACAAGGAGAT GAGCAAGNTC AACCAAGTNCC TCAATGANTG TGCTGGTTCG GNCTGGNNGA	360
AGCAACAGGG GNGCAAACAN CTTTCACGGT NAAGGCCCG NCCCNTTGAC AACGGGNCTT	420
GAAAAGGGGT ACAAGGGGCC TTTTAACCTC CAGTGGTTC CCTTGCNGGN ANCCCCGGGG	480
TTCCGGGTTA ACCAGGGGCC A	501

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGGCACGAGT GCAGATGAAG ATGTTGATCG GAAACACTGG GGCAAGTTTC TGGCTTTTA	60
TCAGTATGCA AAATCATTTA ACTCAGATGA CTTTGNTTAT NAAGANCTGA AGAATGGAGA	120
CTACGTCTNG ATGAGGTGGA AGGAACAGTT TCTGGTCCCA GATCACACGA TCAAAGACAT	180
CAGTGGTGCT TCTTTGCCG GGTCTACTA CATCTGCTTT CAGAAGTCAG CAGCCTCCAT	240
AGAGGGCTAC TACTACCATA GGAGTTCAGA ATGGTATCAG TCCCTCAATC TAACCCATGT	300
TCCCTGAACAC AGTGCACCCA TCTTATGAAT TCCGGTGACA ACGGGTTNAG NNCAGCAACC	360
AAATTAAAAC TNGAACTTNG GCAAAAAAAG	389

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GGCACGAGGA CACTGCCGTG GAGAACATGC CCAGCCTGAA GATGAAGGTG GTGGAGGTGC	60
TGGCTGGCCA CGGTCACCTG TATTCCCGCA TCCNAGGCCT NCTCAGCCCC CATCCCNNTGC	120
TGCAGCTGAG CTACACGGNC ACCGACCGCC ACCCCCAGGC CCTGGAGGCT GNCCAGGCCG	180
AGCTGCAGCA GCACGANGTT GNCCAGGGCC AGTGGGATCC CGNAGACCCT GCCCNCAGCG	240
	240

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GGNACGAGCC CGACGGAAGN ATCCAGGGCA CCCCANAGGN TACCAGCTCC TTAACCCACT	60
TNAACCTGAT CCCTGTGGC CTCCGTNTGG TCACCATCCA NAGCGNCAAG CTGGGTNACT	120
ACATGGCCAT GANTGCTGAG GGACTGCTCT ACAGTTNGCC GCATTTNACA GCTGANTGTC	180

GCTTTAAGGA GTGTGTCTTT ANGAATTACT ACGTCCTGTA CGCCTCTCCT CTCTACCGCC	240
AGCNTCGTTG TGGCCGGGCC TGGTACCTCG GCCTGGACAA GGAGGGCCAG GTCATGNAAG	300
GGAAACCGAG TTAAGAAGNC CAAGGNAGCT GCCCACTTTT TNCCCAAATT TCTGGNAGGT	360
	360

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

AGGAGGCCGG CCTCACCTTA ATGAGGACGT TNTCGTAGCT GGTGGGATTN ATGACGTCAT	60
AGCAGATGAC CACGAGGTGG GTGTNCTGGT AGGACAGGGG CCGCAGCCGG TTNATAGTNT	120
TNTTGCCTG AANGCACAGA GCAGCGGGGG TNAGGGGACG TCCCCTTCCC TGTTGGACT	180
CTGAACGGGT GAAGGGGAAG GGGCCAGGCA AGTAAACCCT GNCTTTAGGG CCTTCAATT	240
CCCTCATCTT ATGACAATGG GGCAGCAAAG CCAGGTAGTG CTGGCACGGG CTNTNTGGGT	300
CGCAAATTGT TTGGGAAGGC TTNAGGNCNG	330

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GGCACGAGCA GCCTGTACCC TAAAATGAGT GCCCATAAGC GCTCCTTGGA TTTCCTCATT	60
NAACTGCTGC ACAAGGATCA GCTGGATGAA ACTGTNAATG TGGAGCCTCT AACCAAGGCC	120
ATCAAGTACT ATNAGCATCT GTGACAGCAT CCACCTTGGC CGAACAGCCT GAGGACTGTA	180
ACTATGNCAG CTGGCTGACC ACATTAAAGT TCCACGGCAG AAGTTGGCCT TTTTTGGTNT	240
TNGNN	245

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ACCAAGGCTTT GGCTCAAAAG AATGGATGGN GTTTCACTCT TGTGCCCCAG GCTGAAGAGC	60
AATGGCGCGA TCTTGGCTCA CCNCAACCTC CACCTCCCAN GCCGGGGTGC TCNTNNCACT	120
GCCGGGNAAG GTGATAGCCG CTCCCNAACG CTAATTAATG CGNCTACCTC ATGATGCGGG	180
AGAAGNTGGG NCGTCAATCT GCCCTGAGCA TCGTGAGGTC AGAACCNNTGA	230

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GGCACGANC GCCCCGCAGC CAACCCCCGA GGAGCGGCCG GNTGGCGTCC GNGCGCCCAG	60
GAAGTTGGGG ATGTCCTACA AACCCATCGC CCCTGCTCCC AGCANCACCC CTGGNTCCAG	120
CACCCCTGGG NCCGGGCACC CCGGTCCCTN ACAGGTAAGC NTCCCGTCGC CGTCGGGCTT	180
CAGTGCCAGG NAGCCGGCGC CTCCTTGAA AACCGCTGTT TTNAACGNAC TTTTG	235

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATCAGGGGAA ATCAAACGGA CTGTCACAAG GATCCTGCCA GATCCTGATG ATCCAAGTAA	60
GTCCCCTGTT GGGTCACCTC TAGGGNGCGC CATTGCAGAG GNCCCCAGCG AGATGCCAGG	120
GGATGAGGTG CCTGTGGAAG AGCACTTTCC TGAGGCAGGC ACAAAATTAG GGAGCCCCCA	180
GGGGGCCAGG TAAAGGGGAC GAGAGCATGA CAAAGGCCAG TAACTCGTCA TCTCCAGCT	240
GCANTTCTGG GGCCCGGGTC CCAAAGGGGG CTTGNCCCAG GTTTNACAGA CAGGCANGAA	300
GCAACAGNGC ACAG	314

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GGCANAGGTC CCCGCAGAGG AACNTNCTGC CCAACCGTT GCTGACCAAG GTGGCCGAGA	60
TGGCGCANAG CNATCCTGGT CTGCAGAAC AAGACCTGTG CCAGGAGCAC CACGAGCCCC	120
TCAAGCTTT NTGCCAGAAC GACCAGAGCC CCATCTGTGT GGTGTGCAGG GAGTCCNGGG	180
TGCACCGGCT GCACAGGGTG TGCCCGCCGA GGAGGCAGTG CAGGGTACA AGTTGAAGCT	240
GGAGGAGGAC ATGGAGTACC TTGGGGAGC AGATTACCA GGACAGGNAA TTTGCAGGCC	300
AGGGAGGAGC AGAGNTTAGC CGAGTGGCAN GGTCAAGGTN GAAGNAGC	348

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATCCAGACCG ACTTCCGCTG CTGTGGCGTC TCCAACATA CTNACTGGTT CGAGGTGTAC	60
AACGCCACGC GGGTACCTNA CTCCCTGCTGC TTGGAGTTCA GTNAGAGCTG TGGGCTGCAC	120
GCCCNCGGCA CCTGNTG	137

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGCACGAGCC GCCTCCTCCC GCCGAGTCAG CAGCAGCAGT GAGCTGGACC TGCCCTCGGG	60
NGACCACTGC NAGTTGGGN TCCTGCAGCT CGACGTGCCCTNCTCCGCA CCCAGCTCCG	120
CGGCTCCCGC CTGCTCGATG CCATGCGCAT GTACCGCCAA GGTTACCTG ACCACATGGT	180
GTTTTCCGAG TTCCGCCGCC GCTTTGATGT CCTGGCCCCG CACCTGACCA AGAACACGG	240

GCGTAACAT ATCGTGGTGG ATGAAAGGCG GGCAGTGGAG GAGCTGCTGG AGTGCTTNGG	300
ATNTGGAGAA GAGCAGCTTG NTGCATGGC CTGAGCCGGG TNTTCTTCCG GGTGGGNACC	360
TTT	363

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GGCACGAGGG CTCCAGGGNA GCCCTCTTCC CGGTGGCTTT AATATGAGTN TCGAGGGAGG	60
TCAGGGTAGG GGCAGCTACC ACGCCTGAAG CCCTAGAGGT CACCAGGCGG CGCGGGTAGA	120
TTCGGGGAA GCGCGCAGGG CTGCGCTAGG GACCCGCCGG GTCACCCCTGG TACATGGNTG	180
GCTTTNTTT ACAGTTGTT CTAACACATCA GAAATGTTG TCCGCTTTA AAAACAAAAT	240
TGGCAGTAAC AGTTTATTAT TGGGTAGCTT GATGGAACCT GTGGATTACT TAATTAAGAA	300
ATTAATAATC TGNCTTTTA ATTGGGGNTT TACCANTTTA GTGTTNTTGG GNTTTAAAAA	359

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GGCANAGCTG CCGCCGTCGC CGCCACCCGA GCGGAGCGN GCTGGGCCGC CAAGGCAAGA	60
TGGTGGACTA CAGCGTGTGG GACCACATTG AGGTGTCTNA TGATGAAGAC GAGACGCACC	120
CCAACATCGA CACGGCCAGT NTCTTCCGCT GGCGGCATCA GGCCCGGNTG GAACGCATGG	180
AGCAGTTCCA GAAGGNGAAG GAGGAACCTGG ACAGGGCTG CCGCGAAGTT CAAGCGCAAG	240
GTGGCCGAGT GCCAGAGGAN ACTGAAGGAG CTGGAGGTGG CCGAGGGCGG CAAGGCAGAG	300
CTTGGAGCGC TCTNCCANGC CGNAGGTANA G	331

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CCAGAGGTTT GCTGGCCACT GTCACTGTGT GTNTGAGGCT GATGCCAAG CGCATGGTCC	60
GGANGAACTN CCTNGTGATG AACCTGGTGN CTGTAGAAC CCTGGGGTCN ACGTCCACCA	120
TCTTCTCAGA TAAGACAGGG NANTNTNACT NAGATCCGCA TGATAGTCGC TNTCATGTGG	180
TTTGACAACC AGTTCCACGA GGCTGACACC ACTGAGGTNC CAGTCAGGGG ACCTCATTG	240
ACAAGAGTTC TNTACACCTN GGTGGTTCCT NTNTTCA	277

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTTGAAGGGG GCCAAACCCA AGCTGATGTC GGCCATCTCC AAGACCTTCT NGCCGGCCCA	60
CAANAGCTAC ATCATCGNTG GTNGTNTGGG TGGCTTCGGC CT	102

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTTTCGCGTCC TCAATTGCCN CGGGGCTCNC GCTGGGGCAC AAACNACTCG ACGCAGCGCA	60
GACGCCAAG GTGAAGGTTG CCCACGGGGA TTGCCCGGTC CATGNCCAAT GCCATGGGNG	120
TGCAACTGCT ATGTTCCATC CGNNCAANCC GCGT	154

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GGCACGACCG GGCTCGAGAG CCNCCNCGA TGCCAGTNCC CATNCGGGGC CGCCGCCAGT	60
NAACGNCGGA GAGGTGTTCC CCCCACACTG GGGCTCCCAC TACTGCGAAG GAGTGACCCA	120
CGAAGGCCAC AGAGATGCCG GGGGCTTCGG TGAAGGTGGC GGTGCGGGTC CGCCCNTTCA	180
ATTCCCGGGN AAATAAGCCG TGNACTCCAA GTGNCATCAT TGCAGATGTT TGGTAAGCAC	240
CACCACCATT GTTAAACCCC AACAGCCCC AGGGAGACGC CCAAAAGGTT TCAGCTTGG	300
NACTNATTGC TAACTGGGTT TGGGACAATC TNGNACCTNG A	341

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTNACTGGTG CTTNCTGCCG TCGACTGGTA TGCAGTCAGC ACTGTGAGCC ACTTACCTNC	60
AGGTGTNANC TCGGGGCCAG CCCCTTGCAT GTGGACCTGG CCACCCTNNG AGAAGCTTAA	120
G	121

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GGCACGNGGT AAATGCTATG AAAATAGTTA CTACACTATT GTTTATNTGT ATTTTATTG	60
AATTGTTTG GGGTGGGGGG CAGCTGTATC TTTCTTAGTA ATAGAACCCC TGGTTTTAGC	120
TGGGCACATG AACTGCCNTC AATAAAGATT AAAGTACCCC AGCCTTCCTT GAGATTGTGG	180
CCATGTGACT GAACTTTAGA CAGTGAAGAT ATAAGCAGAT ATCTNCTGTG GCAGTGTAG	240
GAAACTATTA AAGACAGTAA GGAACATTGC CCTTTGCCTT CTTTGTTCCT TNCTTCATTT	300
TTCTGCCTGG GAATGCAANG TGNATGGNTA ACACCCTAGC AGNCTTTT	348

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CCTGGACCCA CAGTCGGCCA GTGGGTACCT GCAGCTGTCA GAGGTCTGNA AGNGCGTAAC	60
CTACACCAGC CTGTACAAGA GTGCCTACCT TCACCCCCAG CAGTTGGAC TNGTAAGCCT	120
GGGGTNTTGG GCAGCAAGGG GTTCACCTGG GGCAAGGTCT ACTAGGTAAG TGGAAGTNGA	180
GNGTGNAGTT NCTGGTTCTT AAGGGATGAA GTAAG	215

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AAAAAAAACC CAACTTGACC TAGTTGTCAT TTATAGANCA CTCCATCCAA CAACAGNAAA	60
ACACATAATT TTTTCAAAT GTACACGGAA CATTGNAAG ATAGNCCACA TTCTGGTCTA	120
TAAAACAAGG CTCAGTAAGT TTAGAAGGNT TCAAGTTATA CAAAATATAT TCTCTGACCA	180
CAATTGANTT AAATAAAAAA TACCNGAAAG NTATCTAGNG ATTCCCCAAA TATTT	235

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GGCACGAGNA GTTGGAGGAG AAGAATCAAG AACTGCAGCG GGCAAGGCAA AGAGAAAAAA	60
TGAACGAGNA ACATAATAAA CGTTTATCAG ACACTGTTGA CAAGCTGCTT TCAGAACATCTA	120
ATGAGAGGCT TCAACTTCAT CTTAAAGAGA GAATGGCTGC TTTGGAAGAT AAGAACTCTC	180
TTTTAAGAGA AGTTGAAAGT GCAAAAAAGC AGTTAGAAGA AACACAAACAC GATAAGGATC	240
AGCTTGTCTT AAACATTGAA GCACTGAGGG CTGAACTAGA CCACATGAGA CTTAAGAGGT	300
GCTTNCACTT TCATCCATGG GCCGACCCCA CTTGGGGCAG TGTTCCCAGA TTTTCAGGTT	360

TCCCCATGGC AGACGGGNCA CACAGACTTC NTACCAGCAN CCAGTGCAGT NGTTGCGGGN	420
GCCCCACAGAA A	431

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GGCACGAGCC GTGATGCCAA GCTGCCAGCC TCGCGCTCCA TCCGCAACCT CTTGGCAGT	60
GGGAGCCTTC GGGCCTCAAA GAGTAACCGT GTGACTGGTG TNTACGAGCT CAGCCTGTGC	120
CACGTGGCTG ACGCGGGCAG CCCAGGGATG CAGCGCCGGC GCCGACGAGT CCTGNACACA	180
TNTGTGGCCT GATGTCCGGG GCGAGGAGAA CCTGGCAGG CTNNNTAGGCC CGGGAGTNGA	240
CAGTTTCAT T	251

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGGGTNCCCC GGGNTGCANG AATTNGGCAG AGGTACAAGC TCGNTGCCTA TAAAGCTGAT	60
GATCCAACAA TGGGGGAGGG CCCAGACAAG GCACGTTCCC AGCTCCTGGA TCCTGGATCG	120
AGGCTTGAC CCCAGCTCCC CTGTGCTCCA TGNAATTGAC TTTTCAGGCT ATGAAGTTAT	180
GAATCTGGCT GCCTATCGAA AATGNTGTAT ACAAGTATGA GACCANNGGC ATCGGGGGAG	240
GNACGTGTNA AGGGGGTTCT C	261

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GGCAGAGGNA CAAGCTCGAT GCCTATAAAG CTGATGATCC AACAAATGGGG GAGGGCCCAG	60
ACAAGGCACG CTCCCAGCTC CTGATCCTGG ATCGAGGCTT TNACCCCAGC TCCCCGTGTC	120
TCCATGNAAT TGACTTTCA GGCTATGAGT TATGATCTGC TGCCTATCGA AAATAATGTA	180
TACAAGTATG AGAACCAAGCG GCATCGGGGA GGCACGGGTG AAGGAGGTGC TCCTGGAACG	240
AGGACGACGA CCTGTGGGAT AGCACTGCGC CACAAGCACA TCGCNGAGGT GTTCCCAGGA	300
AGTTCAACCG GTTTTGNAAG AGATTTTTTC TTTTAGCAAG NGGATTGAAT TACTGGAGGG	360
AAGGCCACC NTGCGGGACC TNTNCCCAAT TG	392

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGCAGAGCCC GACGGAAGCA TCCAGGGCAC CCCAGAGGAT ACCAGCTCCT TNACCCACTT	60
NAACCTGATC CCTGTGNCC TCCNTTGGT CACCATCCAG AGCGCCAAGC TGGGTCACTA	120
CATGGCCATG AAATGCTGAG GGACTGCTCT ACAGTCGCC GCATTTNACA GCTGANTGTC	180
GCTTTAAGGA GTGTGTCTTT GAAGAATTAC TACGTCTGT ACGCCTCTGC TCTCTACCGC	240
CAGGTTCGTT NTGGCCGGGN CTGGTACCTC GGCCTGGACA AGGAGGGCCA GGTCAATGAAG	300
GGAAACCGAG TTAAAGAAGA CCAAGGCAGN TGNCCAATT TTGNCCAAGA TNCTGGGAGG	360
TTGGNCCATG TAACCAGGGG	380

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GTACTGCTTC CAGTTCTGC CCTTTGGCAA AGGCCTCATC AAGAAAGTGCC GGACCAGCCC	60
TAATGCCTTT NTGCAGATCG CGCTGCAGCT GGCTCACTTC CGGGAACAGG GGTAAGTTCT	120
GCCTGACCTA TGAAGGCCTC AATGAACCAG NAATGTTCCG GGAAGGGAAC GGACTGAGAA	180
CTGTGNCGTT CCTGTNACCA GCGAAGTTCC ACAGCCTTN TGGCAGGCCA TGNATGGGAG	240

GGGTCCCACA CAAAAGCCAG ACCTGCAAGA ATCTTTTCC AGAAAGGCTT GCTNAGNAAG	300
CACCCAGGAA TATGTNACCN GCCTGGGNCC ATGAAACCGG GGGCAGGGG ATTGNAAN	360
GGCANCTTTT TNTTGGCCTT TTAATTGGG TTNTTCCAAG TTAACTTAGG GGGTCANTT	420
TTTCCTTTT CCTTGNTTGA GGGTGGTTT NGGGGAANCC TTGGGGGNTT TTTCCAACC	480
AGGCCAGT	488

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GGCAGAGGNC AGGACGAGCT CAGCTTAAG GCCGGAGACG AACTCACCAA GCTGGNGAG	60
GAGGATGAGC AGGGCTGGTG CCGTGGCGG CTGGGACAGC GGGCAGCTGG CCCTCTNACC	120
CTGCCNAACT AACGTGGAAG GCTATCTAGA AGGCCNCCTN CCCTGCCATA CTGCCCGTTA	180
ACTCCTCCCC ACTGCCGCC CTTCCCCTNC CCACTNCTGC GTNCTCCTTC CCCTGCCAT	240
AGAAGTTTCC AGACATATTT TCCCGAATTC AAGCTTTTT ATTGTTTAA AAAGTTCAAA	300
ACCAGGAACA AAAACAAAAG TNATGCCANG AGGACAGAGN CATTNGCAG GGGCCCANCT	360
GGNAGGGTTT GGGGTGCTTG GGGGTTTGG GGAGTGGGC CCCCAGGGTT AGGTTAACCA	420
GTTNTTNAGG TANTTAGGC CCCAAGCATT CAACAAACAT CTGGGTTCCCT TTTGGGGGT	480
TTCCACCCAA AN	492

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TTCCATAATG GCTGTNCTGA TTTACATTCT CATCAACAAT GNACAAAGTGC CCTTNCTCT	60
GCATTCTCCC TAGCATTTTT TTTTTTTNT CTTTTNG	97

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GGCACGAGGG ACCCGCCCGC NATGGGGGAC GAGGACGACG ATGAGAGCTN CGCCGTGGAG	60
CTGCGGATCA CAGAACCAA CCTGNACCGG GCACGAGGAG AAGGTGAGCN TGGAGAACTT	120
CGAGCTGCTC AAGGTGCTGG GCAGGGAAGN CTACGGCAAG GTNTTCCTGG TGCGGAAAGG	180
CGGGTCGGGC ACNACGCCGG GTAAGCTNTA CGCCATGAAG GTGCTGCGCA AGGTGGNCGC	240
TGGTTGNCAG GGCCCAAAGT ACGCAAGNGT CAC	273

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GGCAGAGGCG CCCCCCAGCC CTTCCTGACG CTCAGCCTCG GGGCCTCTCT CCAACTCTCC	60
CGGCCACCG TGGCATCGGG AGGCCATGCT CAGGTCTGAA GCAGGTTTGG GGCCTGCTGA	120
CAGCAATAGC CCGCCTTTGG GAAACCCCTT GCTGTGAAAC TCTCTGCACT GCAGTGAACC	180
TTCAGTCACG AACCTGCCTC TGCCCCTTCG GGGGACGCC ACACAAAAGG GNAAGTGCTT	240
GGCCGTGCTG GTTCCTGCC CGCTGGTGGG CCTGNCCGGG GNTTGGGCGG CCGGTGAAGC	300
GGGATTGAA TGGGGATGAG GGTGNACAGG GGCCTGGTTC CTGTTCTGA GNGCCNCAGT	360
NTTGTCCCT CCTGNCCAGT TCCTGTTCCA AATGCATG	398

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GGGCACGAGA AAACTTTAC AATNAGCATG AAGAGATAAC CAACCTCACT CCACAGCAGT	60
TAATAGATCT CCGGCATAAG CNCAATCTTC GGGTCTCTGG TGCTGCACCT CCTAGACCAG	120

GAAGTAGCTT TNCTCATTTC GGGTTTGACG AACAACTTNT GCACCCAGATT CGGANATCTG	180
GATACACACA GCCCACTCCA ATACAGTGCC AGGGTGTGCC TGTGGCATTA AGTGGTAGNG	240
ACATGATTGG TATTNCCAAA NCAGGTAGTG GGNAAACTNC AGCCTTCATT TGGCCCATGT	300
T	301

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

ATNGTTGGA AAGCGCATAT TGCTTCCNTC TTCCCCGAAT TCTGGCAACT NTTCCCTCTG	60
CNATNATGGG CCCTTGGGCA TCATGAACCTT NATTACTCCT CACTGGCTGG AATTCAAAC	120
GCCCCATCTGT AGTGGTCCCG TGCCTTGACC ATGCACCTNA GAATCCACGN GANACGGAGC	180
CCTCCTTGNC GGACGGGCTG GACGNTTTG	209

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GGCACGAGGA GGAGCAGACA GCGGTGGNCA TCNCCAGCGT CCAGCAGGGCG GCGTTCGGCG	60
ACCACAAACAT CCAGTACCAAG TTCCGCACAG NGACAAATNG AGNACA	106

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TTATGAGCAG GGAGATGAAG AAGCAAATCT TGGTCTGCC ATCANTCCAT TCATGGATCG	60
TNCTTCTCCT CAACTAGCAA AACTCCAAGA NTCTTTATC ACCCACATAG TGGGTCCCCT	120

GTNTAACTCC TATGATGCTG CTGGTTGCT ACCAGGTCAG TGGTTAGAAG CAGAAGAGGA	180
TAATGATACT GAAAGTGGTG ATGATGAAGA CGGGTGAAGA ATTAGATACA GAAGATGAAG	240
AAATGGGNAA ACAATCTAA ATCCAAAACC ACCAAGGAAG GGAAAAGCCA GNCGGGCGNA	300
TATTTTNNGT CCAGCTTAAT GGCACCAACCC TTCACTTNGN AAAACCCCCA AGGTTTTT	358

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GGCACGAGGA CAACCGGGAG CAGCAGCATT TCCTGCAAGA TTGTNACGAG CTGAAGCTCT	60
GGATCGACGA GAAGATGCTG ACAGCCCAGG ACGTGTCCCTA TGACGAGGCC CGCAACCTGC	120
ATACTAAGTG GCAGAACGAC CAGGCATTCA TGGCCGAGCT GGCTGCCAAC AAAGACTGGC	180
TGGACAAGGT GGACAAGGAA GGGCGAGAGC TCACCCCTGA NAAGCCAGAG CTGAAAGCCC	240
TGGTGTCGGA GAAGCTGAGA GACCTGCACA GGCGCTGGGA CGAGCTGGAG ACCACCACCC	300
AAGCCAAGGC CCGCAGCCTN TTTTATTGCC AACCGAGCTG AGCTNGTTG NCCCAGAGCT	360
GTTGTNCCT GGAGAGCTTG GCTGGAGAGC CTGCAGGCCN CAAGTTGCAC TCCNGTTGAC	420
TACGGNAAA GGACCTTACC CAGCGTTNAA CATCCTTNTT CAAGAACGAG C	471

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GGCAGANGAT CTACTGTGTN AGGNGAGAGG GCAATTAAAA AGCTGAAGAG AAAGGAGGCC	60
CTCTNTGTAT TCCGTTCCCT CCTCCTTAAT GCCTCCAAGG GTCCTTGCAT CCCTAGTCTC	120
CTAAACTCCA GCTCTGAATT CGCCATCAAC CCATGGAGCA ATTCCAAGGC CCCAGTTACC	180
CATCACCTCC ACACCAGGTG CAAGTTTG TTCAGCCCCA AAGGCAGTGA GCATTTCTAG	240
TTTGCCCCCT CTGCCCTGNA ACCCCACAGC ATGCCTGTT GCAGCTCCCT GTGCCCTCGG	300
CACTTCCCCA GGCTCATTTG AAGCAGGTGT GCCTCGGCA GTTCCCCCAA ATTCCCAGGT	360

GCCTCATNCC TNATGNGNTA ATGGCNGTGA GGGGAAAANT TTTCAAGAAG GTGGAAGAGG	420
CAGCNGGATT NGTTAGGGGT ANCTGTNGTT CANCTTGAGA TGCACAGTGA AGGTTAGGGT	480
AGNTGGGACA GGCCTACCTG	500

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TGTATTCACC TATTNATTCT GTGGNTATAAC ATAGTGTNG GGTAGTGGAA ACACTGGAA	60
GCTTGGGCAG TAGTTNCTCA AGGATTGAAG CTTGTTCTT TAGATCTGNA GGTAGATATG	120
ACTAGGGGGA AAAACANTGG TNGAGATAAA GGCTACCATT GAAAACCCTG TAGCTCCTAT	180
CTGTGCAATT ACAATCTGGA TGCTTCAGGN AGCCCTTTT CTGGGTGCAC ANATGTAANA	240
TANCCTACAA GTCTTGGAGC AANCCTGTT TCCTTACGT TCACAGCTGT GTTCC	295

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GGCACGAGCN AGTATATGCG GCAGGCGGGA TGGGCCTGGA CCTACGTCNA CACAACCACC	60
TCCAACACTA TGACATGCTG AAGGACATGT GGGTNTCCCT AGCACCCATG CCCACCNCGA	120
GATATGCTGC CACCTCCTTC CTCCGAGGNT CCAAGATCTA CGTGCTGGGG GGACGNCAGT	180
CCAAGTACGC GGTCAACGCT TTCNAGGTCT TTNACATCGA GACTNGNTCC TGGACCAAGT	240
TTCCCAACAT TCCCTATNAA GCGGGCCTTN TCCAGCTTG TNACCCTGGA CAANCACCTG	300
TACAGNCTNA GGAGGCCTGC GGGCAAGGTC GCNTNTTACC GGAAGTCCCA AGTTCCCTGAG	360
GGACGATGGG ACGTTTTCC GNAATGGNAA ACAGGGGGGG GTTNGCTGAA GATGGAAAGG	420
TTCGTTNTTT TCCTTNA	437

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GGCACGAGCC TCAGCCTCGC TCATGCGCAN TNTCTNAGGT GCTTTGGACC ATGGTGATCC	60
ACATCGGCCT GAGCGTNAAG AGCTTGGCGG GAGGTTGGT GCTGTTCTTC TTCTTCAG	120
CCTTGCCAC CCTNACCGTG GCCATCCTCC TGATCATGGA GGGCTCTNG GCCTTTNTCC	180
ACGCACTGCG CTTACACTGG GTTGAGTTCC AGAATAAATT CTACAGCGGG ACCGGTTCA	240
AGTTCTTACC CTTCTCCTTC GAGCATATTG GGGAAAGGGN AAGTTGAAA GAAGTGAAGN	300
CCCTTTAAAG GGCCC GTGTG CCCCAATGT TAACCTTCCC GGCNTTCCTT TCCAAAAGTG	360
GATTAAAGTN GTGGCNTTTT TTTGCCTTNT G	391

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GGCACGAGCC ACAGTGCAAG CCCCTGTCCC CTGGAGAGAT CCTGGGCTGC ACATCCCCC	60
GACTGTCCAG AGAGGTGGAG GCCGTTNTGT ATCTTGGAGA TGGCCGCTTC CATCTGGAGT	120
NTGTNATGAT TGCCAACCNC AATGTCCCCG CTTACCGGTA TGACCCATAT AGCAAAGTCC	180
TATCCAGAGA ACACATATGAC CACCAGCGCA TGCAGGCTGC TCGCCAAGAA GCCATAGCCA	240
CTGCCCGNTC AGCTAAGTCC TGGGGCCTTA TTCTGGGNAC TTTGGGCCGC CAGGGCAGTC	300
CTNAAGATTC TTGTAGCACC TGGTAATNTN CGATTNCGAA GCCTTGGGCC TTT	353

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GGCACGAGCG GANCCACGGA GCCCACGGAG GAGCCCACGG AGGAGCCCCA GCGTCCGAAC	60
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GGGCAGACCC CCTCGAGCCG CGAAGGAGCC CGAGAACGAG CCACGATGTG CGGAATNTTT	120
GCCTACATGA ACTACAGAGT CCCCCGGACG AGGAAGGAGA TCTTCGAAAC CCTCATCAAG	180
GGCCTGCAGC GGCTGGAGTA CAGAGGCTAC GACTCGGCAG GTNTGGCGAT CGATGGAAT	240
AATCACGAAG TNAAAGAAAG ACACATTCAAG CTTGGTCAAG AAAAGGGGGA AAGTCAAAGG	300
TTTTTCGATG GAAGGAACCT TTACAAAACA ANGTTCAAGGC ATTGGGCTTA AAAAGTNGGN	360
GTTTTTNAGN ACCA	374

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GGCACGAGGC CCCAGGTACT ATGCAGCTGT GGAGGCCAAG AAGGAGAGAA TGAGCAAACA	60
CGCCCAGACC TTTGGGGCCA AGCAGCCCAC ACATCAGGGG GGCCCTGCAC AGGACCGCGG	120
AGTGTACCTG TCCCTCCTGG CCTCCCTCCG NACACGTNCC CAGTTNCCCG TGGTGGTGT	180
CANCTTCTCC CGGGGCGCT GTGATGAGCA GGCCTCAGGN CTNACCTCCN TTGACCTCAC	240
CACCAAGTTCG GAGAAGAGCG AGATCCACCT NTTCCGTNCA GTGCTGCCTT G	291

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GGCACGAGCC TGTGGAAACC TCTNCNAGTC CTGGAGACTG GTGCCCTGAG CTCCAACCAG	60
CGGGCCTCAT CCTACACCCCT CACCACCGCA ACTTNTNACC CGAGCAAGAA GCAGCTCCCC	120
GAGAGAAAGA ACGTTCCCAC CTGCNTAGCC ATGGGAGAGG ACGCTGCACA GGCGAAAAG	180
TTCCAGCACC CTGGGTCTGA NATGCGGCAG GAAAAGCCCT CGAGCCCCAG CCCGNTGCCT	240
TCNTTCACAC NAAGNC	256

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCCCCAGAGC TGGACAGCCG GGNTGGAGTG CAGTGGTGA ACCAAGCTCC CTGACAGCCT	60
CTNTNTCCCA GCTAAGGTGA TCTTCCTGCC TCGGNCTCCC AGGTAGCTGG NGTTACAGAT	120
CGAGCGGCAC NTT	133

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GGCANAGGNA TCCGCAGGGA CTGGCTGACC ATNAACAACA TCAGCCTGNA TGAAAGGC GG	60
CTCCAAGGAA GTACTGGTT GTGCCTGACT GCCGAGTNAC TGTCCCTGGTT ACAAGGATGA	120
GGNGGAGAAA GNGAAAGNAG TACATGCTGC CTCTGGACA ACCTCAAGAT CCGTGATGTG	180
GAGAAGGGCT TCATGTCAA CAAGCACGTT TTCGCCATCT TNANCACGGG GCAANGAAC	240
GTNCTTNCAA GGG	253

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GGCAGAGCCC CTATCAACTC TTTGGTCGAT CGGCTGGCCC TTCTCCAGGT CAGGAGGATT	60
CTNCAGCAGC TGGGCCTGGA CAGCACGTGT AAGGACAGCA TCGTGGTGAA GGAGGTGTGC	120
GGANCGTGTC CCGGCGNGCG GCCCAGCTCT GCGNTGCTGG CCTGGCCGCT ATAGTGGAAA	180
AAAGGAGAGA AGACCAGGGG CTAGAGCACC TGAAGGATCA CTGTGGGTNT GGACGGCACC	240
CTGTACAAGC TGCACCCCTCA CTTTTCTAGA ATATTGCAGG AAACTGTGAA AGGAACCTAGC	300
CCCTCGATGT GATGTGGACA TTTCATGCTG TTCAGAAGAT GGCAGTNGNA AAAGGGCAG	360

CACTGNTTCA TTGTTGTGGG CCAAGAGTTT ACAGNAGCAC AGAGGGGGAA NTAGGAACCC	420
TGGG	424

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GGCAGAGCAG GTCTGGCGG GGCACGTTTC CACGGTCTGA CCCGCCTNTC CCGCTGGTGC	60
CAGGTTGTNT CCAGCGGTTTC AAGTGCTGCC AGGTCAACAT CGAGGNAAGG GCTAGGCAAG	120
TTTTGGTGGAA TCCTGCGGAA AACCTGCTTC CTCATCGTGG AGCACAAC TG GTTTAAGAAC	180
CTTCATCATC TTCATGAATT CTNCTGAGCA GTGGCCCCCT GGTGAGGTCC AGGGGAGAGT	240
NTGAAGGAGG GATTGGCTGG GGAAGGGTGT AGAGAAGCCA GTGGGAAAAG GCTGAGGCCA	300
AAGCCCAGTG GCTCTNAAAA CAGATTGGCT GTGGTNCCAA GAAGAATGAT CTGTTAAAAT	360
GCTTTAGGC TGCTGTGGG AGCCTNTGGG ATTAGGATTG CNAATTGTT ACATNGTGT	420
NCCCTTTAGC ACTGTNCCC	439

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

AAATATGCTG CCAAGATGGG GAATCCAGCT GCTGAGCTTT GACAATAAGA TGGAGCTGGC	60
AAAGGTGGTA AAGAGCCACC CCAGTGCCAA GGTTTGTCCA GCAGAGGGGC ACTGCGTGT	120
TGCATCAGGA TGGTTCTGTG NCATTGCTAC CGATGACTNC CACTCCCTGA AGCTGCCTGA	180
GCCTNAAAGT TTGGGAGTGT CACTGAAATC CTGCAGACAC CTGCTTGAAA ATGCGNAGGA	240
AGCACCATGT GGNAGGTGGT GGGTGTGAGT TTTNACATTG GGCAGTGGCT GTNCTGAACC	300
CTTCAGGCCT ATGGTNCAGT TCCATCGCAA ACGGCCCGGN TTCTGTGTTT GAAAATGGGG	360
CACCCNGGTT GGGGTTCAC A GTTTGCCAC GTTTCTTGGG ACCCTTGGGT GGGTGGGGTT	420
TTCCNTGGGC ACCAAAAGGG GGGCCNAAAG TGNAGGTTT NNAAGGGTT T	471

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GGCACGAGAA TGAACCGTGG GGATGACACC CCCCTGCATC TGGCAGCCAG TNATGGACAC	60
CGTGATATTN TACAGAACGCT ATTGCAGTAC AAGGCAGACA TCAATGCAGT GAATGAAACA	120
CGGGAAATGTG CCCCTGGCAC TGATGCCTGT TTTGGGCC AAGATCAAGT GGCAGAGGAC	180
CTGGTGGCAA ATGGGGCCCT TNTNAGCATC TGTNAACAAG TTATGGAGAG ATGCCTGTGG	240
ACAANGNCAA GGCACCCCTG AGAAGAGNTT TTTCCGAGAG CGGGCAGNGA AGATGGGNCC	300
AGAATTTCA ACCGTATTT	319

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CCAGGAGGTG TTGCAGTNAA CCAAGATCAC ACCACTGCAC TCCAGCCTAG GCAACANAGA	60
CTCTNTNTCA AAAAAAAA AAAAAAAA AAAAAAAN	97

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

AATTCAGTA ACCGAAAAT TAAGCCTTAG TATGAAAAC TGAGGATTAA TAATTGAAAA	60
TGAAAAAAACT ATGTTACTNT CTATCATCAG AATTATAGTC TTTGGTGCTN NGTTTTCAAT	120
GGGGCATATT ACATAAGGTT GTTCTTTCA CCCCAAAGAG ACTACTAGGT TACCACTCTG	180
GGGCATTGNC TTTCCACCTT AACCCCTNAA CCAGTAAGNC TNTTACACCC TNTTGTAGGC	240

CCACT

245

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

CTGCTGCCCA ACCGGTTGCT GACCAAGGTG GCCGANATGG CGCACAGCAT CCTGGTCTGC	60
AGAACAGAAGA CNTGTGCNAN GTGCACCACG AGCCCCCTCAA GCTTTTTGTC CAGANGGACC	120
AGAGCCCCAT CTNTTTGGTG TNCAGGGAGT CCCGGAGCAC CGNCTNGCAC AGGGTGCTGC	180
CC	182

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GGCAGAGGTT CCTTGCTAT GGCAACCGTA CGTCAAAGA CAAGAGTGG A GCCTACCTCT	60
TCCCTGCCGA TGGCGAGGCC AAGCCCTACG TCCCCAAGGA GCCCCCGTG CTGCGTGTCA	120
CTGAAAGGCC CTTTCTTCTC AGAGGTGGTT GCGTACTATG AAGCACATTC ACCAGGCGGT	180
CCGGCTTTAC AATCTGCCAG GGGTGGAGGG GCTGTCTCTG GACATATCAT CCCTGGTGG	240
CATCCGGGNA CTACGTCAAC AAGGAGCTTG GCCCTGCACA TCCATACAGA CATCGACAGC	300
CAGGGGTATC TTTTTCAAA GACCTCAATG GTTTCAAGG TGGCAAGCCC CGAANGTTA	360
TTNTGAAAGG AAGTTNCCNC TTTCCNGGGC C	391

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TTTNNNCACG GCTCTCTNGT AATGCAGAAT CTGGGTGANA CTTCCACCCC CACACAAGNC	60
TCGNTGCTCT TCGGCACGGG TCAACGGCAT GATAGGGCTG GTNACCTCAC TTTCAGAGAG	120
GCTGGTACAA CCTGCCGTCT GGGACATGNC AGAACATGANC TCAATTAANG TCATNCAAAA	180
GTGTGGGTA AGATCGAGCA CTGCCTTGCT NG	212

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GGCAGAGNAT CAAATATGCT GCCAAGATGG NNAATCCAGC TGCTGAGCTT TGACAATGAG	60
ATGGAGCTGG CAAAGGTGGT AAAGAGCCAC CCCAGTGCCA AGGTTTGTC AGCAGAGGGG	120
CACTGCGTGT NTGCATCAGG ATGGTTCTGT GCCATTGCTA CCGATGNACT CCCACTCCCT	180
GAGCCTGCCT GAGCCTAAAAA GTTTGGGAGT GTTCACTGGA AAATCCTGTC AGACACCTGC	240
TTTNAAAATG CCGAAGGAAG GCACCATGTG GNGGGTGGTG GGTGTGAAGT TTTCACNTTG	300
GCAGTGGCTG TTCCTGAACC CTCAGGGCCT GATGATNCAG TTCCATNGNC AAACGG	356

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GACTTTGGAT CCAGCTAAA ATCTNACCTT NTCCTGAGCC CTTGCCTAGC CCCCACCTCC	60
ATCTTCGCTG CTCTGCTGCC TGTGCCGGGN AGGGGCTCTG TTTTTCCCCT AGAAATCTAT	120
GCCTTGCCT GGGGGCCAGG ACACCACAGG GGTAGGCTCG TNTACAGCCT CACTAGCCCA	180
AGGGCCTACG AATGCCCTCT TGGGACAGAG AAGCCTGGAA TGGAAGAAAG CTNATGCCAT	240
TNCCTTGGCT GCTGGTTCTT TTGGCATTGG GAANTCTTCC TTCTCTCTAA TGTCATNCTT	300
GCTGCTGTNC CGCTGCATTA TTTCCCTTA AATNTTTCNG GGANTTGGGG GTGAACNGNT	360
GTGGCACCNA ACCCTGGGG ATGTGCTTGG GGGAGGAAGG GGAGGGGAA GGTCTGGAA	420
NTTTTNTNTN TTTGGCCAG TTNAGGTTGN AGGNCAAGGGG GGNCCCCGTT CTGGAGGAAG	480

GAGAGCNTCC 490

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GGNAGAGGTG GCTTGAACCC GGAAGTTAA GGCTGCAGTA AGCTATCATG GCACCCACTG	60
CACTCCAGCC TGCNTAACCC AAAGAGACCT TACCTCTAAA AAACAAAAAA ACGGAATCCC	120
CAAGTAGTTA GTGTTGCATT GTCTGCTGCC GTCCAGAGCC CAGAACGCTT CCTCCAGCTT	180
GGCGCCAAGG TCCCAAAGGG CGCACTGCTG CTCGGCCCCC CCGGCTGTGG GAAGACGCTG	240
NTGGCCAAGG CGGTGGCAC GGAGGCTTCA GGTGCCCTTN CTGGNGATGG CCGGCCANA	300
NTTCGTGGA GGTCATTGGA GCCCTCGG	328

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

NAGAGCACAT CAAGGAAGAN CACAACATGT GGGCACTATC TNTNCTTCAT CGTCCTGGTG	60
AAAGTNAAAG GAACTCCACC GAATATACTG GGCCTGAGAA GTTACGTGGC AGAAATGAAT	120
CAAGGAAAGA AACCTTGACT GGTTCCCCAG GATGAGAAGC CATGTNATTG GTCAGCAGTG	180
AATTCTGAAA GGAGNACAGT NTNGNCCTGN GGAAACCTG	219

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CAGAGGACCA CCCGGACGAG GAGATGGGT TCACTATCGA CATCAAGAGT TTCCTCAAGC	60
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CGGGCGAGAA GACGTACACG CAGCGCTGCC GCCTNTTCGT GGGAAATCTG CCCACCGACA	120
TCACGGAGGA GGTACTTGAA GAGGCTCTTC GAACGCTATG GNGAGCCCAG CGAAGTCTTT	180
CATCAACCGG GACCGTGGGT TCGGCTTCAT CCGCTTGGGA ATCCAGAACCC CTGGCTGGAA	240
ATTGGCAAAA GCAGAGCTGG GACGGGCACC ATTTCTCAA GAGNNAGACC TCTTACGGNA	300
TTTCGCTTTC GTTAACAACA TGGGNNTNAG	330

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

TGCTGGAGAA CCAGACCCCCA GAGTTCTTNC AGGACGTCTG CAAGCCNAAG TACAGCGGCA	60
CCCTGAACCT GGACAGGGTG ACCCNAGAGG CGTGCCCTGA GCTGGACTAC TTTGTGGTCT	120
TCTTCTCTGT GAAGCTGCGG GNGTGGCAAT GCGGGACAGA GCAACTACGG CTTTGCCAAT	180
TCCGNATGG GAGCGTATCT NTGAAGAAC GCGGTACGA AGGCCTCCNA GGCTGGNCCG	240
TGCAGTNGGG GCGCCATCGG GACGGTGGGG CAATTTGGG TNGAGACGAT TGAGNAACCA	300
A	301

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GGCACGAGCC CAATNGGGNT CCCTNCNNCA GCCTCTACCT CTCCTNAANC CTNTGANANC	60
CNCCTACACA CACACACAGG CATACTCAGN CCCACTCAA GCTGAGAATG ATCCAACCTCA	120
GCCCTACTTT NCGGATGGAC ATATTAAGGC CANGAGGGGC GGGNCTTNCC CCAGGTCGTA	180
TGGCAGNGGG G	191

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GGCACGAGCA GGTCTGGCG GGGCACGTTT CCACGGTCTG ACCCGCCTTT CCCGCTGGTG	60
CCAGGTTGTC TCCAGCGGT CAAGTGCTGC CAGGTCAACA TCGAGGAAGG GCTAGGCAAG	120
TNTTGGTCCA TCCTGCGGAA AACCTGCTTC CTCATCGTGG AGCACAACTG GTTTNAGACC	180
TTCATCATCT TCATGATTCTT CTTGAGNANT GGCGCCCTGN TNAGNNCCAG GGTNAGAGTT	240
TAGAGGAGGG ATTGGCTGGG GAAGGGTGT AGGAGAAAGC CANTNGGGAA AAGGCTNAGG	300
CCAAAGCCCA GTGGGCTTNT TNAAAACAGA TTTGGCTGTG GGTCCCAAGA AGAATGATCC	360
TGTTAAAGTG CTTTAGGCT TGNTTGCTTT GAGCCTTGG GATTAGAATT CCATACTTT	420
TCACATTGTG ATNCCTTNA GCAATTNCC NA	452

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GGCACGAGCC CCTATCACT CTTGGTCGA TCGGCTGGCC CTTCTCCAGG TCAGGAGGAT	60
TCTNCAGCAG CTGGGACTGG ACAGCACGTG TNAGGACAGC ATCGTGGTGA AGGAGGTGTG	120
CGGACCGTGT CCCGGCGGGC GGCCCAGCTC TGNGGTGCTG GCCTGGCCGC TATAGTGGAA	180
AAAAGGAGAG AAGACCAGGG GCTAGAGCAC CTGAGGATCA CTGTGGGTGT GGACGGCACC	240
CTGTACAAGC TGCACCCCTCA CTTTTCTAGG AATATTGCAG GAAACTNTNN AAGGAACCTTA	300
GCCCCCTCGNA TGGTGATGTG GACATTTCAT GCTGTCANAA GATGGNCANT GGGAAAAGGG	360
GCAGCACTGA TTCACTGNTG TGGGCCAAGA GGTTTACA	398

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GGCACGAGGG TAAATCCTAG CTTCTCGGA AACTAAGGCA AGAGGATCAC TTGAGCCCAG	60
GAAGGTGGAG GCTNCAGTNA GCTGTGATTG CACCACTGNA CTTTAGCCTG TNTGAACAAA	120
TTTGTGGCA TAGGAATTCT TCATAATGTT CCTTTATTAA TCCTTTNTTT TTTTTTTTTT	180
TNAAAAGGGN GGCCNCTGAC C	201

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GGCAGAGGTC AATGTACATT TNATATTAAA AAAAGCCAAA ATAACAATGG GGTGAGANCA	60
GGAGGCCACT ATACCAGTGG CCAAGNAGTT CANATCCTTG GAGGCCGTCT TTGGAGAGGC	120
TCANTGGAC TCGTATTCTG GGCAGCAGCA CAGCACCGTN TGGGAACAAG GTACACCCTC	180
CCCACACCTG NGCCTTTCA CCCACAGGGC AAGGGATGTG GCGAGAACTG NNGGGCACAC	240
GTGGAAAACA GTTCAGCCCT GCCCGGGCGN TCTTTAAAG GNNGAGCTCT AAGGGATCAC	300
A	301

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GGGAGGCGGG NGGCCATGCG GNTTNCAGCC CTGAAATCTC CCAGCCGCAG AAGGGCCGGA	60
AGCNCCGGGA ACCTAGAGCT TCCACTCAGT CCGAGCCTGC NAGGTGGGCC GGGAACCGA	120
ACGGACCCCCA GGATCGGGAA GTGGCTCCGG CCTCCAGGCT CCGGGGCCGG CGNCTGAACC	180
CCATCCCTGC TTCCTACGGC ATGACATTGA ACCCCGGTGN TTGCTGACAC CCAGCTCGCT	240
GCCTCCTAAG CATTNCACTT CTGGAGCACC CTGAGTCCA TTNCGNCCCC GTAGCCCGGC	300
CAAGTTTCC TTTCCATTTC CATCCAGTGG GCAGNGCCAG GTGCACATNC TTTTTNTAAG	360
GTGGATGGGC TTTTGACCCC GTGGGTGGTT TTNCCCAGGG NNCCAAAANN CTGATTATTA	420
ANCANCAACA ANAACAAACCT TTTNGGGTNA ATTTNNAGCC AGTTTTTTN CAGCAAGCAT	480

507

TTTAAGGGGG AAANTAGTTN AATTGAA

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

CCACCTGGGA GCAGGTACAG GNTCTCTGAC ATATCTCNAT GGGNTACAAA ATGAAGNTGT	60
ACTNCCAGAC TAACCCCTAC TTCACAAACA TGGTGATTGT CAAGGGTTC CAGCGCAACC	120
GN	122

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 181 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CGGCAGGCCAT TCGGAAAAAC TTCCCCACGG CTACTGCGTC CACGTGGNGG TGGCGTGGGG	60
NACTCCCTGT AAAGNAGAGN GAGCATGGCG CCCGGAANGT CGTGAGTCGA GTCTTCCCG	120
GGCTAATCCA TGCCNGNGTG GAGGCTTCTG ACGCAAGTTG GNGCCCANGT GCTGGATCGA	180
C	181

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GGCACAGGTC TTTGCCACG GCTCTCTGGT AATGCAGAAT CTGGGTGAGA CTTCCACCNC	60
CACACAAGGC TCGGTGCTCT TCGGCACGGT CAACGGCATG ATAGGGCTGG TGACCTCACT	120
GTCAGAGAGC TGGTACAACC TCCTGACTGG ACATGCAGAA TCGACTCAAT AAAGTCATCA	180
AAAGTGTGGG GAAGATCGAG CACTCCTTCT GGAGATNCTT TCACACCGGA GCGGTAAGAC	240

AGGAACCAGC CACAGGTTTG CATNGACGGT NNACTTGAT TGNAGAAGTT TCCTGG

296

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GGCANAGGTG GCATATTCCCT GTAATCTCAG NCTCCTNGGT AGCTGGGACT ACAGNNACAT

60

62

GC

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GGCAGAGTNT TTTATTTAAC ATGATTTC TATATCGTTA CTGTCGAATG CTAGANGAAG

60

GCTCTTCCG AGGTCGGACA GCAGACTTG TATTTATGTT CCTTTTGTT GGATTCTTAA

120

TGACCCCTTT TGGTCTGTT GTGAAGCTTA GTTTCTTGG GCCAGGCCTT TACAATAATG

180

CTCGTCTATG TGTGGAGCCG AAGGAACCCC TATGTCCGCA TGGAACCTCT TCGGCCTTCT

240

CAACTTCCAG GCCCCCTTTC TGCCCTGGGT GCTCANGGA TTTTNCCCTG TTGTTGGGA

300

ACTCAATCAT TGTGGGACCN TTTTGGNAA TTGCAATTG GACAACAAAT AATNTTCCT

360

TGGAAGATGT AATTTCCTAA TCAAACCGGG NGGNATAAGA ATTNTGAAAA AAACCAATTN

420

431

TTTGAAAAG G

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TGAATGGTGG GCATGGNTCA GAAGGATTCC TATNTGGCG AACGAGGCC AGAGCAAGAG

60

101

AAGGCATCCT TCACCTTGAA GTAACCCNAT NGNAGCACGG T

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GGCAGAGNCA GGCCTTCTCA GGAAGAAAGT GGAGGTCTG GCTGAGGCCT GCACAGACCT	60
GCTTTCGCAC CAGAACGAGC TCACCGTGGG CCTGCCGCC GAGCCCCGGG AAGAAGATCA	120
TCTCTGNGNC CCCTTCCCCC AGAGGAGCTT CANAAAACTN CATCTACGNA GGCCAGTGGG	180
CAGGACATCA GCATTGCCGT CCTTCACGCA GGAGGATTGT GGTTTACCTG GCCATGTTAT	240
GTTCAGGGNC GCACAGACCT NCTTTNTGG GAGATTGCTT GAGACTNCGG ATTGGGANTG	300
ATCATTCAAGG TTGTTGGGCC ACGGGAGCNT NGGCACGGAG CCTTGAAANT GNTTCAAGGA	360
GGAAGAGGNT TTTTNGAAAN TTTTGATGGA ACCTTCAGNC CTTTGATT ATGNAAAAT	420
TTTCCTGNAA CCATATTTT AAGTGGGGGA AAAAGTTTG GGGTTGAAA GAAGTTTNCN	480
	480

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

TTGGCTGGGA CTGTCTCCAC GCTGGGGTAC AAGTTCTTCA CGCNCATCCT TGAATCAAAA	60
TTCAAAGTCC AAGACACATG TGGAGTNAC AACCTCCATG GGATGCCGGG GGTCTGGGG	120
GCCCTCCTGG GGGTCCTTGT GGCTGGACTT GCCACCCATG AAGCTTACGG AGATGGCCTG	180
GAGAGTGTGT TTCCACTCAT AGCCGAGGGC CAGCGCATGC CCACGTACA GGCCATGCAC	240
CAGCTCTTCG GGCTGTTGT NACACTGATG TTTGCCTCTG TGGGGCGGGG GGCTTGGAGG	300
CATCATATTG GTNTTATGCC TCCTAGANCC CTGTGCCCTT TGGGATTGGG TNNGCAACCT	360
TCTTCCAAGG TGGGGGGCA AAGAAGNCTT NAAAAATTCT TCCCTTAACC ANCAACCA	418

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GGCACGAGCC GGTGTTATCC TCCAGTGCTG AGACAGGCCG TCTCCCTGGC CCGGCGCATC	60
CAGGACCCTC TGATTGAATT TGCCCAGGTG TGCAAGTCCG ATGAAGACAT CCTGTGTCTC	120
AAGTTTCACC CCTTGCAGGA GCATGTGGTG AAAGAGGAGC TGCTAACGC CTTGTACTGT	180
GTAATTATC AACCGAGTCA ATGAGGTCGG GGTTGATGTC AACCGTGCCA TTNGCCCACC	240
CTTACAGCCA GCCCTTGATC CAGTATGTTT TNTGGCCTNG GACCTTGGAA AGGGACCCAC	300
CTACTGAAGA TCCTGGAAGC AGAACAAACAA CCNGGTTNNG	340

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

TACACACTTT TAAACAAACCA GCTTCACAG GAATTCACTC ACTATCATAG GAACAGCACC	60
AAGGGGGAAG GTGTTAAACC ATTCAAGGAGA AACTGCCCC ATGCATTGGN TAATNATCTT	120
CCACCAGGCC CTACCTCAA CGTGGAGAT TNCAATTGCA CATGAGATTG GGGCAGGGAC	180
ACAGATCAA AACATATCAG ACCTAAAAGC AGTCATGGG AGACCACTGA ACAAGCGCAA	240
AGTCNCCTGA GAATGTGCGT TCAGGGTGT NCACANAAGA GGCANAGNGG TCGATGTGGT	300
TTG	303

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GGCACGAGCT CGTGCNGTTC TAAGTCACTA GGAGATGGTA AAAGCAATAC CATGAGACTT	60
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CCGAGGCTAG GGTACGAAAG GATGGCTTCT GCGTGGTGCT CANTCTCTCC CAGATCCCTT	120
GCTCTGTAGG AAACCAACCC CCTAAGGCCT AAAGATGGAA GTGACCCAGG TGTCTACTGA	180
TGGATGAACA GATCAACAAA GTGGGATGTA TTCACACAAA GGAATATTAT TCAGGGGGGA	240
AANGGAAGNA AATTCTTGAC ACATGGNTAC AACATGTAAT GAACCTTNGA AAGACATGAA	300
TGCTGGAGTG AAAATAAAC TTAGTCACAA AAAGGACCCA ATTAACTNGC ATTGAGNATC	360
CCCANTTTNT TATTGGAA	378

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GGCAGAGGAT TTTATTTACT ATTATTTAG AAAAAGTAGG CAGTAATTTC GAGTCAACTG	60
CTTTTTCTAA ATCATTTAAC GTGTTAAATG AGGAACCCTA CTGCACAAAT GTAGGGTTAA	120
GTATCACTTT TGAAGGTTA CTTCAAAGTA AGTGNAAATTA AGGCTATCAA GGGAAAGAATG	180
TTTTTGGCTA TAAACTGGCA TAAAGAAAAN GAAGAACTGG GNGAAATTAC TGAACTAGAG	240
GAAGTNCATC GGAACTAGAG GTGTTGAAC AAATTATTTG TAGACGTGAA TCCGGCTTTC	300
CATTGTNCCG GGGGAAATT TCCCATGGTT TTNGTTGGT CTTCTTCGNC CCAGGTTCCA	360
TTAATGGGCC ANGNNCCACA CATTGGGGG TGGGTTAAG GGNACCGGGN AAATTAAAC	420
CCGTTAAAAA AGGGGGGGGG GGGGGGNCCA AGGNTTCCCC CCNTTGGGG AAAGTGGGTT	480
	480

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GGCACGAGGC AAACANCTCA GCAAGCTCCT TCTTGTCCAT GGACACTGGT GTTATACACG	60
GGTTTCCAAC ATGATTCTCT ATTTTCCTA TAAGAATGTG GNCTATGTGA AACCNCCCTT	120
TCTGGTACCA CNNCCTTTG NGGGATTTTC AGGG	154

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GGCANAGGGA AAAAGCCATT CTACTAACGT CTGTCCTTGG ACAATAACAC CAGTAGGNNA	60
ATGCTGAGTT GGAAAATTA GCAAATCTAG AGTCTTCTCT GGTTCTATTTC TATTNATTAA	120
AGCTTTATGG GACTTGCTTT NCGATTAGCT GCAGCTCCTG CCCTTAGCTT CTTTNGTTNA	180
ATTGCCAAG GGCTAGTGAA GACTTAGGTT CTCCTCCAAG GTTAGAAAAT TNGNTAA	237

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GGCAGAGCAC AGATGCTGTC CTGAGCAGAT GGCATGTAAT GCCCGCACCA NCCGTTCTGG	60
GGTCACGTGC AAGAGGCTGG CTGGAAATNA TGCCAGGCAT GCTCTTGCCA CCAGAGAACCC	120
TCTTGCCCTG TTCTNATGTG CCCCAGAGCC CAGTNTTGGG CCTCCCTTG AACGCTCCCC	180
TTCGTGCCCTG CTACCTGTGG GAAGGTCTCT TCTGAACCTGC CCCTGTCTG TTCCCAACAG	240
GTTCAAGGCCA ACAAGGTGAA GAAACTCTCC ATCGTTGTCT CCCTGGGGAC AGGGGGGTTTC	300
CCCACAAGTG CCCTGTGAAC CTGTNTGGGA TGTTTTTCGT TCCCAGNAAA NCCTGGGGA	360
GGTTGGGCCA AAATTGTTT TTGGGGGCCA AGGNAATGGG GGAANATGGT TGGTGGGATT	420
TTTTNAATTT TGGGG	435

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GGCAGAGCTT TTGACCCCTCA TTTCAAGATC AACAAATGCAG TTTCCAATAT CATTGCTCC	60
ATCACCTTCG GAGAACGCTT TGAGTACCAAG GATAAGTTGGT TTCAGCAGCT GCTGAAGTTA	120
CTAGATGAAG TCACATACTT GGGAGGCTTC AAAGACATGC CAGCTCTACA ATGTCTTTCC	180
ATGGATAATG AAATTCCCTGC CTGGACCCCCA CCAAACACTCTC TTCAGCAACT GGGAAAAAAC	240
TGAAATTGTT TGTTTCTCAT ATGATTGACA AACACAGAAA GGNTTGGGAT CCTGCCAGAA	300
ACAAGAGACT TTATTGATGC TTACCTTAAG GAATGTNCAA GGCACACAGG CAATCCTACT	360
TCAAGTTTC CTGGAGGAAA ACNTCNTTGC GGCACCTGGA CNTTTTTTG CCGGANCGGG	420
ACAATTCCA ATTGGGGTTG GGTTNG	446

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAGCCGGCCG TNCTGCCAGC TGCNTGTAAT GCAGGAACCT GGCTGCACCA TGGGTATCTC	60
CTCCANCTGC AATTTTCCTT TCTNTACTTT NTGCAGGTTN ACCTACCATG GGGTCTCCCC	120
ATGTTAAGGT GACTGCAGAG AAAATTAATG GACTTACGAA ATGATTACCT GCANNCGGAT	180
GAGGCTAATA AAGATTTTG GTTCAAAGGT ATGGTAAGAG AGTGAATTCA GAAAGGCACT	240
GGNAAGAGAA TGGNAAAGTT AGGGTGTGGC TAGAGANGGA NCTTCAAAGA GNCTGCCCAT	300
GTTGTGGAAC TTCCCATAG	319

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GGCACGAGGA AAAGAATTAG AGTTCTTGAA AAAACTTAAT GATGCTGATC CTGATGACAA	60
ATTCATTGT CTGAGAACTC TTCAGGCACT TCTATCACAA GCAGCATCTT TGTCTGGTAT	120
TCGAGCCTCT CAGCATGAAC TTACGAGAGG TGTTAAAAAA ATATGGTAAA GATGTTGGTC	180
TTCATATTAA AGCTGTAAGA TCCTATAGTT CAGCAGTTGT TCCTGGCATT GAAACTCCTT	240

AAAAGATGCA TATNGTACAT GCCGATATCA AGCNAGACAA TATTCTGGGT TAATGGNATN	300
CCAAAACNT	309

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GGCANAGGGC AAAGTCCACA CTGGGAAACG GCCCTATGAA TGTAGCCTGT NTGGGAAAAC	60
CTTCACTACC AGATCCTACC GCAATCGGCA CCAGCAGTTC CACACTGAAG AGAGGTCTTA	120
TGAAATGTAC AGAGTGTGGG AAGGCCTCA AACATAGTTC CACCCTCCTT CAGCACAGA	180
AAGTCCATAC TCCAGAAAGG CGTCAGGAGG ACAGGGCACA TGGGGAAGGT CGTTAGCTGC	240
TTAGCACCGT GTTCCATCAG GAAAGGTCTT ATTNCAGAA AGGNGGTTAA GGAGAGTTGG	300
CCCTTNAGAN TTCCCTTCCG AAAGGGTTA AAACCTGGC AAATTCCCAA CAACCCACCC	360
CCAGGGNG	368

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GGCACGAGCG GCACGAGGGG AGATCCTAAT GAGGACATTG TGGAGAGAAA CATCCGAATT	60
ATTGTTCCCTC TGAACAAACAG GGAGAATATC TCTGAATCCC ACCTCACCAT TGANAACCAG	120
ATTTGTGTAC CATTGTCTG AACCTCTGTG AAAAATGTG AATCCTACAG AAGTGGAGCT	180
GGATGAATCA GATAGTTACT GCTTACCCAG AGCAATATCT GTGAATGGAA GNCACTGCTT	240
ACAGAGACCT GCTTACACTT ATGNACAGAA ACAAGTGCTT ACACAGCTGT GGGTCCCCA	300
CTTCGTNATT ATGGGTTGGT GAGGACCCAA AATTGGGTGG GGAAAACAGG CCTTTAAANC	360
CCCCAGATTG GCCTTGTAA TTCCCTG	387

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TGGGGGCTCT	TGGGTTCCCTC	GTCTGCTACA	CAGAAAGTGAG	GAGATTCCCC	TGACTGATCT	60
CATGTTGTTA	AGTGTCTAT	CCATCCCCAC	CACACCCCAA	CTTCTTCATG	NAAGCAGGTN	120
TCCATCCTTA	TAACCTGAGA	GGCTGTGAAT	CATTCCATAG	ATGTNGGTCT	TCTGCTACCG	180
NTCTTCACAT	TGCCTCTACA	TACCAGGTCT	TCAGCTGCAT	TCTAGGAAAC	ATCATATACT	240
ATTGGATTGC	AAATCTATAA	ATAATATAAG	ACAATGGACT	GACAGGGGAA	AAAAGTTTTT	300
TTTTAAGTTT	ACAAACTNCA	ATCCCACTTG	TTGGCATTTC	NAAGGGGGCN	ATACTTTTTC	360
CTTNATTCCA	CCGTTAAAG	AAGTTTNGGA	ATT			393

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GGCACGAGTG	GNAATTAA	GGGAATGAAA	ATTAAACCTG	GCTCAATGGG	NAAACCTTCT	60
CCTGCTTCG	ATGTTAAGNT	TGTAGATGTA	AATGGCAATG	TTCTACCTCC	TGGACAAGAA	120
GGTGATATTG	GCATTCAAGT	TCTACCCAAC	CGACCATTG	GCCTTTTAC	TCATTACGTG	180
GATAATCCTT	CAAAAACAGC	TTCAACTCTA	CGAGGCAATT	CTATATCACT	GGGGACAGAG	240
GATATATGGA	TAAAGATGGG	TATTCTNGT	TTNTTGCAA	GNGCAGATGT	TGGCANATAT	300
NCCCTGGTTN	TCGATTGGC	CCCTTGGGT	GGNAAATCCC	CCATTNNCAC	CCCTTANTTT	360
AGAGTNCCCT	TTTCAAANG	CCCNACCCCT	TCAAGGGGGG	NGGTNAAAGT	TTTNGGNTTT	420
AAAACCCNTT	TCNANGNCCA	NTTCAGGGCC	CCTTTAAGG	GGTCCGGGG	CTTTAAAAAA	480
CTCCGGGCCT	TNAATTCCCC	CAGGGGGG				508

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GGCAGAGNCA GAAGC _{AA} AT CAGGGACTGC TACTCCACAG AGATCGGGAT CAGTTAGCAA	60
CTATCGATCT TGCCAAAGGA GTGATT _C AGA TGCTGAGGCT CAAGGAAAAT CCTCAGAAGT	120
TTCTCTTACC TCATCTGTGA ACCTCACTTG ACTCTTCTCC TGTTGACCTA ACTCCAAGAC	180
CTGGAA _G TCA CACAATAGAA TTTTTGAGA TGTGTGCAA _A TCTAATTAAA ATTCTTGAC	240
AATAAACAGA AAAC _{TT} GCT TATTTC _{TTT} GCAGCAATAA GCATGCATAA TAAGTCACAG	300
CCCAATGCTT CCCATTGTAA TCCAAGTTAT ACCTAATT _{TT} TAACCGGGGG TTNGGGNTTT	360
NGGATTGCAA TTTGN _C ACCG GGGTTGGGA CCAGGTTTT TN	402

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGCANAGCNG AAACCGNGTG CGCANCGATN AAGCAACCTN AAGGACCCC _A GGAACCCNGG	60
NCTGNGANGG AACGTGCTCA GTGGGGCCAT CTCCGCAGGC TTATAGCCAA GATGACGGNA	120
GAGGAAATGG CCAGTGAATG AACTGAGGGA GTTGAGGAAT GCCATGACCC AGGAGGCCAT	180
CCGTGAGCAC CAGTGGCCAA GANTGGCGGN ACCACCACTG ACCTNTTCCA TGNAGCAAAT	240
GCAGGAAGAG GANTGCAC	258

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GGCACGAGCA GATGTTCACA GCAGCACTAT CCATAATAGC CAGAAAGCAG AAGCAGCCC _A	60
GATGCCACC AGCAGGTGNA TGGATGGACA GACTGTGGTC TGTCAGTGAA TGGAATATTA	120
TTCAGCCCTT AAAAGGAATG AGGGACTGAC ACAGCACACA TGAGTNTGGG AAACAGGATG	180
CTGAGTAAAN GAAGTCAGAC ACAAAAGGCC ACACATTGTG TACTGTGTGA TTCCATTCT	240

GTGNAATGCC CAGATTAGCA ANTCCGTAGA AACAGAAAGTA GATGAGTGGT TGCCAGGAGA	300
TGGGGGAGAA GGAGCGGGGA GTATGTTCAT TCAGNCTGGA TTTCNTTAAC AAATGCCACA	360
GANGTTGTTT TAAACAAACAG ACATTATTT TCANGTTTG GAGGTGGAGT TCTAGGCGNG	420
GTGCCTCAA TTTCATTCCC ATGAGGCTTG TTCNTGGTTG CAGAGGCCAC CTTTTATTTG	480
TTCCCCACNAN TTTTCC	496

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ACGNNTNAGT NGCCAAC TAC GTGGTCCAGA AGATGATTGA CGTGGCGGAC AGGACCAGCG	60
GAAGATCGTC ATNGCATAAG ATCCGGCCCC ACATCGAAC TCTTCGTAAG TACACCTATG	120
GCAAGCACAT TCTGGCCAAG CTGGAGAAGT ACTACATGAA GAACGGTGT GACTTAGGGC	180
CCATCTNTGG CCCCCCTAAA TGGTATCATC TGAGGCAGTG TTCACCCGNT GTTNNNCNT	238

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GGCAGAGGGA AATGGATCAN AGGATTCAAG CTGCAGAAC A TAAGACACGG AAAGACGAAA	60
AACGCAAAGC TGAGGAAGCC CTCAGTGACC TCAGACGTCA TATGAANCTG NAAGTAGGAG	120
ATCTGCAGGT GAACCATTAA AAAGCTAAGA AAGCTCGAAG AACAAATCAA ACGCGTAAGT	180
CCAAAAGGAA GATGTGGCTG CATTGAAAAA ACAAAATTAT GATTTATCCA ATGGGNAAAC	240
CAGAAGTTAA GAAAGACCTT TTAGAAGCAC AGACAAACAT AGCCTTCTT CAGAGTGAGT	300
TAGATGCTTT TGAAAAGTGG TTATGCTGAT CCGAGTCTGA TTACTGNAGG GNTCTTGAA	360
TTATTCCGGG CTTACCCNG AGGTTCGAAT TNGTNNTT	397

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GGCAGAGTTT CAAACAGGTA TCTAAGAACT TCAGTGAAAGT ATTCCAGAAG TTAGTACCTG	60
GTCAGCAAGC TACTTGGTG ATGAAGAAAG GAGATGTGGA GGGCAGTCAG TCTCAAGATG	120
AAGGAGAAGG GAGTGGTGAG AGTGAAGAGG GGTTCTGGCT CACAAAGCAG TGTCCCATCA	180
NTTGACCAGT TTACTGNAGT TGGAATTAGG GTGTCATTAA CAGGAAAACA AGGTGAAATG	240
AGAGAAATGC AACANCTTC AGGTGGACAG AAATCCTTGG TAGCCCTTGC TCTGATTTTT	300
GCCATTNCAG AATGTGACCC GGCTCCTTT ACTTGTGGA TGAATTGACC AGGTCTNGGT	360
GTTCCAGCAC AGAAAGGCTG TTTTCAGTTT GGTTTGAA CTTGCTGTAC AGTCATTAA	420
TTACACTANT TTTNGGCNGA ACTGTTGGGT CANTGNCATT T	461

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GGCACGAGCC AGTATTGAGT ATCTNTNTCT AGAGCGAGCA AGAGAGGGAG AGAGGAGGAA	60
AAAATACACA TANTACAAAC ATACATGCAT GCACACATAC ATACACATGT ATACACACAC	120
ATAATTTGAA AACTGNTTGG CACTTCAACG NTGCTGAAAT TGTTTTAAA TTGAAGTTTC	180
TTTCTTCCAC AAAGCAGCCG TTTCTATTCA AATGGANATT CAGTACCAGA GNNTAAATGT	240
CTATGTAGTC ATACTGATTT TAGATAGNTA AGGGCTACAG CATACTANNT CGACAACCAA	300
NTTTGTCATG TGACTAAACC GTTTACTTTC AGTTGGGCT TACCATTACT GGTTTCCGC	360
TTGGGGNNNT TTTT	374

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GGCANAGCCA GACGGAAC TG GAAACCAGC TGGAGTACAA TAAGAGGC GA GAAAGAGAAC	60
TGCACAGAAA GCATGTCATG GAACTTCGGC AACAGCCAAA AAACCTTAAAG GCCATGGNAA	120
ATGCAAATT A AAAACAGTT TCAGGACACT TGCAAGTACA GACCAAACAG TATAAAGCAC	180
TCAAGANTCA CCAGTTGGTA AGTTACTCCA AAGATTGAGC ACAAAACANT CTTAAAGACA	240
CTGAAGGATG AGGCAGACAA GAAAAC TTGC CATTGGCA GAGCAGTATG AACAGGGTAT	300
AATTGNNATG ATGCCCTCTT CAAGCNTTAC GGCTAGTTGA GGCTCCAGGA GGCAGTTGCC	360
CGGGCCTTGN GGNTACCG	378

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GGNAATGGTT ACAAAAGCAAC CATTGATTAG AAGTATGCGA ACTGTAAAAA GGGGAACCTTT	60
AAAGTTAATA TCTGGTTGGG TGAGCCGGTC CANTGANCCA CAGATGGTCG CTGAAAATTT	120
TGTTCCCCCT CTGTTGGATG CAGTTCTCAT TGTTTATCAG AGAAATNTCC CAGNTGGTAG	180
AGAACCCAGGA AGTGNTNAGT ACTATGGCCA TAANTTGTCA	220

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

TTTTTTTTNTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNNNTTTTN	50
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(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GTAATGCTCC TTTNNCCCC CGGCAAGNTC TCAACGNCCC TAAACCTCTA TATCCCCACG	60
ATGGCCTTCA TTACTTACGT NCTCCTGGCT GGAATGGCAC TGGGCATTCA NAAAAGGTTC	120
TCCCCTGGNA GGTNNTGGGC CT	142

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GGCANAGTTG GCACCCCTG GCAAGGCNGG TGGGGCNCC GGGCCCANCC TCCCCCAGGC	60
TTGGTGTACC CATGTGGTGC CTGTCGGAGT AAGGTGAACN ATGATNAGGA ATGCNAGNCT	120
GTGTAAGGCC TCCTGCCAGA AATGGTTCCA CCGTGAAGTG CCACAGGCAT GGACTAAAAG	180
CGCCTATGGG CTGCTGNACC ACTGTNAGCT TCTNCCGTCT GGGCCTGCAA TCTCTGCCTC	240
AAGACCAAGG AGATCCAGTT CTGTCTACAT CCGTNAAGNG GCATGGNNGC AGCTNGTGGC	300
TNCTAACGGA ATGGG	315

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

TGCCCTGGGC CTGNACTGNG GGTTCTGGTG GGACATNATT TATTGGGAAC CATGTTGCAT	60
GCATNAAGGG AGTGNCGCAA AAGCAATGCA GCAGAACGCA GGGNGCCTCT GTGAGGNCAC	120
ATTGTGGNNG ATGGTGTGT CTTAGNTGAG AAGATCACTG NTGGAAACTT CCTGGCT	177

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

CCAGCTGAAT TTTAAAAANT ATTTAATAGT GACAGGTCTN ACTGTNTTGC CCAGGCTCGT	60
TTTGAACCCC TGGGNCCAGG CGCTCCTCCN ACCTTGAACC TCCCAAAGTT CTGGGAGTTA	120
CACATGTGAG GCCANCACAC CAGGNCCAGA CTGGGTGAAT TTATGAANGA AATTAACTT	180
CTGCCACAC CGNCCNGCCT CCCCGCGAGA	210

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GGCACAGCGG GCTGAGAGGA GCGTGGCTGT CTCCTCTNTN CGNCATGGNT GTGCTCGGCC	60
ACNGATATCG GTGTACTCCG AAAAGGGGGG AGTCATTGG CAAAAATGTC ACTTGCCCTG	120
GCTGTATTCA AGGCTCCTAT TCGACCAGAT ATNGTGAACT TTGTTCATCG CGNACTNTGC	180
GNCAAAAACA ACAGNCAG	198

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

CACATGAAGT GTTACAAGTG TTGAGGACTG CGGGAAGCCC CTGTNCGNTT GAGGCAGATG	60
ACAATNGCTG CTTCCCCCTG GGACGNTCAN TGCTGTGTG	100

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GGCAGAGCGA AAAAACTTCC ACTTCCACGA CTGGAGTGTG TGCCAGCCTG TGGTGAGGGC	60
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TTCTACCCAG AAAGAGATGC CGGGCTTGCC CCACAAAGTG TGTTCGAAGG TGTGAACGAG	120
AACTGCTTGT AGCTGTGCAG GCTCCAGCAG GNAACTGTGA GCAGGTGTGA ANACGGGCTT	180
CACACAGCTG GGGNACCTNC CTGCATCACC AACCAACACGT GNCAGCAACG CTGACGAAGA	240
ACATTCTGCA AGAATGGTGT AAGTNCCAAC CGGCTGTGCG AAACGNTAAG CTNCTTGCAT	300
TCCAGTTCT GGCTGGCCNG CACGTTGACC TCCTGGNCC GGGGT	345

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

CATGCACTTT GCCTTCGGAA ATGGCTGTAC ATTCAAGATA CTTGTCCAAT GTGCCATCAG	60
AAAGTATACA TCGAAGANAT NATCAAGGAT AATTCAAATG TATCTAACAA CAATGGATT	120
ATTCCACCCA ATGAAAATCC AGAGGAAGCT GTAAGAGAAG CTGCTGCTGA ATCTGACAGG	180
GAATTGAACG ANGATGACAG TACAGATTGT GAATGATGAT GTTCAAAGAG AAAGAAATGG	240
GAGTGATTCA GCACACAGGC GCANAGCTGA AGANTTAAT GATGGATTAC TGACTGATGA	300
AATTAGCTTT TATTAATGGT TGAGGTATTG GTTTNAAATT CCAGTTCCNT CCAAATGGGG	360
TAATATCCCT TCACCTTCAT GTGTAACCAG GCACAAAAAC AGTTTCATGT GGATCCGTGG	420
ATGGGTTTTN CNTTTACNGT NGATGTGNTA C	451

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GGCACGAGGC CAACGGTACC TGTTTATGCG AGGAGGGCTA CGTTGGTGAG GACTGCGGCC	60
AGCGGCAGTN TCTGANTGCC TGCAGTGGGC GAGGACAATN TGAGGGAGGGG CTCTGCGTCT	120
NTNAAAGAGG GCTACCAGGG CCCTGACTGC TCAGCATTGC CCCTCCAGAG GACTTGCGAG	180
TGGCTGGTAT CACGAACAGG TCCATTGAGC TGGAATGGGA CGGGCCGATG GCAGTNACGG	240
AATATGTGAT CTCTTACCAAG CCGACGGCCC TGGGGGGTNT CCCAGNTCCA GCANCGGGTG	300

CCTGGAGATT TGAGTGGTGT CACCATGANG GAGCTGGAGC CAGATCTTC CATNCTCAAG	360
GGCTACAATT TAAGACGTTA ACAGNGACCA CCTTGGAGTG CAANGGGNGC CTTTT	415

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GGCANAGGGT AGACGGAGCC GCCATCCGCA CTGCAGTCCC CTCTCGGCTG CTTGCTCAGC	60
CTGCTCCGGC CCCGGTCTGC CCCCACGGAG CTCCGGGCAC TTGTGGCAGA CGAGCCCGAG	120
GACCTGGACA CGGAGGACGA GGGCCTCATC AGCTTCGAGG AGGAGCAGGC CCAGCTGTCC	180
TTCAACACGG ACACGCTCTG CTGACCACCC AGAGCTGGC CANGGAGGAC ACGCTCCACT	240
GACCACCCAG AGCTNGCCA AGGACTAAC AATGGGGAC ANAAGTTCCC CANTTGCCTG	300
GCNAAGGGCT GG	312

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ACAGGAACCT NGTGTCTNGT GGCTNGCCCG NGTGCCTGAT NATGAAGGGA GATTCTATG	60
TCATTGAATA TGCTGCCTGT AATGCCACCT ACAATGGAAA TTGTTNACCC TGGGAGCGAC	120
TTCGGCCAGN TAATCCAAT CCCCTGGCA ACCAAAGGNC AGCTTCTTGA AGGTTACCAT	180
GGGCTGTGCC CGNGGGATCT NGAGAGNAAG	210

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAAAGNGGAC GCCCAGGGGT GCTGCATNGC ACAACCAAGT TTTTGACAG CGGGAGNGGN 60
CCCGGGNGCA GAGGTAGTAC GCTAACAAAG ATGTGTTAAA GAAATCTTAC TCCAAGGN 118

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CACCTCCGAG AGCCTGGATG TNATGGCGTC ACAGAAGAGA CCCTTCCCAG NGGCACGGNT 60
CCAAGTACCT GGNCCACAGC AAGTGACCAT NGGACCATGC CAGG 104

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

ACTTTGGACG TTCAATGTCT GTGGAGAAGA TAGACATTAG TCCGGTTTN CTTCAAAAG 60
GAAGCACAAA GATTGCNCTA TATGGTTAG GATCCATTCC AGATGAAAGG CTCTATCGAA 120
TGTTTGTNAN TAAAAAAAGTA ACAATGTTGA GACCAAAGGN AAGATGAGAA CTCTGGTT 180
AACTTNTTTT TGAATTTCATC AGAACAGGTG TAAAACATGG GAGTACTAAC TTNNNTCCAG 240
AACAAATTTTT GGTTGANNTTC ATTGANCTT 270

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GGCACGAGGT ATTTTNACT GGATATTGCC TTTNTNCTTT TNCTTGGTGC TGCCTTGTAA 60
TACTTNCTCT TGTCTTGGGT GANAAAATTT ATCTACAGAN NAATCAAAAG TTTGTGGTCT 120
AGAAAATAAGC ATAGCACAGT TAATGGNCAT TACCACAATG GAATCCTCAA TGGCAAGTAC 180

ANAAGAAATG GCCATATTAA ACATGAAAAG AAAGTAAAT GAGCCAACAG CCCAGGTGAT	240
AGAAATAAAT TGGTTCACTC ATTGAATTTC TATTGCTATT ATTAGTCTA ACAGCTTACT	300
TAAAAGTAAA ACATCAGTAA ACAATTCTTA ACATGCCCTT ATGAGANCTA CTTAATGAAA	360
TTCCCTGTGGG ATTNAAGGTG GCTGTAAAAA GCACAAACCT AAAATNGCAG AAATGTNNNTT	420
NATTCAAAT ACTGATGTAG GGGGTTTTTG GCA	453

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

TTACAGAGAA CATATGCACA CTANNNNGAT CTCACAATTAA TCAACAATGA AATTNATGAG	60
ACAATCAGAC ATCTGGNGGA AGCTGTTGAG CTCGTGTGCA CAGCCCCACA GTGGGTCCCT	120
GTCTCCTGGG NCTATTAGGN CTNTCCCCAG ATATCTGGGG CATAACTGGG AGCACCTCAT	180
TTGTGGAAA GCCTCTTGT TATCGGGCTT GTGTCAGCAG GTCATGGTCC CTAGAGACTA	240
CCTAGTTGTT AGTGTGACC TACATTGAT AATTAATTGT CAGTTNCNAN TAGTTANGGG	300
GGGGGAAAAA NCATTTACAC ACT	323

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GGCANGAGGN GCCCCGGGA TTGTTCAACC GCGCCGTGAG CCGGCTGAGC AGGAAGCGGC	60
CGCCCGTCAGA CATCCACGAC AGCGATGGCA GTTCCAGCAG CAGCCACCAAG AGCCTCAAGA	120
GCACAGCCAA ATGGCGGNC ATCCCTGGAG AATCTGCTGG AAGACCCAGA AGGCGTGAAA	180
AGATTTAGGG AATTTTAAA AAAGGAATTC AGTGAAGAAA ATNTTTGTT TTGGCTAGCA	240
TGTGAAGATT TTAAGGAAA TNNAAGGTT AAGACGCNGA TGCAGGAAAA GGCAAAGGNG	300
GTTCCTACATG ACCTTTTNT TCCAGCAAGG GCCTTCNTCA CAGGTCAACG TTGTAGGGGG	360
CCAATTTTCG GGTTCAACNG GAAAGNTTCC T	391

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AAACAGGCTG AGGAGGTTCC GAGGCTAAA GGAGGGGAAG GAGCCCCGAG GAGGCTCTGN	60
ANTTGATGTC ACTTAGGTCC AGGGCATCCN TGGGAAGGAG AGAGTAGTGA CACTCAGGAT	120
CCAAAAGCTA GCCCTGCCCA CCCCAGCCCC TGGACCTGCT TACCTGGGTG TGCNACCTGC	180
TCCGGGGGGT GGAGGTGCTC CCCACAGTCC GGGCCAGGAC AGCCTCAGGG GAGAGTNAAG	240
GCCTGCAAGA GGGNAAGCGG AGACAAGGAG GGTGTCCAGG GCTAGGGAGT NCCGGTTGAA	300
ACCAGTTTG TCCCTGTTGC AAGNTTCCAG GTTNCCGNTN GACAAAACAA GCAGG	355

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AAACAGGCTG AGGAGGTTCC GAGGCTAAA GGAGGGGAAG GAGCCCCGAG GAGGCTCTGN	60
ANTTGATGTC ACTTAGGTCC AGGGCATCCN TGGAAAGGAGA GAGTAGTGAC ACTCAGGATC	120
CAAAANCTAG CCCTGCCAC CCCAGCCCC GGNACCTGCT TACCTGGGTG TGCACCTGCT	180
CCGGGGGGTG GAGGTGCTCC CCACAGTCCG GGCCAGGACA GCCTCAGGGG AGAGTNAAGG	240
CCTGCAGNAG GGNAGCGGAG ACAAGGAGGG TGTCCAGGGC TAGGGAGTNC CGGATGAAAC	300
CAGTTTGTTTC CCTGTGCAAG TTCCAGGNTC CCGTTGACAA ACAGCAAGGT GCCACATTCA	360
GGNCATTAAA AATTNGTGCA TTTGAAGCAG CATTTGACAG TTTNAAATTC TTCCTTGNT	420
GNATTCCAGG CCCTTTTCT TTTAAACAAN GGATTGGGG CATTT	465

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

TGACCAAGCT TCGGGANGAT GGGCAGGGAG AAATGCCACC ANTACTGGCC AGCAAAGCGC	60
TTCTGCTCGC TAACCANTAC TTTTTTGT TAACCCGATGGC TGANTACAAC ATGCCCCATT	120
ATATCCTGCT TGANTTTCCA AGGTACACGGG ATGCCCGGGA ATGGGCAGTG CAAGGAACAA	180
TCCGGGCAGT TCCANTTGCA NAGACTGGCC AGAGCAGGGC GTGCCCAAGA ANAGGCGAAG	240
GGAATTGCAT TGANNTTCAT CGGGGCAGGT GCNATAAGAN CCCAAGGAGC CAGTTTGGG	300
ACCAGGATGG GGCCTATNCA CGGGTGGCAC TGCANT	336

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GGCACGAGGT TATTTTTTAC TGGATATTGC CTTTNNTNCTT TTNCTTGGTG CTGCCCTGTT	60
ATACTTTCTC TTGTCTTGGG TGACAAAATT TATCTACAGA NNAATCAAAA GTTTGTGGTC	120
TAGAAATAAG CATAGCACAG TTAATGGGAC ATTACCACAA TGGAATCCTC AATGGCAAGT	180
ACANAAGAAA TGGCCATATT AAACATGAAA AGAAAGTGGG AATGAGCCAA CAGCCCAGGT	240
GATAGNATAA ATTGGTTCAC TCATTGAATT TTTATTGCC ATTATTTNGT CTAACAGCTA	300
CTTAAAGGTA AAACCATCCG TNAAACCATT CTNACCAGGC CCTTTNGGGG TCCN	354

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GTGTTCGANT GGAACATGCT CAAATTTGGT GCCAGCCGGG CCGCCGATGA CGCCGAGCGG	60
GAAGNCCAGG GACCGAAAGG AGCGGCTGAA ACACCTCGCGG AACCCGGCTA CCCGNGGCCT	120
CCCTTCCACA GCCTCCGGCC GCCTGCGGGG GAACGCAGAA GTGGCTCCCC NCANACCCCT	180
TNACCCCTAC CTTCANACAC GGNTAACAN CTTCCCCCG GCCCGTTTTC CGGCATNGGA	240

GAGAGAGCGG AAAGTGAAGT TATGGGGNT GCAACCGGGG GGGGCCCG TTAAAACATT	300
TTCCTTGGTT NCGAACCTTA ANAGGNCCGA CAAAGATTAN CTTTT	345

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GGCACGAGGG AAGGTGAAGA AAACGGAGAT AATACTATTT CCACTGGTCT GTTGTACAGT	60
GAGGCTGACA GATGCCAAT ATGTCTTAAT TGTCTATTAG AAAAGGAAGT TGGTTTCCA	120
GAAAGCTGTA ATCATGTCTT CTGTATGACT TGTATTCTTA AATGGGCAGA GACACTGGCT	180
TCATGTCCTA TTGACCGTNA AACCTTTCA GGCAGTGTAA AAATTCACTG CATTGGGAAG	240
GTTATGTTAA GGTTCCAAGT AAAAACAG CTGAGGGAA ACAAAAGNCC AGGAAAAATG	300
GAAAACTCCT TTGGGGAAAC AGGTCTCCNG TCCNGGAAAA TTTCTTAAAA GGCTGTTTA	360
GGGNGGAAAA GNCCCT	376

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATGATGAGT TCTATACTAA ACAAGATGTA ATTATTACAG CATTAGATAA TGTGGAAGCC	60
AGGAGATACG TNGACAGTCG TTGCTTAGCA AATCTAAGGC CTCTTTAGA TTCTGGAACA	120
ATGGGCACCA AGGGACACAC TGAAGTTATT GTACCCATT TGAACGTAGT CTTACAATAG	180
TCATCGGGAT CCCCCAGAAG AGGAAATACC ATTTGTACTC TAAAATCCTT TCCAGCTGCT	240
ATTGAACATA CCATACAGTG GGGCAAGAGA TAAGTTTGAA AAGTTNCCTT TTCCCACAAA	300
CCTTCATGTT TAACAAATTG TGGGCAANCN NTTCATCTGC AGGAGGAGTC TTACAGAGGT	360
TCCGGGTGGG NCANATTGG GANGGNTTT TCAAGTTTA AAGGTNCTTT GGCCGGGGCC	420
CGGGAATTGG TCCCCGT	437

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

AATGNTGAGA TCTATACTAA ACAAGATGTA ATTATTACAG CATTAGNTAA TGTGGNAGCC	60
AGGNNGATACG TAGACAGTNG TTGCTTAGCA AATCTAAGGC CTCTTTAGA ATCTGGANCA	120
ATGGGCACTA AGGGACACAC TNCAAGTTAT TGTCCNCAT TTNCCGGNG TCTTCNCAAN	180
AGTCCATCGG GNTCCCCAG AAGCGGGANA TCACNTTTGG GTACTCTAAA AACCTTTTC	240
CAGGTGCTTT TNGAACNTGN CCCTAACATG GGGCAAGAGA TAAGTTNAA AGTCCTTTT	300
TCCCCACAAAC CTTNTTTTTT	320

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGCACGAGCT GTCCTGACCC TNAGGCCTAT GCTCAGTCCA TCGCAGACGN CCGGNTCGTG	60
TTTGAAATGG GCACCGAGCT GGGTCACAAG ATGCACGTNC TGGGACCTTG GTGGTGGCTT	120
CCCTGGNCAC AAAAGGGGCC AAAGTGAAGA TTTGAAGAGA TTGCTTCCGT GAATCAACTC	180
AGCCTTGGAC CTGTACTTCC CAGAGGGCTG TGGCGTGGGA CATCTTGCT GAGCTGGGC	240
GCTTACTACG TGAACCTCGG CCTTCACTGT GGGCAGTCAG CATCATTGCC AAGAAAGGAG	300
GTTCTGCTTA GACCAGCCTG GGCAGGGAGG AGGNAAAATG GTTTCCANCT CCAAGACCAT	360
CGTGTACCA CCTTGNATGA GGGCGTGTAT GGGATCTTTC AANTCATNC	409

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AATGTGATGG TGTATGTTGG GATTCCCATC GGGGAGGGTG CTCATNAATG AAGAGGTACT	60
CAAGACAATT NACGAGGGAG ATGCCGATGA GGTGACGAAG CAGAGGATTG ATGATGGAAA	120
AAAGAAGCCA GGTGCTTTNT NGCACATCTT TNCAGCCAAG GATGCAGAGA AGATCCNNGA	180
GCTGCTCCGA AA	192

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

AGCTCCGCAG GCACTNCANT AAAAGCCTGA CCCAACATT TGGAGATGAC AAGTACTCAC	60
TGGCCCGCAA GNGGTGCTCA CCAACATGTG CTCCCGNCC ATGCAGATGG CACTGTACTT	120
CTGCTCGGGG CTGCTGCAGG GACCCAGCGC ATTCCGGCAC TACGCGCTCA ATGTGCCCT	180
GTACACACAC TTCACCTCGC CCATCCGCCG CTTTGCCGAC GTCCTGGTGC ACCGCCTCCT	240
GGCTGCCGCG TTANGCTTTT AGGGGAGCGA TTAGACATGG TCGCCTGGTN ACCCTGCAGA	300
AACAGGCAGGG ACCATGTTAA CGGACCGTCG GCATGGGTNC CCAAGCGNGT GCAGGAGTTT	360
CAGTTACCAT TTTNTTNTTT GGTTGTTTTT GGGTTCAAGG ANGAGTGG	408

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GGCACGAGTA CATGGCTACA TTTTATGAAT TCTTCAATGA GCAGAAATAT GCTGATGCGG	60
TGAAGAACTT CTTGGATCTG ATTCGTCCT CGGGGAGAAG AGACCCCAAG AGTGGTGAGC	120
AGCCCATCGT GCTTAAAGAA GGGTTCATGA ATCAAGAAGG GCCCAAGGAC GGAAGCGCTT	180
TGGGATGAAG AATTTTAAG AAGAGATGGT TTGCGTTGAC CAACCATGGA ATTTACCTAC	240
CACAAAAGCA AAGGGGACCA GCCTCTCTAC AGCATTCCCA TCGAGGAACA TCCTGGGCAG	300
TGGAGGAAGC TNGAGGAGGG AGTGGTTCA AAATGGAAAA ACNTGTTCC AGGTNCATTC	360
CAGTCCAGAG CGTTGNNTG TTACATCCAG GG	392

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GGCANAGGGG AGCTGCCTGG ACCAGCCAA TGGTTATAAC TCCCAC TGCGGCC CGCATGGTTG	60
GGTGGGAGCA AACTGTGAGA TCCACCTCCA ATGGAAGTCC GGGCACATGG CGGAGAGCCT	120
CACCAACATG CCACGGCACT CCCTCTACAT CATCATTGGA GCCCTCTGCG TGGCCTTCAT	180
CCTTATGCTG ATCATCCTGA TCGTGGGGAT TTGCCGCATC AGCCGCATTG AATACCAGGG	240
TTTTTCCAGG GCCAGCCTAT AAGGAGTTCT ACAACTGCCG CAGCATTGCA CAGCGAGTTT	300
CAGCAATGCC CATTGCATTC CATTCCGGCA TGCCCAGGTT TTGGAAAGAA AATCCCGGGC	360
CTGCAANTGT ATGATGTTGA GNCCCCATNG GCNTNTNAAG GTTTACAGTN CCTGNTTGAC	420
AAAANCCTTG GTCANAATGN TTNAAAANTA AAGGTTGTA AAACTTTTT TGGGTTATTT	480
TTTCAAAAGG TGGGGTTTTT CACCC	505

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GGCAGAGCCA GAACCTACTG GACCGGGATG TTACCTCCAA GTCCGACCCC TTCTGTGTCC	60
TCTTTACAGA GAACAATGGC AGATGGNTCG AGTACGACAG GACAGAAACC GCGATCAACA	120
ACCTCAACCC CGCCTCTCC AAGAAGTTCG TGCTTGACTA CCACTTGAG GAGGTACAGA	180
AGCTCAAGTT CGCGCTCTTT GACCAGGACA AGTCCAGTAT GCGGCTGGAC GAGCATGAAC	240
TTCCCTGGGCC AGTTCTCCTG CAGCCTGGGN ACGATTCGTT TCCAGCAAGA AGATCANTAG	300
GCCTCTGCTG CTGCTGAATG ACAAGCCTGC GGGGAAAGGG CTTTGATTAA GATTGTTGC	360
CCCAGGAGTT GTTCCGACAA ACCGGGTTCA TCACATTAAG NCTGGGGGG CAAGAAGGTT	420
TGNNAAGNA AGGGACCCTT TTTGGGAAGT TCANA	455

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

CCTTTNAGGA TGCTCCTACA GCAGCTGCCT AATACTTTNA GTTGCAGTNA GATGTTGGCT	60
GGGACCACAG TCATCTAAGG NTACTGCTCA AGATGGCTGT TGTNTNGNAA ACTCAGCTGG	120
GGCTACTGAT CAGAGCACCT GNCATGTGGC TGTCNAGCAA GGCAATGTTA AGGAACATGG	180
GTGACATTTG GAGGTCAAAT TTCAGATGAG GTTGCTGAAC GGCTGATGAC CATCGCCTAT	240
GAAAGTGGTG TTAACCTCTT TGAATACTGC CGAAGTNTTA TGCTGCTGGG AAAGGCTGAA	300
GTGATTCTG GGGAGCCATC CTTCAGGAGG AAAGGCTGGA GGAGGTTCCA TTTGGTTCAT	360
AAACAAACAA ACTTTACTGG GGTTGGNAAA GCNTGNAACC NGAAGAGGGG TTNTTAAGAA	420
AGCCTTTTTT TTGA	434

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GANAGACCCT TTAAGTNTCC TGANTNTGGA AAAGNCTTCA AAGAAAAGTC AACTGTCATC	60
ATACATTACA GGACTCACAC AGGTAAAAAA CCTTATGAAT GTAATGATTG TGGAAAAGCC	120
TTCACTCAGT AAGTCCAACC TCATTGGTCC ATCCAGAAAA CCCACACTGG TGAGAAAACC	180
TATGGTTGCN CTTAAATNTG GAGTNTCTTT ACATTACAGA AGCTTGATCC TTAGTTGATN	240
NC	242

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

TTATTGAGAA TCTCTTGCATAGCTGGTG ATGAAGAACCA GAGGTACGG AAAATGTGT	60
GCCGAGCACT TGTAATGTTG CTCGAAGTTC GAATGGATNG CCTGCTTCCT CACATGACAT	120
AATATAGTTG AGTACATGCT ACAGAGGACT GAAGATCAAG ATGAAAATGT GGCTTTAGNA	180
GNCTGTGAAA TTTGGCTAA CTTTAGCTGA ACAGCCANTA TGCAAAGATG TACTAGTAAG	240
GCATCTTCCT AAGTTGATT CCTGTGTTNA GTGAATGGGC ATGAAGTAAC TTNGGACATN	300
GATATTTATC CCTACTTAAA GGGTNGATGT TTNGAAGGAA GTCGGAAACG G	351

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GGCACGAGCT ATGCCTTAAA ACTNCCGAGC CCCACTCCAT GTAATAGGAT TCCTGGCCTT	60
CCTCAATGGG GGTCATGTC CTTGGACTGC GGGCCCTCAG TCCTTAAGTG GAAAGTGAAC	120
CGTCCACTGC CCCATGGAGC CCATCTGGAC ACAGCACAGC CCCAAAACCG TTAGCAGCTG	180
GCTCTGTTTC CAAGCCTGGG GAGGGGTTCC TCAGTGCCAG GAGTTGGGGA CAGGCTGGGG	240
ATCCAAGCTG CTTGAGGGGG TCAACCTTGG GACCAAATTG CCTTAAAGCC TGTGGTTAAA	300
AGGGCTTNAG GGGAAAGGTTA ATGGGGCCAC NTGCTGGAA GTTGGCCAGT TGCCCGGTTG	360
GCAATGGTGT GAATNTTTG GCCNTGTTG CCTGCCCTGG GGTTCCANCA AGTTNATCCC	420
TCCTTNTTNT NTNTNCTTTG GGGTTGTTTC CNGTNGTCAT NGGTAAATNT CCCCTAGTTT	480
CAAGTTTAC ATAGGGCCTC C	501

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GGCACAGTAG AAATGGAAAG AAGGNGGGGA TTGTGGTGGC TTGTGCCAG ACTGGAGCCT	60
GGANTAAATGG CAGCTCAGTC AAGGAGCAGA CCTGGNACTG GAACAGNTTG AAAACCAGNG	120
TTTTGTACTT TGAGAGGAGA GATTCCANGC TGCTTCTTGA ATCAATCCAA NTTTCATTAA	180

CAGCTCTNGG AACACTTTGG GNGCTGATT GTCTCTTAG GGGGNCATCC CCAACATGGT 240
TGAATTCCA CTNCTTCAGA TCTTGNGGCT T 271

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

TGTAAATTAA TTGTGATATT TTANGTTTT CCCCCCTTTA TTNCCGTAG TTGTATTTA 60
AAAGATTCGG CTCTGTATTA TTTGAATCAG TCTGCCGAGA ATCCATGTAT ATATTTGNAA 120
CTAATATCAT CCTTATGAAC AGGTACANTT TCAACTTAAG TTTNNACTCC ATTATGNCAC 180
AGTTTGAGGA TAAATGAAAT TTT 203

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GGCACGAGNG CAGACTATTG CCTCAAGGAA CAGTCATTT TGNAGATATC AGCATTGGAC 60
ATTTTGAAGG AACTNGAACC AAAGTTATCC CAAAAGTACC CAGTAAAAAC CAGAATGAAC 120
CCATTGGGCA GGACGCATCA AAGTTGACTT TGTGAATCCC TAAAGAACTT CCCTTGAG 180
ACAAAGATGA CGAAATCCAA GGTGGACCC GCTGGGAAGG TGACCATGTT AGGTTAAAT 240
NATTTNCAAC AGACCGACGT GGNCAAATT AGGAGCGGGG CANCCAATA TAGNAAGTT 300
CTGT 304

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GGCACGAGCT GGGGCCACGC TGGTCTGGGA ATAGTTGGGC AGGGAGGCTG TCTACCTGGT	60
CTCCAGAATG GACGGCCCTG TGGCAGAGCA TGCGNANGCAG GAGCCCTTTN ACGTGGTNAC	120
ACCTCTTTG GAGAGNTGGG CGCTGTCCC A GGTGGCGGGC ATGCCTGTT TCCTCAAGTN	180
TGAAGAATGT GCAGCCCAGC GGCTCCTTCA AGATTGGGG CATTGGGCAT TTCTGCCAGG	240
AGATGCCAA GAAGGGATGC AGACACCTGG TGTGCCTCT TNAGGGGTA ATGCCGGCAT	300
CGCTGCTGCC TATGCNTGCT AGGAAGTTGG GCATTCCGTG CACCATCGTG CTTCCCCGAA	360
AGCACCTTCC CTGCCANGTG GGTGCCAGAG GCTTGCAAGG GGGAGGGGN CCNAGGGTTC	420
CAGTTGACTG GNAAAGGTTT TTGGAACGAG GNCCATT	459

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GGCACGAGNA AAATTGGAAG AGAAAATACT ATTCTGGTT GGGTATCCTT AAGGATTAGA	60
ACCGCAGGAC TCCTCCAAGT CTGTAGGCCT ACTTTCTCTA TGAGAACCGT NATGTTAGTC	120
CATCTAACTG AACCTCATCT CTCTTCAAT GCAGGTATCA CTACCATTAA AGTTAACATT	180
CGTAAATGCC AATTCCCTGG GNGGAGGCTT CCATTGCTGG ACCTGCGATG TCCGGTGNTG	240
NGGCACCCTA CAGTCCTANT TGGACTGAAC AGGCCTGATG GAGGTTGTGG CTGGNCTCAG	300
TTACACCTAA GAAGNTTGG GGCAAGGTTC ATTCTNNNTGC TTTTAAAAAG TGGCATGGAA	360
CTGTAGTGGT TTNAAACATT CATNTNGTTT AACAGGGTC GTAAGCCTGG TTTGG	415

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

TGGNCTNATT CCCCAGCATG AAGGCCCTGA GCCCGGTNCC CGGNTGCAAC NAAGGCGGTG	60
TCCTGCCTGT GGGAAAGCAT CTGGCCATCG CCCGGGGCCG AGGGAAAGGG CCCGGNAAGC	120
TNAGGAGCCG CTGAANCTTG CTGGGACGAN ATGNAACCAC TG	162

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

CGGCATTGCG NCANAANGNC CNAAGGAGGA GTCCTTCGGG CCTGTAATGA TCATCTCTCG	60
GTTTGCTGAT GGGGACTTGG AATGCCGTGC TGTTCGGGC CAATGCCACG GAANTTGGC	120
CTGGNTTNTG GTGTCTTCAC NAGGAACATT NNCAAGGCC TGTANTNAGT GAACAAGCTC	180
CAGGNAGGCA CTGTGTTTGT NAAACACGTA CAACAAGACC GACGTNGCCG NTTCCCTTC	240
GGAAGGGATT CAAACAGTCT GGGATTGGG CAAAGATTCT TAGGGAGAGG CGGGNTCTGA	300
AACGAGTNAC CTGNGGGTT AAAGACCAGT GAACCTTCG GAATACTTNA AGNAAAGGTC	360
TTTGTGAAGG AAG	373

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GGCACGAGCA ACCCGGGNGG TCGCCACGCA CCGCATGCNA CCTNANCCCC AGCCCCGATG	60
GTNAGGCCTA CACACTGGCT TCGAGACCAC CCGTCCGCCT CAATNATGTC ATGCTCAGGC	120
TGGTGACGGA GCTGCGCTGG CAGAAGTNCG TNATNTTCTA CGACAGCAAG TATGGTGAGT	180
TGTCCGGCAG GCGAAGCTGG GGCTGCTTGG GGACAGGGAT GGCCAGATGC TGGGAGACCT	240
GAGAAGTGGG TGGGGCCCTG GACCGGTNGG GGGTGGTCTG TGCTGAGTGG GCCTCCAG	298

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TTAAGTGTAG AATCAATGAA AAGACTTAAC AGCCTTCTCA ATATCCCAGA AAAGTGCCT	60
GAACAGGGAG GGATGATTG GAAGATATCT GAAGATAAAC AGCTAGCAGT TTGCCTGAAA	120
TATGCTGGAG TATTNNAGA AAATGCAGAA GATGCTGATG GAAAAGATGT ATTTANTACC	180
AAATCTGTTG GGCTTTCTAT TAAAGAGGCA ATGACTTATC ACCCCAACCA GGTAGTAGAA	240
GGCTGTTGTT CAGATATGGC TGTTACTTTT AATGGACTGA CTCCAAATCA GATGCATGTG	300
CTTGATGTAT GGGGTATACC GCCTTAGGGC ATTTGGGNCA TATTTCCAN TGATGCATTG	360
GTTTCTTAC CTCCAANGGT TCNGCACATG NANTGAGANT GGTAGAAAGC GTGATATGAN	420
NTTGTNTAGG ACTGTGTTGT NCATANTTGT GGTAGTAACC ACANNTCCAT TACAGCTGTA	480
NGTTTCTCTT CCTTTCNAAT TTGGTG	506

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GGCAGAGTNG AAGATGGGA CCACGGTCTC ATTCAAGGGGA TCCTTGTGTTT TTTCCAGCCA	60
GCCCACAATG CTGTANGGCA CCTGGAGAGA CAAGTCAGGT GCTGAGCCCG NGTGGGAGAC	120
CTGGAGCAGG GCGNGAGGAG ACNNGCCGAG GGCTGGGTT CNAGNAAGCA CCTACCACGC	180
CTGCTTAGTG GACCACCTCG AAAGTGGGCC TGGTACTTGC GCCTTCTTGT CAGGCCGAGG	240
CTGCTGGAAA TTGGGTGACT TCCCCGCGTG GTTNTGCGTA GAGCTTGGCC CGGAAAGCTG	300
GCGTCTGAGG CCTTNNGGAA CATGCATTCC TNCTACCAGG TTGGACAGGT TGCCCAAGTGG	360
CTGGGCAACA GAACGAGCTT GAAAACCACC ATTCAAGCCA TNCCATNGTA AAGTGAATGT	420
AACCCCTGGTT CCCCAGTCCA ANTTNCTTTT GGGAGCNTNC CNAAATTCCC CAGTTTCAGC	480
ANTNTCCCCG GNTGGTTCAG ACAACACAAAC CATTC	515

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

AGAACTAGTG GATCCCCCGG NCTGCAGGAA TTCGGCANAG GGNAGCGTGC NGNATTCAA	60
GCTTACCGAG ATGCTGATGG CCTGGTTATT GACCAGCATG AAATATTTTT GGACTACNAG	120
CTGGAAAGGA CTCTCAAAGG GTGGATCCCT TGGNCACCTT GGAGGCGGTC TTGGGGGAAA	180
AAAGGAGTGC TGGGNCAACT GAAAATTGG GGGACGGGAC CGGCCTTTC GAAAACCTAT	240
TAAACTTGCC CGTTGTTNAN AAACGACCTC TATAGAGAGG GAAAACGGNG NAAGGCGGGN	300
	300

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

AGGGAGCACC GGGAAATGCC AAGGGGATCG TCCATACCCA GGCAGGGCTAC CTGCTCTATG	60
CCGCCCTGAC TCACAAGCTT GTGTTTAANC ACCAGCCAGG TGACATCTTT GGCTGTNTGG	120
CNGGACATCG GNTGGATTAC AGGGACACAG CTNACGTGGT GTATGGGCCT CTCTGCAATG	180
GTGCCACCAG CGTCCTTTT GAAAAGCACC CCAGTTTATC CCAATGACTG GTNCGGTACT	240
GGGAAGACAG TAGAGAAGGT TGGAAAGATCC ANTCAAGTTT CTGATGNGGC GGNCGCAACG	300
	319
GTCTGTTCCG GGCTGGTTG	

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GGCACGAGCT CGTCCTTGNA AACTNATCCA ACAGCCTCAA AATGCGAGCN TGTTTGTNAA	60
CAGACCCGCC CTCGGAATCC TGCCTCCGGA GAACTTTGTG GNAGAAGCTC CGGCAGTCCT	120
TGCTCTCGGT GGCTCCAAA GGGATGTTCC CAGCTCATCA CCATGGCCTG CGGCTCCTGC	180
TCCAATGAAA ACGCCTAAA GACCATCTTC ATGTGGTACC GGAGNAAGGA AAGAGGGCAG	240
AGGGGCTTT TCCCAGGAGG NGCTGGAGAC GTGCATGNTT AAACCAGGCC CCTGGNTGCC	300
CCGATTACAG TATCCTTNC TTCATGGGGG GGNTNCCTT GGGAGGACCC TGGGTTGTT	360

TAGNGCCCCA GGAAATTTA AAGCCCTTCA AAAGGTTGGG NAATCCCTT CC

412

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GGCACGAGNA CACCCTGGGC CTCACACCCC TGCATCACGC CTCTCGGGAA GGCCACGTGG	60
AGGTTGCCGG CTGCCTGCTG GACAGGGGTG CCCAGGTGGA TGCTACCGGC TGGCTCCGAA	120
AGACCCCCCT ACACCTGGCT GCAGAGCGAG GGCATGGGCC TACCGTGGGG CTTCTGCTGA	180
GCCGAGGGGC CAGCCCCACT CTGCGGACGC ATGGNGCCGA GGTGGCCCAA ATGCCTGAGG	240
GGGACCTGCC CCAAGCGGTT GCCTGAACCTT GGAGGGGGGG AGAAGGAGTT TNAAGGCATA	300
GAGTNCAAGG GGGTTTTAGC CAAACAAGCA AGGTTTCCAA GGTTTCCAAC NGGCCAATT	360
GANTTTCCA AGGTTTTTTT GGGTTTNAAG GTTNNCCTTG CNTTGGAAAGG GGGACAATT	420
AAGGNAAGAG GTTTTTCCG GAGGAAGGGG NTTGGGGAA AATTAAAGGG GTTTTGGGT	480
TTTNACTTTN AATTAAAAA NGGCTT	506

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAAATACGTN TTGCTTNAT AACTCTNATT GCTTCTTGC TGTTGGGTG TGTAAAGTAA	60
GCATTGATTT NAGTGTGAG NAATGTGAAA CGGGACTTAC AGGNATGCTT GGATTAGTNC	120
ATCACAGGTT CTNATGAAC TTNCTACCA CAGTGANTA ATATTTNTCC TCAAACCTGT	180
GTGCCCTAAG GANTNTGTTA NAATAATTGT TGGATAATT CTAGGTGGGT GTTTATCCAA	240
GGCGCNAGAA ATTCCCTGCC CTTGGACCAG ATGTGTGGGG GCCNTCTGAC AAAATGGTAT	300
GNTNTGGTTT ANTTTACAC AC	322

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GTCTGGTCGC NAGCAACCTA ANTCTAAAAC CTGGAGAGTC CCTTCAANTG CAAGGCGNGG	60
TGGCTCCTAA CGCTAAGAGC TTTCGTCTGN AACCTGGGCA AAGACAGCAA CANCCTGTGC	120
CCTGCCCTTN	130

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GGCACGAGCC TCANTCCTTA ACTGGAAAGT AACCGTCCAC TGCCCCATGG AGCCCACATCTG	60
GACACAGCAC AGCCCCAAAA CCGTTAGCAG CTGGCTCTGT TTCCAAGCCT GGGGAGGGGT	120
TCCTCAGTGN CAGGAGTTGG GGACAGGCTG GGGATCCAAG CTGCTTGAGG GGGTCAACCT	180
TGGGACCAAA GTTGCCTTNA AGCCTGTGGT AAAAGGGCTT CAGGGGAAGG TAACTGGGCC	240
ACCTGCTGGA AAGTTGCCAG CTGCCCGGTT GGCAATGGTG TGAAGTTTT TGCCCCCTGT	300
TCCCTGGCCC TGGGGGTTCC AGCAGGTGCA NTCCCTTCCC TTGCTTACTN TNCTNCTTT	360
GGGGGTTTTG TTCCCTGTNA GTTCACTGGG GGTTAA	396

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GGCTATTGTA GGGCACCTNA CATTGCACAA GAAATGCCCT TTGCACTGGT GAATNTGTGC	60
CATTTCGTAG GGTCGGNATC CTCTGNTNAG CGTGGTTTAC CA	102

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGCATNGTGN CAGGTNTGCA GCAAGTTGTT TCTTAGTGTC CCAACGGAGG AACCACTGAA	60
GCAAAGCTTT ACCTGTGCTC TACAGAANGA AATACTATAC CAAGGAAAGC TGTTTGATC	120
AGAAAACCTGG ATTTNTTTTC ATTCCAAAGT CTTTGGAAAA GACACAAAGA TCTCTATTCC	180
AGCTTTCTCG GTAACCCTAA TAAAGAAANC CAAAACGTGCT CTTCTAGTGC CAAACGCCCT	240
GATCATAGCA NCAGTCACAG ACAGGTACAT ATTTGTTCTN CCTTNACTTT TCCAGAGATT	300
NCAACTT	307

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

GGCACGAGGN AATCATCTT AANATCACTT TCTNCTTCTT TGTNATTGTN ATTCTCTTGG	60
CCATAATACA AGGTCTAATT ATTGATGCTT TTGGAGAACT AAGAGACCAA CAGGAACAAG	120
TCAAAGAAGA CATGGAGACC AAATGCTTCA TCTGTGGGAT AGGCAATGAA TTACTTCGAT	180
NACAGTGCCA CATGGCTTG AAAACCCACA CTTTACAGGA GCACAACTTG GCTAAATTAC	240
TTGTTTTTC CTGGATGTAT CTTATNGACA AAGNTGGAAA CAGNNCACAC AGGGNCAGGA	300
ATCTTATGTT CTGGGAGGGAT GTTATT	326

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

TAGGAGGATA TNACGGCTTG AATATCTNAA ATNCAGTTGA GAAATACGAC CCNCATACAG	60
GACATTGGAC TAATGTNACA CCAATGGCCA CCAAGCGTTC TGGTGCAGGA GTAGCCCTGN	120

TGAATGACCA TATTATGTG GTGGGGGGAT TTGAATGGTG ACAGCCCACC TTTNTTCCGT	180
TGGAAGCATA CANCATTGN ACTGNTTCCT GGGACAAC TG TN	222

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

TGATATTCAC CTTCTGGTC TGTNGGNTTG CCTTATATCG TNATCTNCTT CTNGGTGGTT	60
AATGGTCATG GTCACCTGGT CACTCCAACA ATATCTGTTG TTTCGTACCT CTTTNNTAAA	120
TNGAACACTG TNTACAATCC GGTGATTAT GNCTTC	156

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GGCACGAGCA ACATATTAAG ACTCTGTCTC TACCAAAAT ACAAAATAAGT NAGCTGGCA	60
TGGTGATGCA CTCCTATAAT CCCAGCTACT CAGGAGGCTG AGGTGGGAGG ATCACTTGAG	120
CTCTAGAGGC CAAGGCTGCA GTNAGCCGTG ATCATGCCTC TNACCCCTAG TCTGGGTGAC	180
AGAAGGAGAC CCTGTCTCAA AAAAAAAA AAAAAAAA AACNNNNGGG GGGGCCCG	239

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

AATCAAAATT GAATATCATT ACTTTTTATA GATCTATTCA GATTTATTCT TTGTNCTTGA	60
GTCAACTTG TTGGATTGT ATGTTCTAG GAATTGTCT GTTTCATCTA GGTTATCCAA	120
TTTTTGAAAC ATATAGCTCT TATACTAATT CTCTTACAAT CCTTTTTATT CCTATAAAC	180

AGTAGTAGTG TCTTCATT CTGAATTTA GTAGTTGAGT ATTCTTTNC CNTAATCTAG	240
TTAAAGCTTT GPTCAACTTT GTGGANCTCT TNCAAAGAAC TAAATTTNG GTT	293

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CGCACTCAAG GTCGACACTA GTGGNTCCAA AGANTTCGGN AGAGGAAACA GCGGTAAACN	60
CCCAGGTCCCC AGGGCCAGTC CCTCACCNNGG CCCAGAGCAA GGCCACTAAG GATGGGCCGT	120
GGAAACCAAA GTGGTCATCT ATTNNANCAT CATNNNCNGC AATTTNCCTN TTATCGGNGT	180
NGAAAGNGNA AGACATTGCA GCCAACTTCA CAAGAAATGT CTAGANAAGA AAGTNCTTTA	240
TGTGGACCNT GAGTTCCAC NGGATGAGAC CTGTCTCTT TATAGCNAG	289

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

CTANTCCNAG CACTTGAAA GCNAAGGNAG GAGGATTNCT TGAGGCCAAG AATTAAAAC	60
CAGCCTGGGC AACATAGCAA GATCCCGTCT CTATAGAAAA NCTGTNAANT TAGCTGGCA	120
TGGNGCCATA TGCCTNAC	138

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GGCACGAGTG GTGGCTCATG NATGTAATCC CAGCACCTTG GGAGGCTGAG ACAGAAGGAT	60
TGCTTCAGCC CAGGAGTTCC TGACTCAAAA AAAAAAAAAA AAAAAAANNNCN	120

GGGGGANTTT TTNGGGGG

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GGCACGAGGT GGCGAGCNCC TGTAGTCCCA GCTGCTGGGG AGGCTGAGGC ACGAAAATCA	60
CCTGANCCA GGAAGCGGAG GTTGCAGTAA GCCGAGATTN CCCCACGGCA CTTNAGCCTG	120
GGTGACAGAG CGAGAACTCT GTCTCAAAAA AAAAAAAAAA AAAAACNN GGGGN	176

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

ATTAaaaaACT CCTCTGGTTG CCGTATTNA TGATCTGGAT ATAGAAGCGG ATGAAGAAAGA	60
TGAACCTAGG GCAAGAGGTC TTACAGGTTT GAAAATATT GGAAATACTT GTNACATGAN	120
TGCAGCTTG CAGGCTCTT CTAATTGCC ACCTTGAAAC ACAGTTTTN CTTGATTGTG	180
GGAGGGACTT AGCTCGNAAC AGGATTAAGN AAACCTGGCC ATTTGTGAAA AGTTAATCTN	240
CAAACCTTAAT GGACAGNGCC TGTGGCATT AAAAGCCAGG GCCAGGTTTC TGTTTGTGGC	300
CTACTTACTC TGTTTCAAG GGATTTAAAA ACTGTTAAAT CCCAACATTT CGGGGGGGTT	360
TTTCTNCAGC CAGGGTGGNT CCAGGAATTN CCNTTCGGTG TTTTAATGGG NTTGNCTTC	420
CAGGAGGGAT TTGAAAGGGG CCAGTTCCCTG GGAGTTGGAA GGAGGNTCCC CGNAANCCTT	480
AACCCTTGGG GGGGG	495

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GGCAGAGGAG NATGACCTTG TGCCCACAGC ACCTTCTCTG GGCACCAAAG AAGGTTACCT	60
CACCAAACAG GGAGGCCTGG TCAAGACCTG GAAAACAAGA TGGTTTACTC TGCACAGGAA	120
TGAACTGAAA TACTTCAAAG ACCAGATGTC ACCAGAACCA ATTGGATCC TAGACCTAAC	180
AGAATGTTCA GCTGTACAAT TCGGATTATT TCACAAGAAA GGGTAAACTG TTTTTGTTTG	240
GTATTTCAT TNCAGGACAT TTTATCTCTG TGCAAAGGAC CGGAGTAGAA GCTGTTGAGT	300
GGGNTCAAGG TATTACGGN TGGGNAAATT TGTTCACCAN ATTAAGGAAA AACCAAGGTT	360
CCAAACCCAG GGGGN	376

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GGCAGAGGGG TAAATTAAGT ATTGAAAAAA TGCTATGGGG CAGAGGAAGA AATGCTAAC	60
TTCTGTGAGA AGAGAAGACA GCTTGTACA CAGGTGAAAA GAACAAGCTG CAGCTGAGAG	120
AAGAAAAGTA TAAGAGTTGC TAGGTGTGAC AATCTCAAGA CTTTTCAACC ACTACAAATT	180
TAAACAGCCA CCCTAAATCA CCCC	204

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GGCAGAGNAT TTAGACATTA TTACTCAAAA TATTCCAGAA AAGGTAAGTT TGTTTGTAAAG	60
ANTTTAAACT TGACTGTAAA AAAAGAATTG TATGTATTG TACCAATTTC TTATATGTNG	120
AGCATTCCCTG TGAAATGTTT GCAATTTCNC CCTTCCCTT CCACTGCCCT GCTAAATGTG	180
CACATGTATT AGNACACAAA TACCCAGTAA ATGGGAATT ACCCATTAC ATGGCATACA	240
CACTGAGGTG GGCTTGNGGT ACATACAAA TTTTGTAGGAC AAACCTTACTG GGGTAAGTTT	300
TTGTGGGATA CTTGTNTNAN AANTGATTAA TT	332

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGCANAGNAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AANAAN

56

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

AGACCTTAAN CCCAGGAGGC GGAGGTTNCA GTAAACCNAN ATTAACCCAC TACACTCCAG

60

CCTGGGCCAA CAAGAGCAAA ACTCNGTCTC AAAAAAAA AAAAAAAA AANC

114

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GGCANAGCGG CCACNCAAA GTTTGGGAA TTACAGGCAT GACCCACCGC CCCTGGNTGG

60

ATTTCCTTG AAAAAGNNAA AAGAAAAAAA AAA

93

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GGTGAACCCT GGCGCCCCAC CTCCCCGCGC AAGTTCACCC CTGNGATGCA CGNTTCCNTG

60

GAACAAAGTTC CTGGTTCTN TGANGCACCG TGCTGACCTC CAAATACCGT T

111

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

TGTAATCAGC ATCANTAATA ACTGTGAAGT CCTTCATTGG CTTAGGTTGC ACTTNTNGGT	60
AGAGGCTGGG GCAAGGNTTT NTTGGGATCA GGGACACTAG GCAGCCACTC CTCAGGCACC	120
AGTAGTGGTG GGCANTGAAG TCAAATGTGC CAGTNTTCAC ATGCCTGGNT AGCATAACACA	180
GATTACCACT GGTGGCTGGT NTGGNTGGGC TGGTCCTTGA ANCCTNCAGG TGGGCATGGC	240
TCCAGGTGCC TGGTGGTGGC CAGTGGTAGG CTTAGGGCAG GTGAGGTGCC TTGGGCCNT	300
TGGAACAGTG TGGCATGGAA TTGGTGGTTG ACAGGNTGG NAACNTNGCC TTGGCAAAAT	360
TN	362

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

AGAACAGT TNCTTAGCTG GGTGAAGTGG CTCATGCCTA TAATCCGGCA CTTTGGGAGC	60
CTGNGACAGG TGGCATTGNT TGAAGCCAGG AGTTCAAGGC CAGCCTGGGC AATAAAAGTGA	120
GAACCTGTCN GTNATAGACA AAAAAAAA AAAAAAACAA AAAANCNGGG GGG	173

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GGCAGAGCTG GCGCATCGGT TCATTCCTA CCTCAACGGC CAGATCATGG CGTGCNACAA	60
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GCCTGCAGA TCTTCGACAC CTGGGTGGC AACCTGTCGT CGCGGCCGTA CCAGGAGTTC	120
TCCCTGGCC TACATGCGCA ANATCGTCAG CGGCCTGATC CGTAAACAGA AGGGCGCAA	180
GTCGGTGA TCATGTTCAC CAAGGGCGGC GGCCTTGGC TGGNAGAGCA TTNCGACGC	240
CGGCGCAGAN CGCTNGGCC TGGATTGGAC CTGCGACCTG GGCAGGGCCC GTCAGCGGT	300
GGGTAACCGG TTGGGCTGCA AGGTTNACAT GGACCCAAT GTGCTTTACG NCAAGCCGGA	360
AGCGATTTGC AACGAATTG GGCGNATNC TTGGCCAGTT NTGGCAAGGG CAAGGGCNT	420
TTTTTCAAA CTTGGG	436

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GGCAGAGGNA GTGGTATGNG CTGGATCTGG TGAAAAACCA GGATGGCGCG GTGGTGGGTT	60
GTACCGCACT GTGCATCGAA ACCGGTGAAG TGGTTTATTT CAAAGCCCCG GCTACCGTGC	120
TGGCGACTGG TGGACAGGGN CGTNATTAT CAGTCCACCA CCAACGCCCA CATTAACACC	180
GGCGACGTTG GNGNCATGGN TATCCGTGCC GNCGTACCGT GCAGGATATG GAAATNTGGC	240
AGTCCNNCC GACCGGGCAT TGGNTGACGG GNNATACTGG TCCACCGAAN TTGNCCGTGG	300
TGAAGGCGGT TATCTGCTTG AACAAACATG GGCGAACGTT TTTTATGGGA GCGTTAATTT	360
TTTTNT	366

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GGCAGAGTNA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAT NNNGGG	57
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(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

AGGTAGAAC CACCATGGTG CTGTCTCCTG CCGACAAGAC CAACGTTAAG GGGGGGNTTT	60
TNTAAAGGTG GTGNGNAC	78

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

AGGGTACCGT ACGTCGTCGC TGNTGAGTGG GCGAAAAGCT GCAAATGAAA CAGCACTGCC	60
CACATCCGGA TCTGTTACAG GTCGATCCGT TCGAAGCCAT CATCGATGAA GAGCTGGAGC	120
CTGGTGATAT TCTTTATATT GGGNTGGGAT TCCCGGCATG AAGGCTACGC GCTGGAAAA	180
TGGCAGGGAA CTATTCCGTG GGCTTCGCG CGCCAAATAC GCGGAACTG ATTAGTGGAT	240
TTGCCGATTA TGTGCTGCAA CGTGAACCTNG GCGGCAACTA CTACAGCGGA TCCGGATGTT	300
TCCACCTCGC GNNTCATCCT GCGGGATGTT TCTGNCCGCA AGNGAATGGN TNAAACTGCG	360
TGAGAAATGGA TGCNTCGGAA TTGNTTCANC CAGCCNGTNA CAATTTAAG CAATGGTTTT	420
GGCGAGTTTT ATNTCCCAGT CAAGTCATGG AANNTGGGTT ATTGGGGCNG CCAANGCCGG	480
CTTTTCAGCC GGTGNAATT ACAGGTG	506

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GGCAGAGCAT GNNTATGGGN TACAAAGNGA TGTTATATT TATGAATATT TAGCTGGCA	60
TGGAAGCTCA TGCCTGTAAT CCCAGCACTT TGAGAGGCTG NGGCAGGTGG AGTGCTNGAA	120
GCTCAGGGGT TNAAGATTAG CCTGGGCAAC ATGGTGGAA CCTATCTCTA CAAAAAAAAN	180
AAAAAAAAANC TGGGGGGGAA TTTTTGNAGT GTTCNGGGGN CCTATGGGTT TTACCC	236

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

TTGGCTATGG GACTATATGT NATCTANTGA CTTTTTAAAAA ACAGATTACA AACTGTAGGC	60
CTTAGATNGG TAAGTAATTT TTCAGCTGGG CATGGTGGCT NATGCCNGTG GTCCCGGGGC	120
TTTGGGAAGG CCGAGGCAGG CGGATCACGA GGTGGGGGT TCGGGAACCA TNCTGGTCGA	180
TGTGGCGGGN CCNCGTGTT TCAGTAAAAA AAGTGCAGAA ATTGGGCTGG GACATGGTGG	240
CGTGCACNTG TGGTNCCGGN TGCTTGGGG TGCTTGGGG CGGGGGGGT CGCTTTGGC	300
CTNNNGGAAGG AGGAGG	316

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GGCAGAGCNG AAAGCGGGCT GCACTACAAC CGACATCGNT ACTACAATCC GGATGTTGGT	60
CGCTATCTGA CGCCTGATCC GGTGAAGCTG GNGGGTGGGC TGAACGGATA CCAATACGTG	120
CCCAACCCGA CGGGTGGNTG GTATCCGTTG GGATTAGTTT GTACACCTGG GGCAGTGCCG	180
GGNCTTCANC AAATAACACA GCAGTTAGCA AAGTCCCTGG AGGGGGATTA GCCGCGCATG	240
AAGCAGCTGG GGGTCATCTA ATTGAAAGGC ACGTTGGTC AGACAACGGC GCAGTAAGCT	300
TTNAAGGCTT GTAGGCAGAG CCCAANTATT TCCAGNNCA TCCACGGTTT CAGANT	356

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GGCAGAGCTG NTTGACCGAA CCGTTGAAGC GGTTTCGAT ACGACGCAGC TNACCGTAGC	60
GCTCGCCCGG GGAGATGTTG CAACCGCTGG AGCAGNCATG GCAGATGCTC GGCGCAAATT	120
GCATGTCCC A CTTACGGTTG TAGCGCTCGG TAGTGGGTCT TGTGCGTGAA CACACCGATC	180
GGGTCAGACC TTCGGNGAAG GTTNCCGGAG AAAACTCGCTT CTCCAGCACG CCGTACTTT	240
AACCGAACCC GAAAGTACACG TTGTCGTGGG ACGCCGAACA CGCCGAGGTC GGTGCCGNCG	300
GGNTAAGTCT TTATAGAAGC GCACGNANCG GTAGCAGGCC GATGNCAGCG GTTTCATTTC	360
CGTGGGGAAA TGAACGGGGC CCNAGGTTCC NGGTTCTGG TTGGT	405

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GGCAGAGNGT TTTNCGGGCT CAGTTCGTGG TGCCAGCTGC CGTGGGTGCG GTCAATGAAA	60
CGAGTTTCAC AGAACTCCC A GANGCGCCGG TACCAGGTTT CGTAATGCAG CTCCCCCGTC	120
CTTTTNANCA GCGCCTGGGC CAGCGGGCAC TGGCTCGCA ATGGGTCCAG TGCAGGCGCC	180
TCGCGCCACC ACGGGGCGCT GGCTTCCANT CGAGGGTTA GACAATNCCN GGGGGGGCCN	240
TTGAAGGGCC N	251

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CCCTGGCTCT CTTGATAGAG GCGNGAGAGT NNGNTTCCAG ACCAGAATTT ATCTTCAAAC	60
GCTTCGGCTT CGCGCGCCGC TGCCTTAAGA ATACGGGTCC GCTGGATAAT AATGGCCCAA	120
GATGCGATTG AAAAACCAAT CAAAATCAAC ATGATAAGTT TAACCAGAAG GCTAGCCTTC	180
AGG	183

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GAGTTGGCGG TCAGGTCAAC GGCGGCTTCC AGGGGCGAAA TCAGGAAGAT CACCGCCACC	60
GGGATAAACG CCACCCAGTC GAACGAAAAA CCGTACTTGA ACGGCACCAG TAGGCTGATC	120
AGTGGCAGCT GGGGCAGGGC GCCCAGGTTC GACGCGGCC ATCCACCAAG CCACCAACAA	180
ACCCAGGGTC AGGCCGATCA CGATCGAAC CAGGCGCAGG NAACGCGTTG TTGAAGCGGT	240
TGAGCACCAC GNATGGTCAG CAGCACCAAG GCCGCCACAT GGTTTGTCG GNNGNGTCCA	300
GGTCGTTGGT GGNCATTAAC CGCNGGT	327

(2) INFORMATION FOR SEQ ID NO:384:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GGCAGAAAAT AAAACCACCG GGGCCTCCCT TTAAACTTTN GTTCTCAAAG GGCCCCTCCA	60
CCTGGCCCTG TTCTGGCCCC CAAGGATTCT ATGGGAAGCA GTGGAGTCCC ACAGATCTCG	120
CTCCANACTC TGCTCCCTGA ATCCCGGGGC TCCTCCAACT CCCCCCTGGCC TCTAANACTC	180
CTTCCCATCC TCCCCTCCCA CTCAGAAAAC TCTTTGTGGT CCCCCGCGGAT GAGGCCAGG	240
CTCGAATCCC ATATGCCCGT GTNAACCACA ACAAGTACAT GGTGACTGAA CGCGCCACCT	300
ACATCGGTGA GTGTTTGAG GCACCACGGG GCGCTTGAAG AAGAGGGGGT TTCAGACACC	360
AGGGCGGNCC CCCGAGGGTG NCCTTATGTT NCACCCTTTN CTTTTTAGGA ACTTCCAATG	420
GTTTGATNGA	430

(2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GCTTCGCTGG TTTTCGGCTG TTCCAGNATG GTGCTGACCT TGTTGTAGGT NAGGCGGGCC	60
TGGGAGTGNA TCACCGCTTC GTAGAACTGG TAGTCGGTCA TTTCGNCGGT TTTCGAGATG	120
GTCATCTCGC ACACCATGGC CAAACGGTCG ACTTTCGGGT TCAGGGAGCA CAAGCCGTTG	180
GACAGNTGCT CAGGCAGCAT AGGGATGACG CGCTCGGGGA AGTACACCGN GTTGCCGCGC	240
ACCTGGGCTT CGTTGTCCAG GGCGAACCG ATCTTNACGT AGCTGGACA CGTCGGCAAT	300
CGCGAACGNA ACAANTTCC AGCCGCCGGA GGAACAGGCG CATTGCCAG GCTTGGNTTT	360
CGCATTAGNC CGCATTNTNC GAATTCGCGG GCANTTCGG CTTCATGGTG ACGAACGNCA	420
GTNNANGCAG TTCGATGNNG TTNTNTTGT NNNTTTNTTC GATTCCGNT TGAGTTGGGG	480
GTTTTTGAG CACAGNNNTGA G	501

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GGCANAGGNC TGTACGTGCG CCATTGCTCG TGCATGGGT TTTTANTGAT TAAGCCTGNG	60
TATGCAACAT CAGCATTAAA NAGCTCGTGT AAANCAGAAT AACGGCATT TGCGAGCATG	120
ATTGGCTTCT GTCTGCTTGG ATCAGTTGTA TAAATTGGAG TTTTAGCTC GAAAAATGCA	180
TGTAATCGTC CGTTTGAGG ATTTTCAGCA ACAAAATTG GCATTGGTAC GCCATCAAGT	240
GGAATATAAA ATTCACTTC AGGGCTGGAT TTCATNAGTC GAGTTCAAG CACAAAGTAA	300
TACTGGATAA AACGGACTAT TTTGGGCTGA ATGTACTTGA ATGCCAGTGC TGGTATTCTC	360
TCGGGACGTA TTTTTAGAC CCGTGNCTAG NTCCNTCCGT ACATNNGGNT TTGGGTCCGT	420
TAAAGTTA	427

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

GGCANAGGTC TCTGTNGCTG TAATTAAGGA TCTTGAGATG AGGAGGCAAT CCTGAATTAT	60
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CCGGGTGGGA CCTGTACCCA GTGACACATC AGGAGAAATT TTTTTATATG AGAAAATGTG	120
GAAGGGAAAT TTGAGACAGA CAGAGGAGGA GCAGCCGAG GGGAGGCAGTT GTGTGCAGGC	180
GGAGGCAGGG ACGGGGCGAT GCACCACCGG CTGAGGAAGG ACCGCGGCCA CCGGGTAGCT	240
GGAAGACGCA GNTGGAGCCT CCCCTAGAGC TTTTGGNAAG GGACACAGCC CTGCCAGCAT	300
CTTCGTTTN GTCTTGCGC CTNCAAAGAC NAAAATCAAG GCTTTTNGA ACAAAT	356

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

NGCAGAGCGC GAAGTGGTGT CGGGTACTCC TTGAGCGAGC TGCCTTCCGG CGCCACATCG	60
GTGTCGTGGA AGCTGTAGTA GTCGATGCC AGCTTGGAGA AAAACTCAA GGCCCGTCA	120
NCTTGACCGA TGGCCACTTC CATCGCTTTA CCGCTGCGTT GCCACGGCG CTTGAAGGTG	180
CCCATGCCAA ACATATCCGC CCCCAGGCCAC ACAAAAGGTGT GCCAGTAACA GGCGGNATG	240
CGCAGGTGCT CGCGCATCGG TTTNCCGAGG ATCAGCTTGT TTGCGTCGTA ATGGCGGAAG	300
NCGAGTGNNA GAGTCGCTNG TCAAGG	326

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GGCAGAGCCA CGGTCAGGCC GNCACTGGTA CCGTTCTTGA AACCCACGGC CGAGGACAGG	60
CCGAAGCCAT TTGCGGGTGA GTCTGGGATT CGGTGGTGCG TGCACAATNT GCCGACCAGN	120
TGGTCAGGTC TTGCAAGGTAC TGGNGGGAAA TCGTGTCCAG GGTTTCGGTT GNCGTNGNAG	180
GCCCATTCC GNCAAGTCCA GNAGTAATTG NACGACCGAT GTGCAGGCCG TCCTGGATCT	240
TGAACGAGTC GTCCAGNTAC GGGTCGTTGA TCANGNCTTT NNAGCCGACG GTGGTACGCG	300
GCTTGTTCGA AATAGACACG GATCACCAAGG TTTNAAGGT GTTCGGACAT TTTNGTNGGT	360
CAGCACTTT CAGGTGGTTN GG	382

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GGCANAGGCT GATCGGNACC CAGNTCGAGC ACGTTCCGGC CATGCTGGAA ACCATCTTCA	60
AGAGCGCCTT CGGCCTCGAC CCGGTATTTG CGGGCCTGNT CGGCAGCGCC ATTGTNATGG	120
GTGTGAANGA GGTGTGTTCG CCAACGANGC TGGCCTGGGC AGTGCGCCA ACGTCGCCGC	180
CGTAGGGCGN TTNAAACACC CCGGTGCNCA AGGCGTGGTC CAGGCCTTCA GCGTGTTCCT	240
CGATACCTTC GTGGATTNNN CACCTGCACC GCGTTGCGNN TTNCTGCTGT CGGGCTTTT	300
ACACCCCAGG NTTTGAAGG TGAATGNGAT CGGGCCTGNA CCCAGAACCTT CGGTTGGGCC	360
GCCCTGGGTT CGGTTGAANT GGGGNCCG	389

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GGCAGAGCTT NGCTTCGCTG GTTTTCGGCT GTTCCAGGCA TGGTGCTGAC CTTGTTGTAG	60
GTNAGGCGGG CCTGGGAGNG NATCACCGCT TCGTAGAACT GGTAGTCGGT CATTTCGNCG	120
GTTCAGGGAG CACAAGCCGT TGGACAGNTG CTCAGGCACA TTAGGGATGA CGCGCTGGG GAAGTACACC	180
CNGTTGCCGC GCACCTGGGC TTCGTTGTCC CAGGGCCGAA CCGATTCTTC ACGTAGCTGG	240
ACACGTCGGC AATCGCGAAG GAACAACTTT CCAGCCGCCG GAGNAACAGG CGCATTTC	300
CAGGCTTGGT TTGCGATTAG ACCGCATCGT CGAAGTCGCG GGCATTTGC CTCATGGTGA	360
CGAACGGCAA TGACGCAGTC GATGGGTTCC TTTGGNCTTT TTTTNGATTT CCGGTTTNNT	420
TTTGGGTTT TTTT TAGGCN A	480
	501

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GGCAGAGNAA GACATCCCAT GTTTATGAGT CTGAAGACTT AACATTGTTA AGATAATACT	60
CTCCAAATTG ATTAAGAGGA TAATACTCTC CAAATTGATC TACAGATTCA ACATGATCCC	120
TATCAAAATC TCAGCTGGCT TCTTGTTAGA AACTGACAAA TTGATTCCAA AATTCATATG	180
AAATTGCAAG GGATGCAGAA CATCAGAAC AATCTGTAAA AGANCAAAAC TGGAGTACTC	240
CCACTTCTCA AAAACTTACT GCAANGCAA AGTAATCAAG ATAGGTTGGG CATGGTGGCT	300
CATGGACTGT NAATNCCAGC ACTTTTGAAA GTTCCGAGGC GAGTGGGTTTC ACTTGAGGGT	360
CCGGGGTTTC AAANCCAGCC TNGGCCAATC TGTTGGAAAC CCCTTTTTA TTAAACTTTT	420
AAANAATTG GNTGGGCTGG TGGCGGGGN CCTNAATCCC GGTTTTTCGG GGGTTGGGC	480
NGGGCATTG	490

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GGCNCTAGAT GTNGTTAACG GTGTAAAACA GACCAACCCA CAGCGGCCGT ACCTTAACCTT	60
CANTCGTCAG GAAGAGGGCTC AGCGTCGGGG CCAATAGCGC TCCGGCAATG CCAGAAAGGT	120
AACGCAATCA GCAGGTAAAG CGGTAAAAAA TGGGGATTAA AGCGGCGTGG TNAACCCGTA	180
CAGACGTTTC ATATTGTTCN TCCCTGTNCC CTNAACGTNT GAAGTGAGGA	230

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GGCANAGTGA ACAGCGTAGG NACTGTAAAG CATGTNTTGG GGTAAAACCTT TCCTTGATA	60
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AAGAGAAACA GGTTCTCTTG GATGAATAGA AGGNACAGAG AAGGCAGATC CAGGCTTATC	120
CTTCTCGTGT AAGGGTATAG TAAAGAAAGG TCTATGCCGG GCGCAATGGC TCACGGCTGT	180
GAATCCCAGC ACTTTGGGAG GCCGAGGTGG GTGGGATTCA TGAGGTGCAG GNGATCAAGA	240
CCATCCTGCC TAACATGGTG AAACCCGTCT TTNACTAAAA NTGACAAAAT NNA	293

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GGCACAGNAG AAAACAGGCA AAAGAGACAC TTCAGGTGGC ATTGATCTGG GAGAAGAGCA	60
GCATCCCTTG GGCACACCCCA CTCCAGGACG CAAGCGANNA AGGAAGGGAG GAGACAGTGN	120
ATTATGAACG ATGATGATGA CGGATGACAG TGAATGGACC AAGGGGATGA AGATGATGGA	180
GGATGAAGNA AGGATAAAAGT AAGGACAAAAA AAAAAAAAAAA AAACCNCCGG GGGTNNNCTTT	240
TGGGAGCGCC CGTG	254

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GGCANAGNAG AAAACTGAGC TCGTTGGCTG GTTTCTCAAA AATCCACTCA TTTGATGATT	60
GTGGTGGTGT TCACTGACTT TATCCCAAAC CTACATGGAA GGGTGTTCGG GACAGACAGC	120
TCTCCCCAA AGAAAATGTC CTCTTAGCTA AGAGTCCATG TTTTCTTTTC TAAGTAAGAT	180
TTTGACAGAG AATGGCATAT GTATATGTGN AGGGCTGGGT CGTGTGTTT CAAATGGAAG	240
CAACAGAAAA GCAGAGCAGG TGTGTCTGGG GAGTATAGAG ACTGAAGGCT GAANGGTGGT	300
TGAGTTTCTG GGTAAATTGG TGGATGGTTA GTATGTATTG ACTTTGAACT TNCCNTTCTG	360
GAGCATTGT TAGAAGGCAG NNAATCCACA ANGACAGGGA G	401

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GGNAGAGNCG TTGAGGNGCG CGGNNGCCGAG GCATAGAGCG TGTCGATCGT GTNGCTCGAT	60
TTGCCACTGC CGCTGACCCC GGTGTATGCA GGTGAAGGTG CCGAGCGGCA GGCTGGCCGT	120
CACGCCCTTC AGATTGTTGG CGGTGGCGTT GTGGACGGTC AGTTTCTTGC CATTGCCCTT	180
GCGATGGGTG GTNGGTACCG CGAACTGCCN NCCTGTNCCG ACAGATAATC GGTGGTTGAT	240
GCTGTTGGGG TTGGTCAAG TGACTTNCCCT TCGTAACGTG GCCCTNCGCG ATNGGATTG	300
GCCCGACCCA TGGGAACGGC GGGNAACCCG GACCCATGTT CGATGNACAT GAA	353

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GGCANAGCTG GNAATGGTTC GCTGAAGAGC CTGGCTGGCA ACTNTTCGCG AAATGGCGAG	60
AGCTGGCAGC CACTCGCTGC CTTCCGGTAT GCCGACCGCG CGGGAATTG CTGTTGGGGT	120
AGTAGCTTTC GCTGCGCTGG NTAGGCGGTG TAGGAACAAT GCCCGGTTGG TCCATTGAA	180
ATCGAACAGC ATGCCCAATG CTTCACGCAC GCGCCTGGTC GGCGAACGC NGNCGCCGGT	240
TNATTCAATGG AACAGCGCCT GGGTGGTGT GGGGAATCCG GTGNAGGTAT CTCGGNCCGG	300
GATG	304

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

GGCAGAGTGA ATTTTNGCCA GTGAACACTT CAGCCACCAC GGTGTATTG CTAAAGGTTG	60
AACAGCCCCAT GTAGTGGAAAG ATTGGCTGGC CGTTGTAAGA AAAACGCGTT GTCCTATCAG	120

GCATAACCCC TTTGACCTG CGTGGCGCGA ACGGCACAA ACAGATTGGT TTTACCTGGA	180
TTTACAGAAC AGGCATTCGC CACATTCTGC AGTGTAAAGC GGAATTAACG TGATCGCCTG	240
GCACAACGCT GGTCACAAC TTGGCCCACT TNTACCACTA TGNCCGGNAC CTTTNGTGT	300
CCCAGCAAGG TTTTGTN	317

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GGCANAGGGA GTGGTATGNG CTGGATCTGG TGAAAAACCA GGATGGCGCG GTGGTGGGTT	60
GTACCGCACT GTGCATCGAA ACCGGTGAAG TGGTTTATTT CAAAGCCGN GCTACCGTGC	120
TGGCGACTGG CGGACAGGGG CGTTATTTAT CAGTCCACCA CCAACGNCCA CATTAACACC	180
GGCGACGTTC CNGGCATGGN TATCCGTNCC NG	212

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GGCANAGCAG CCCTCAGGCA GCTCCAGCAG CAGATATTG GCCCGCCGCT GCACGCTAAG	60
CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ANTNCCTTG	120
CGCACCACTG CATGAAGAAT GGTTGCACCA ACGAAGATGC GGTTCTATGC CGCGGCGGCT	180
GGTTTCAACT TCGGGGTAAT TCAGGCATAG CATCTCCAGG TAATGGAACA GAATGACAGT	240
CAATATGGGG GTCAGGCAGA TNNTCCAAAA AACCCCGGCG GAGGCGAGGT TTTTTTTTNA	300
ACATCAAAGG CGAGGANTTN TTTGATT	327

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

TGCACGTTNN TTGATCATGA CGTGCATGNT GTGTCTGGG CATTGACANC AACCATGAGG	60
TTGCCACACG GTGCTTGTG GACAATNGCC ATGTAGGAGT CCACAAGGTT CTGGGTGGTT	120
TCCATTTGCC GNTCCAGCTA TGGGTCCATG GAGTTTATN AAGCTGTCNN TGCCAT	176

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

ACAGAGTTG TCAACCTCAN NNCTACTGAC ATTTGGNGCT GTGGTGTGGG GCCGCCCTGT	60
CCCTGGGNAG GAGGTTGAAA AGCATCCATC GTCTTCACCC ACTTGGTGNC AGGAGCGCCC	120
TCTAGCTATG AATGGACCAA GTTGCCACGT GTGCCTCTAG TGGCAGGGTA GGGAAATGCAG	180
TCACCCCCAG GTGAGGGACC ACGGCTTCC CTCAAGTGTC CAGGGATAGC CTCTNCCGAA	240
TTGGTGACAT TGGGAATCCA GATGTGGAGG AGGTGGGAA AAGGGNCCTG TGGGATAAGG	300
TTAGGGGAAG AGTTTTTCC AGGTTCGTTA GGTGGGAAA GGTTTNCCAA GGGCANGGAA	360
TNTTNCCCCC CGGGCAANC AGAAAAGGGC CATT	394

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GGCAGAGCAG GTCCAAGGCC TCGCAGAACCC GCAACATACC TGTAAGCACC TGGGCGCCTT	60
TAGGGTCATG CTGGGCAACC ACAAAACTGC GGTGATCTT GATGAAATCC ACAGGAAACT	120
GGTGCAGATA GCTCAACGCA GAAAACCCAG TGCCAAATC ATCCAGATAG ACCTTGGCGC	180
CCATGGCCTG CAACTTCTGG ATGGTCTGGC GGGTGGCCGG GATGTCGCTG ACCAGGGCGT	240
CTTCGGTAAT TTCCACTGAA ACTTGCCCCAC GGGCCTGGCG AAGAATTNC ACCAGGGCGT	300
CGCCATAGGG GCGTCCTTG NAGCGTGGTG CTGGAAATNT TGATGGGTCA TCGGCAGTTT	360

CAAAACCCAN CTTTGNCCA TTTCTGATAA TTGGNGGCAA CAACCTGGGG ATTGCCACCC	420
ACAAGTTAN GTNCCGGGA	439

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GGCAGAGACT TGAACCAGGG AGGTGGAGGT TGTAGTAAGC CGAGGTCGTG TNACCACACT	60
CCAGCCTGGG CGACGGAGTG NGGACTTTGT CTAAAAAAA AAAAAAAA AAAAAANNTC	120
GGGNGAA	127

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

AAGACTGNAN CANCCNAACA GGNCCAGGAA GTACACGAGA AGCTCTGTAG GATGGCTTAA	60
GTCCAACGTC TCTGAATGCG GTGGCTCAGA GCACCCGTAT CATTATGGA GGCTCTGTGN	120
ACTNGGGCAA CCTGGAAGNA GCTGGCCAGC CACCTNNNTGT GGATGGCTTC CTTGTGGGT	179

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGCACAGCGA ATACGTACAC CGTATCGGTC GTACCGGGNG GGCCGGCAAC GATGGCCTGG	60
CGATCTCGNT GATCTGCCAT GGCGACTGGN ACCTGATGTC GAGCATCGAG CGCTACTTGA	120
AGCAGTCGTT CGAGCGCCGC ACCATCAAGG AAGTCAAAGG CACCTACGGC GGGCCGAAGA	180
AAGGTCAAGG CGTCGGGCAA GGCTGTTGGC GTGAAGAAGA AAAAGGTGCA CGCCAAGGGG	240

GACAAGAAGA AGGCCGGTGC CAAGTCGCCG ACCAAACGCA AGATTGCCAA CCGTCCGTAG	300
ACCGACAACC TGTCGTTGG TTCAGCAAGG TTGGGCATGG GGNCTTGAA AGCGNCGNAA	360
AGCCNGNAAG CA	372

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GGTCACGAGG TACCCAGTGT GGTCCCTGCC TGGACCCAGC CTCTNCTGTT GTCCCCAGAC	60
CACAAACGAGT NTNCCACCAG CACCATGTCG TNCTAACGGC GTGTGTCCTA ACGAGGATGG	120
CAGCTNCTCC TGCCTCTGCA AACCCGGCTT NCTGTTNGCG CCTGGCGGCC ACTAACTGCA	180
TGGGTAAGCC TGGAGCCAGA NTGCCAGCG GTNG.	214

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GGCACGAGCG GAGATGCCGG TGGTCACGCC GGTGGNGCTT TCGATGGACA CGGTAAACGC	60
GGTGCTGAAC ACGCTGCCAT TGCTCGGCAC CATCTGCTGC AGGCCGAGGC GCTGGCAGTG	120
TTCTCGGTG AGGGTCAGGC AAATCAGGCC ACGCGCTTCC CGGGCCATGA AGCTGATAGT	180
CTCGGCGGTG CAGCACACCC GGGNCAGCAA CAGGTCGCCT TCGTTCTCCC GATCCTCGTC	240
GTCCACCCAGG AGCACCATTT TGCCCTGGC GGTAGTCTTC GATGGTGTCT GCGANTGTTG	300
TTGAAAGACA TGGTGGNTGN TCCGATTAT TGGTTGTNAT GTATTNTGGT NTTACCACAA	360
AACCAAGCAA GAGGATGTTC ACGATGGAAG GTTTNANTGG GTTTNCCNT GTGAANGTGT	420
TCCGTTGNCA GAGCAGTAAC ACGCATTACA CCCAGCGGNG GGCCTGGGGC CTTTCGGGAA	480
TTTTGGCGGG CGTTTCTGG GCCANGGGN TN	512

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GGCACGAGGT AAGCCCCCCC GTCGNTGTAG TGGAACAGAA ACGGGGAAAG TTTACTTTT	60
GGCGCCGTCC GGTAGTCCGT TGAAGCAGAA ATAATCATCG TAGTTTCTCG TNATTNTTGT	120
TTTGGTAAAC GGTGTAGTGG TAAAGGTTGT CCCCAGCAAG TGTAGTTAG ATAAATCAAG	180
GTGATGGAAA TTAAACCAAC GAGATGCCA TAAACAGACT AAGCTCCAGA AGAGACGCTC	240
GCTTCAGGTG TCCTGCGCGN AATGCCTNCG NNGCCTTGGA CCN	283

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GGCACAGGCC GGTTGCCGNT AATCCGCAGC NACTGGTGGG CGGCACTGCT TTACCGCCTG	60
CGAGGCACCC TGCGGAAAAC AACCTGNACG GCAAGACCGG CTCCATGAGC GGCGTGTGCGT	120
CNTTAACTGG GTATGTNACC GATGCCAATG GGCGCAACTG GTGTTTCAA TGGTGACCAA	180
CANTTACGTG GTCGCAGGCG CGCGGNTCAA GGCGCTGGGA AAACCGCCTG GCCACGGCAC	240
TGGGCCAACA GCACGGACTT ATTGAGCACC GAAGATCAA TTGTACGNNGG GGCTTGCTCC	300
GGAATGGGGT NGTGACANTC CAACACNTGT TACTGATTTG NTCCCA	346

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GAGTGCAGTG GTCTGATCAT GGCTCACTAT AGCTTCANTN TCTAATCCTC CCGCCTCANC	60
CTTCCGGTAG CTGGAACTAC AGGCGGACAC GCATGCGCAT ATTTTAAGTA GAGACGGGTT	120
TCGCCATGTT GCCCAGGCTA GTCTCTCCAA CTCCTGGCCT CAAGCGAATC CTGCCGCTTT	180

GGCCTCTAA AGTGCTTGGC TTACAGGCCA GCCACCACGC CTGGCTCCAG ACTTTTTTTT 240
TTTTTTTTT TTTTTTNAA AAAAGGGNTT TTTTNATAANN AG 282

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GGCAGAGCGC CNATCCAGCT ATTCAATNGGG TGCGGTTGCN CCGGGTTTCG ATNATGTTCG 60
GCAACTGGGA AATCCGCCCC AGCAACCGTC CCANTGCGTC CAACCCCGGA ATCTCGATGG 120
TCAGGGACAT CAACGCATTN TGNTCTTCCT TGTTCGAACG GGTGTTGACC GNCAGCACGT 180
TGATCCGCTN GTTGAGCAGG CACTTGTGAA GAACGTCACG CAGCAAGCCG GGAACGTTCG 240
TTAGGCACGG TTGGATAATG TGCCACCGGG ATACGTGAGT NACCGGCANC GGCCCCCAGC 300
TGNACCTGNG NTG 313

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GGCANAGTTG GAAACTTACT TGAAAATCGG NCAAGGCAAA ANTTTTTTT GTTTGTTTT 60
GTTTGTTTT TAGTTCCATG TATACTTCAA AAAGAAACTT GTNTTCGGAA GTTGAGAATG 120
CCACTGGGCG CGGTGGCTCA TCCCTATAAT TCCAACACTT TGGGAAGGCT GGAGTGGGCG 180
GATCACTGGG AGCCCAGGAG TTCCAGATCA GCTTGGCAA CATAGTGAAA ACTCCTCTCT 240
ACAAAAAAAT TAGCCGGTA TGGTGGCAGG CGCCTGTNTT CCCAGCTACT CCGGAGGCTG 300
AGGCGGGGAG GATCACTTGA GCCCCGGGGA GTCGAGGCT GCCATNCAGC CATGATTCCC 360
ACCATTACAT TCCANNCCGG GGNAACAGGT TTAAAAAAA AAAACNCGGG GGGTATTTTT 420
AGGGGGCCCG GGGGCCCTG CGTTTNCCC CCCGG 455

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

ACTTTTNAAA CCCGAAACTG AAGACACTCA TCATCAACCG AAATGTCGAC TGNCGTTCCG	60
TCTCTCGGGG AAATCAACGC CCTCAACGTG CCCTCCCTTC CGGGCAACCT GAACAAGCCC	120
AATCAGACCC CCGCCTGGAC CAGCAACCCT CTGTTTGTNT ATTNACCGA GACGTACAAC	180
ACCATTGCNT CGAACGCGNAG TGGNCCTGAA CCTCCTTAAA CCCCGGAACC CTGGAGAAC	240
TCAACAAAGGA GGTGTNCAAG GACGTGTTCC TCACCAACTA CTTCTTCAC CGGTTTGCGG	300
GCCGAGATCT TCCAAGACAT TTCAGCATGA ACCCNGNCTT TCCAGTGTTC CCATTCTTT	360
TTTTGGGGGT TCCAAGGTGT TNCCCCCTTA GGGNTTTN	398

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

TCANCATATG CATTTTTGG TGCAACTTTN CGGGAGGNGC ATAAGAAGGA AGTCACCCGG	60
ATGCTTCANT CAACTTGCTC ANAGGTTCT AAGAAGTGGC TCAGAGNGGT T	111

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GGCACAGGTG ATCGGNACCC AGNTCGAGCA CGTNCCGGCC ATGCTGGAAA CCATCTTCAA	60
GAGCGCCTTC GGCTCGACC CGGCATTCGG CGGCCTGGTC GGCACNCCAT TGTNATGGGT	120
GTAAANGAGG TGTGTTGCC AACGANNAG GCCTGGCCA GTGCGCCCAA CGTCGCCGCC	180
GTANGCCGAT TNAAACACCC CGGTGCNCAA GGCGTGGTCC AGGCCTTCAG CGTGTTCCTC	240
GATACCTTCG TGNATCGGCA CCTGCACCGC GTGNCTGAT CCTGNTGTCG GGGTTCTAAC	300

353

ACCNAGGNT TTCAAGGTG AATGGGNATC GTGCTGGACC CAGAATTGGG TGG

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

CGGGAACAGG TTGGNATCAA TATTCTCCNC TGGCGTNAAG ATCANCCGT NATCCGNCGC	60
AAACTNTTAT TACAAACAC GCAGGAATCG ATTGAGAACC ATTGGCCGTT TCGTCGGCTA	120
TGAANGATCA GCTGTATTTC TGGCGGGTAT TCCGCAAGCG GGTGGAGTG AAGCCCGANT	180
AATTTGGTC GCCGCACGTG GNAGATTAAT TATCCTGCTA AACCGTATAA AGGCCGGCG	240
GGATAAAATGC GAATTGCATA CCATTTTAA GGCTTGTAA AGCCTGAGAG TTTTTTTGCA	300
AAGGGAACCG CTTGCTAAGG GCGGTTTNC CACCTTTCC CTCGGNGTGG ATTTTTGAA	360
ACGGGAACCA CAGGNTTTT AAGGGTCCAC AAATTNCCC CGGGTTCAGG GTTCCTTTT	420
AAAAAAAGGC GAGATTGGTG CGNATCCAAA AATTNCNCTT GAACGGATTG GNCAGGGTTT	480
	481

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(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

TCGAATTCCCT GGACTCAAGC AATCCTCCCG TNTNAGCCTC CCAAATTGCT AGGGTTNTAG	60
GTGTAAGCCA GCCCTGGCAA CAAAGTGTGA AGACCTGNT TCTGACAAA AAAAAAAA	120
AAATTNAAAN CA	132

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

CNGNGCTTCC ATCGGNTNAC CGCTGCGTTG CCACGGGCAG TTGAAGGTGC CCATGCCAAA	60
CATATCCGNC CCCGGCCACA CAAAGGTGTG CCAGTGAACA GGCGGCCATG CGCAGGTGCT	120
CGNGCCATCG GTTTGCCGAG GGATCAGCTT GTTTGCNTCG TAAATGGCGG AAGGCGAGGG	180
GAGACTCGCT GGCAAGGCCT TCGAAGCGCA CCTGATTGCA CAACGGGGAN NTTACGGCA	240
TGGGNNTTTT CCTTATTGTT CTTGGCGAT GTTTGGGTTA TTAGCAAAGG NACCTGGGT	300
TGCTGNTTTT TGGAAATTAA CCAAGGTGTA NTNGCGGTT TGAGTTGGNG AGGGTTA	357

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 517 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GGCACAGCAG CNCTCAGGCA GCTCCAGCAG CAGATATTAA GCCCGCCGCT GCACGCTAAG	60
CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTGCCGTTG	120
CGCACCACTG CATGAAGAAC GGTGCACCA ACNAGNATGC GGTTCTATGC CGCGGCCGCT	180
GGTTTCAACT TCAGGTAATT CAGGCATAGC ATCTCCAGGG ATGAACAGAT GGAGTCAATA	240
TGGGGCAAG CAGNTATCAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATGCAAAG	300
CGGAGAATTA TTTGATTTTG CGCTTCTTTG TAGATNCACG TGGCTGGGCG GAACAACCTGG	360
GNCCGAATT TTTNANTTNC CAATTTTTTC CGGCTTNANN ACGTTTGTN CCTTCGTAGT	420
GGNTNTAGAA GNGNCCCACT ACCNGNAGGA GGAACCCACT TTGNTTTTTT CAAGGATAAC	480
CTTAGNCCA GGNTTTTTTC CCNTAAGNAT TNAGACT	517

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GGCAGAGCAG CCCTCAGGCA GCTCCAGCAG CAGATATTAA GCCCGCCGCT GCACGCTAAG	60
CNCTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTNCCTT	120

GCGCACCAC TGCATGAAGAA TGGTTGCACC AACGAGATGC GGTTCTATGC CGCGGCCGCT 180
GGTTTCAACT TCGGGTAATT CAGGCATAGC ATCTCCAGGA ATGAACAGAT GCAGTCAATA 240
TGGGGCAAG CATNTAACAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATCAAAGC 300
GAGATTATTT GATTTCCGC TTCTTTGTAG ATCACGTGCT NGCGAACAAAC TGGATCGATT 360
TTTTTCAGTT CCCATTTTC CGGTTAGTA CGTTTNCCN TCGTAGTGTT ATAGAAGTGA 420
CCCATTANCC GCAGAGGAAA CCATTGATT TTNTCANGG 459

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GGCACAGGTT TTTNGGGCTC AGTCGTGGT GCCAGCTGCC GTGGGTGCGG TGAATGAAAC 60
GAGTTTCACA GAACTCCCAG AAGCGCCGGT ACCAGGTTTC GTAATGCAGC TCCCCCGTGC 120
NTTTGAGCAG CGCCTGGCA CGGGCACTGG CTTCGCAATG GGTCCAGTGC AGGCGCTCGC 180
GCACNANGGG GCCTGGCTCC AGTCGAGGGT GTAGACAATG CCGGGGGCGC CGTCGACGGC 240
CCAGGCGTAT TCACAGGCAG TGGCGAACAG GCCCTGGCG TCGGTCACTA ACCACTCAGG 300
GGTGACGAGC CGGGCATCCA GGCGCGACT TCAGGGTGCA AACCANTCGN GCCCATTGAA 360
ACCNTGGCCC GGGGGTGATN CCNTAGGGAC G 391

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GANTTGGCGG TCAGGTCAAC GGCCTTCC ANGGCGAAA TCAGGAAGAT CACCGCCACC 60
GGGATAAACG CCACCCAGTC GAACGAAAAA CCGTACTTGA ACGGCACCGG TACGCTGATC 120
AGTGGCAGCT GGGCAGGGC CCCAGGTG ACGCGGCCA TCCACCAAGC CACCACAAAA 180
CCCAGGGTCA GGCGATCAC GATCGAACCC AGGCGCAGGA ACGCTTTGTT GGAAGCGGTT 240
GAGCACCACG ATGGTCAGCA GCACCAGGNT CGCCACCATN NTTTNCCGG CGGNGCCAG 300

GTCGTTGGCG CCATNAACCG CCGGNATGT TCGGTGACGG NCACTTGNTC AGGGACAAAC	360
CCTTCAAGGT AATGATGGTG CCCGTGAACC ACCGGGGTGT TTAATTGGC CATTNCCCG	420
TTGAAATGTT TGNGNACCNT TTGNTAAAAA GC	452

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

ACACCAACTA CCAGTATCAC CGGCAGTTGT NCCTGTNTTA CCCANTCTGC ANAAGTGAAA	60
GTNTCAGAAA GCGCGTAAA CCAGCCGCCA GCACCTTCCA CTAACACCCA GTCAGCCTGT	120
TGTNCAAGCG CCGCGTAAAT CCGCGCTCA TTACCAATGA ATTCTATCGG TCTGCCCTCT	180
TGCGCCGCTG GATGATGTGC GGCGNAGTGG GTTCTGCGAA NGTGTGAAGG NTTTACTGTT	240
GCGTAATCCA GCTGCAGGCT GCTGTTGCCCG TGTGAACGCC AGGCGTCGCT ATTGCGTGAA	300
CCCTTCCGGG GTNTTTCCG NTGNCANTGG NGACCGGTTT TT	342

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GGCACGAGGN CAGCCAGACC TTGCCGGTTC CCGACGGCCT GGACTGGATT CAGGCGGCAC	60
GAATCCCGGA AACCTTCTTC ACCGTATGGG CCAACCTGTT CGGCATCGGC GGTGCGCATA	120
AAGGCCAGCG CGTNTTGATC CATGGCGCA CCAGCGGCAT CGGCACGACC GCGCCTGATG	180
CTCTGCCGCG AAGTCCATA TCGAAGCGTT CGCCACCGCC GGCAGCNTGG NAAAAATGCG	240
CCGNCATCCG CGAAGCTGGN TNCCGAGCCG ATCAACTACC GGGAACAGAA TTTCGCCGAG	300
GTCATCGCTG ACAAGACCGC AGCGANAGGN TGTCAATGTN GGTCCCTTCGA AATCATGGGT	360
GGCTNCTACC TGANCAGG	377

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GGCACGAGGG AAGCACGGCC CANCCNTCCG GAATTCAACA TTGGCTCAGC AGGAAATTCA 60
GCCCANCCCA CGGNACCTGN 80

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CNNCTGCAGG TCGACACTAG TGGATCCAAA GAATACAGCC GAGTTTCACA CCAACTACCA 60
GTATCACCGG CAGTTGTNCC TGTNTNACCC AATCTGCAA AGTNAAAGTN TCAGAAAGCG 120
GCGTAAACCA GCCGCCAGCA CCTTCCACTA ACACCCAGTC AGCCTGTTGT NCAAGCGCGC 180
GTAATCCGGC GCTCATTACC AATNATTCTA TCGGTCTGCC CTCTTGCAGC CTGATGATGT 240
GCGGCGAAGT GGGTCTGCG AAGGTGTAAG GATTACTGT TGGCTAATCC AGCTTGAGG 300
CTGCTGTTGC NCTGTAACGN CAGCNCGTCG CTATTGCGTA AAACCTTCCG GGGTCTTTTC 360
GGTTGCCAGA GGCGANCCGG TTTATAAACCTGCC GGTAGCCTGT NGGCTTTTC 420
NGGGTTGGTA AAAAGTNGCA CAATTGGGGG AACAAATTTT CCCCCANTTT GGGGTATCCC 480
GTTTCCGGTG 490

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GCTGAATATN ATCGAGTGCT GGGGCGATGA TGTACCTCAG GGGCAGGTNA CCTCNTTTCC 60
CATGGCGGTC AAGCTCAAGG AGGATGAAAC CNTGGTGTTC TCCTGGATCG TNTGGCCGTC 120
GCGGCAGGTG CGTNTCGNCG GGAATGAGCA AGGTGAATGG NAAGACCCGC GCCCTGAAAG 180

GCAGACGTCA ATCCGATGCC GTTGATGGG CAACGGGATG GATCTATGGC GGATTAAAGA	240
TGATCCTCAA CACCTGAGGC CAGGCCTCA TGGGACGGCG GCTTTANTCC CGATTCGTCT	300
NTTCGCANGG TTAGGACCGA CGATAAATTC TGGGTTGCAA GACCANTGNC GAAAAAAAGT	359

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GGCACGAGCA AAACTCTGCT AAGGACCATA AGCATATTTN ATCACTTGCA GAGAGGCATC	60
ACTGTCACCC CAATTTACAG ATGGGAAACT GAGCAGAAAG TTGTTAAAAC ACCCAGCACT	120
TTGGGAGGCC GAGGTGGATG GATCACTTGG ATCTCTGGAG GTTGGAAAGCC AGCCTGGGA	180
AACATAGCAA AACCCCCATCT CTACAAAAAA AATCCAGAAA TTAGTTGGGT GTGGTGGCGC	240
ACGCTGTGAG CCCCAGCTGC TTCAGAAGGC TGAGGCTTGC AGTAAAGCTG AGTTTGCCA	300
CCCACTGGCA CTTCGGNGCC TGGGGGCAAC AGGNGACCCT GTTTCAAAA AAAANNNN	357

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

NCGATATCGC CACGNTCGTT CAAATACTTG AAGTCGACGT TCTGTGAACC GCTGCCATGC	60
AGATGAATTN NTCCTGTNCG GCCGGCAGTN CGTTGAACGG CACTTCCAGG GCTGAACTTG	120
TAGTGCAAA NCAGACGAAA CCCAGCATCT GGAAGTAATA GACGTTACGC CTGTCCCCAG	180
NCACGTATCG CACCCTTCCG NCAGTNTGNA GGTCACCGTT GAACCAGGCG CTTGATTGTT	240
CGAAGAATTG CTTAACCCN CAGGNACATCA CAGGTTCGGG CAAGTGNCCG GCCGGGGTTG	300
TTTNAAAGGG AAAAACAAAGT TTCGGTTTCC AANTTCGCT	339

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GGCAGAGGNC GNCGGC GGNG GCGGC GGGGN ACTCGGACTC CTGGGACGCC GACGCTTN 58

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GGCANAGTTT GCATTTAGGA GAAGGGCAGA TGGTGTGTGG TCGAAAGCTC ATGGGACTGT 60
AAATTGGTAG ACTTTTTAA AAATCCAGCT TTTGCCCTA ACTTTGGTC TCGGAGACCT 120
CTGTCCTTA ATAACTAGAA CTGTAGGCCG GGC GTGGCGG CTTCATGCCT GTAAATCCCA 180
GCACCTTGTT AGGGTGAGGC GGGCGGATCA CAAGGTCAAGG AGTTTCGAGN ACCAGCCTGG 240
CCCAGCATAG TGGAACCCTG TCTCTAGTAA AATTACAAAA TTTAGCCAGG CATGGTGACG 300
TGCCTGTGA GTCTTCAGCT ACTTGTTAAG GGNTGGGGC AGGNGNTTG CTTTGNAACC 360
CGGGGNG 367

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

AGCTTCCAGG TTGAAGCCGG NGAGCGCGTG GCGATCATCG GCCCGAACGG TATCGGCAAG 60
ACCACCCCTGC TGC GTACCCCT GGTCAACGAA CTGACTCCGG ATGCCGGTAC GTGCAAGTGG 120
TACCGACGCG GCTGAAACTG GGCTATTAAAC GCCCAGAACC ATGCTTCGGA ACTTCAAGGA 180
CGAAGTCAA CCTGTTNCGA CTGGGTTGGG CCGCTGGACC AAGGGAAGGG CGAGCAAGTG 240
NGTTCGCGGT ACCCTGNGGC CGCAAACCTGG TTCTTCCAAC GANGNGG 287

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GGCACAGTAA AAAGGTTGAA AATGGCTTT TTCCACTAGG AAGGCTGTGG GGACATAAGC	60
TGACAACATAC CCTACATGGA ACAGGCAACC CCGTCATGCA AGTAGGCCTC TCTCCCAAAG	120
GCACCTCCAT CCCTGCTGTC ATGTGGCACA GATGAGCACA CCTACTACGT ACAATGCAG	180
TGTAGGCCACG CCAGACTGGA CCAAGGACAC ACTCTTAGCC TTCTCTTCTC TCCAAATTCA	240
CTTTATTAAT CTTTAANCCC ACACATCCGT GGTTGGGAAA GGTGTCCTTT GATTCTCCA	300
AAATTCAAAA GGGCNTTCCC TGNTATGGNT GTCTGGGATT TATNTT	346

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GGCANAGCTA GTNCTTNNTT CCATAAAAAAA AAGTCGTGCC TGTGGTTATG AAAAAATGTT	60
CAACTAACCT AGAAGAGTTC AGCTACCAAG TGAAGGATTA TGGGAAAGCA GTATTTTTTC	120
AGACCTGGGT ATGCATGAGT GAATAACCAT GAAAGCTTTA TGAAAAATAT ACATCTCCTG	180
GGCCCCTATT AATCAGAATT TCTGTGGGTG TGGCCTCCAA GTTCATACTT TAAAATGGGA	240
TCTCCACATA ATTCCATGTA CACCCAGGCT GGGTAAACAC CTGAGTTCA TGTATTTATT	300
ACTATTCCAG AAACAAACAC AAACCTTTGG GGTGGGATTT TAAAGGGNGC AAGGTTTTTN	360
GGNTGGTGT AAGCAAAGCC ATTTTTNAAG TTGGTCTNTT GGCAACTCCA AGG	413

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

AANCTANCAGC NANGNGCGCC TGCAGGTCGT ACACTAGTGG ATCCAAAGAA TTCGGCACGA	60
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GGGTGCACCT	GGCGATTCCG	AAAAGCTCGG	TGTCGTGCG	TNATGAACGC	AAGCCCAGCG	120
CCTCGGTCCCT	GGTCGAACTC	TTTGCCGGCC	GCTCCCTGGA	GCCTGGCCAG	GTATTGGCGA	180
TCATCAACCT	GGTGGTCCAC	CNACNTTCCT	GAATTGAGCA	AGTGCAGAGA	TCACCGTAGT	240
CGACCAGAAG	GGCAACCTGC	TGTNCGNAC	CTTGCGGAGG	AACTNTTNG	CTGACCATGG	300
CCGGNCAAGC	AGTTCGGACT	GACAG				325

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GGCACGAGGN	AGAAAAGGAA	GGGTGGAAGG	AAAAGAAAAG	AAAAAAAGGA	AAGGAAAGAA	60
AGGGAAAGAC	AGGAAAAAAA	AAAAAAAAAA	NCNCGGGGGN	NCTT		104

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GGCACGAGGC	CATGGTGTG	ACCAGGNGGC	TCGGTTCATC	AATGCTGTTG	AGCGAAGACA	60
GGACTTCAGC	CGGGACTTTN	TTGCCCAACT	GCACATATTG	CTCGAACTGC	GACANAGCTT	120
GCGCACGNAC	AACTNGGATT	NATGATCCCG	GGCTTCGA			158

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

NNGTANNGCG	CCTGCAGGTC	GACACTAGTG	GATCCAAAGA	ATTGGCACG	AGCCGNCACC	60
CAGCGTGGCA	TGACCTTGGA	ACTCAGAGGT	CGGCTTTTG	CGTACCAGGT	TGATAGTGGC	120

CCCCAGTGAA CCAGCACCGG TCAGCAGGNC ANT CGCGCCC TTGAAGTACT TCAACACGGT	180
CGTAGATCGC CAT GTCGCTC AGCGTGTCC CCGTCGAGTA AGCCACGTTG CGTGC GGTTGG	240
AAGGGNATCC CGTNATATTN GGAAGTTGTT GATAGAGAAA CCACGAGCGT AGTAGTTGCT	300
GCGCTCAGTA TCGAAGGCTT GAAACGGNAA TGCCCGGC GT NTGGNGCATC AAGTTNGNCG	360
ACACTGGTCA GG	372

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAGTAGGNNGC CCATNCATCT TTGCTGTGGA GCATTNGCTC CTTTTNGGG GTGGGAATNT	60
GCCTTGCCCG GTCTGCCGGA AAC CAGCAGG AGCAACCTGC GGTNCCCACA AAATTTNGGG	120
TGTACTGGAC CCACTNGCA	139

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GGCAGAGTGN CATNCAGNTC GGACCGAAAA AAGTGGTTA ATT CGGGCTG GCTTGTGCG	60
GTGTGAGCGG TCTGTTTAT GCCATGGCTT TTTGGTCAC TGGTCTGCCG TTGCTGAGTT	120
TAATTCTGCT GTGCATTGGC AGGGTGTTC TC GGCGTCGG CNAAAGCTTT GCCAGTACGG	180
GGTCTACCCT ATGGGGGATT GG CCTGGTGG GG CGTTGCA TACCGCCGG GTTATCTCAT	240
GGGAATGGGG TGGC GACTTA CGGTGCGATG GCTGCCGGGG CACCGCTTCG GTGTTTACC	300
TCAATCAGCA CTGGGGGGTT GGGCTGGGGG TGGCGGC GTT GATCGTGTG GNCGGTGGNC	360
GGTTTCGCTG TGGGNTGTC GAATTNCAA CCAAACGTGA ACGATTNNC GNCGTTAANG	420
GTAATTGCC TTANC GCAAT TTTNGGGGC TTATTTGGAC TTAAGGTTT GGGACTTGCA	480
ATGGGTACCT GGGTTTGCC GGNANC GNA	509

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GGCAGAGCTT GGCTTCGCTG GTTTCCGGCT GTTCCAGGAT GGTGCTGACC TTGTTGTA	60
TCANGCGGGC CTGGGAAGTN AATCACCGCT TCGTAGAACT GGTAGTCGGT CATTTCGCCG	120
GTTTCGAGA TGGTCATCTC GCACACCATG GCCAAACGGT CGACTTTCGG GTTCAGGGAG	180
CACAAGCCGT TGGGACAGCT GCTCAGGCAC ATAGGGATG ACGCGTTCG GGGAAAGTACA	240
CCGGGTTGCC GGGCAACTGG GGCTTCGTTT NTCCAAGGCC CGNACCNGTT CTTTAAGGTA	300
GCTTTGGACA AGTTGGGCAA TCGGGGACGA AACNAATTTC TCCAAGCCNG CNGGAGGAAC	360
AAAGGGGCAA NTTTNNCNA GGTTTGCGGT TTCGCAATTAA AAACCCCCAT TGTTGGAAA	420
TTCNCGGGG NAATTTNGG CCNGAANTGG GGGACGGAAC CGGAAATTTC ACCGCAAATT	480
	480

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GGCAGAGGAA GACATCCCATT GTTTATGAGT CTGAAGACTT AACATTGTTA AGATAATACT	60
CTCCAAATTG ATTAAGAGGA TAATACTCTC CAAATTGATC TACAGATTCA ACATGATCCC	120
TATCAAAATC TCAGCTGGCT TCTTTGAGA AACTGACAAA TTGATTCCAA AATTCAATATG	180
AAATTGCAAG GGATGCAGAA CATCAGAACATCTTGTAAA AGANCAAAAC TGGAGTACTC	240
CCACTTCTCA AAAACTTACT GCAANGCAAA AGTAATCAAG ATAGGTTGG GCATGGTGGC	300
TCCTGGACTG TAATCCCAGC ACTTTGGAAA GTCCGGGGCG AGTGGGGTTC ATTTGAGGTT	360
CAGGGGTTCC AAAACCAGNC TGGGCCACCT GGGTGGAACCCCTTTNTA CTAAAACATT	420
TAAAAAAATTG GGNTGGGGCT TGGTGGGCAG GGNCNGTAAT TCCCGGTTAC TCNGGGGGT	480
TT	482

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GGCAGAGGGC TTCCAGGCAC ACCAGGCCA GGNAGTAGCG CAATTCGTCA TCGTCCGGGT	60
ATTGCNGCAC GAGGTTGGCG AACTGNACCT TGGCGTCTTC CATGCGGTCC TGTTCGACCA	120
GCATGCGGGC ATAGGTCAGC AGCAGGCGTT TGTCGCCCCGT GTACTTCTTG ATGCTTTTT	180
CCCAGCAACG GGAATCGTT NCTTGCCNGG GTTTGAGGTT TTNCAACAAG CGGGCGCGCA	240
NANGGATTAG GGG	253

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GGCACAGGAA GGAAGAAGAA GAAGGAGGAG GAGGAGGAGA AGGAGGAAGA NGAAAGAAGA	60
AGAAAGAAGA GGAAGAAGAA GAAAGGAAGA AGGAAGAAGG AGAAGGNGGA GAAGGNGAAA	120
AAGCGNANAG AGGGAGGAA GANGAAGGGAA AAAAAAAA AAAAAACC	168

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GGCAGAGGNA AAAAGGGAGA TACTATTTN AGTAAATTG AGGGCAAGGA ATATACAAAG	60
GAGTTAGGTG GCTTGGAAAGA AGATTTTG C TATATATGTA AACTAAGCTG TGTGTGGGTG	120
GGTATTTGC TTGTTGGTTT TTGAGACAGG CTCTCACTGT AGTCCAGGCT GGAGTGCAGT	180
GTGGCAGTCA TAGCTCACTG TAACCTTGAA CTCCTGCACT CAAGCCATCC TCCCACATTCA	240
GCCTCCTGAG TAGTTAGGAC TACAGGTGCG TGCTACCACA CCCTGCTCAC TTTGGCATT	300

TTTTNTNTT TNTGTTNNNT TGATTTTTT GGGACATAGT

340

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GGCAGAGTCT GGACCGGNCT GGCCAATATG GTGAAGCCCC CCTCTCTACT GAAAATGCAA	60
AAGTTAGTCG AGTGTGGTGG TGGGCACCTG NTAATCCCGG CTATTTGGAA GGCTGAGGCA	120
GGAGAATTAC TTGACGCTGG GAGGTGGAGG TTGCAGTGAG CCAGGGTCGT GCCGCTGCAT	180
NCCAGCCTGG GNAGACAAGA GTGAGACATT ATCTAAAAAA AAAAAAAAAA AAAAANAAA	240
AAAAACCCGG GGGGGTTTTT TTTGGGGGGC CCGGGGCCNN TGNTTTCCC CCCGGGGGGG	300
GTGNCCCCG	309

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

AGCTTCCAGG TTGAAGCCGG TGAGCGCGTG GCGATCATCG GCCCGAACGG TATCGGCAAG	60
ACCACCCCTGC TGCCTACCCCT GGTCAACGAA CTGACNCCGG ATNNCGGTAC GTNCAAGTGG	120
ACNGACGCGG NTGAAACTGG GCTATTACGC CCAGGACCAT GNTTCGGAAC TTCAAGACG	180
GAGTCCAACC TGTCGACTG GATGGGCCGC TGGACCAAGG NAAGGCGAGC AAGTGGTTCG	240
CGGTTACCCCT GGGCCGCATN GTTGTCTTN CAACGNCGAG NTCCTTTAAT TCGGTTGTAG	300
GTGAATTCC CCGTTGG	317

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

GGNACAGCTC GCGGGAGCGA TATGCCACG GTCGTTCAAN TACTTGNAGT CGACGTTGTG	60
TGAACCGCTG CCATGCAGGA TGGAATTCT GCTGTTCGGC CGGCAGTTCG TTGAACGGNC	120
ACTTCCAGGN TGAACCTGTA GTGCGANNCA ACGAAACCCA GCATCTGGGA GTGAATAGAC	180
GTTACGCCTN TCCCAGGCCAC GTNATCGCAC CCTNNNGTCA GTNTGTAGGT NANNNNTGTGA	240
CCANGCGCTT GGATGTTCNT AGAATTGCTT AACCCCCAGG CCATCACANG TCGGGCAAGC	300
GCCGGCCGGG TTGTTGAAGG AAAACANCTT CNGTTNCCAG CTCGTGAATG GNATGGCCTC	360
AGATTCTGTGC A	371

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GGCAGAGCAG CNCTCAGGCA GCTCCAGCAG CAGATATTAA GCCCGCCGCT GCACGCTAAG	60
CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTGCCGTTG	120
CGCACCACTG CATGAAGAACAT GGTTGCACCA ACGAGATGCG GTTCTATGCC GCGGCGGCTG	180
GTTCACATT CGGGTAATTG AGGCATAGCA TCTCCAGGGA ATGAACAGAT GNAGTCAATA	240
TGGGGGCAAG CAGATANCAA AAAACCCCCG CGGAGCGAGG TTTTTTTTTT ACATCCAAAG	300
CGGGNATTNT TTGATTTCG CTTCTTGTA GATCACGTGC TTGGNGAACAA ACTGGTTCNN	360
ATTTTTTT	368

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GGCAGAGGNA TGGGTGCCTG TGGTCCCCAG CTGCTCGGNA GGCTGAGGCA GGACAGTCGC	60
TTGAACCCGG GCAGCAGAGG TCGNGGTGAG NCNAGAATTG TGTCGCTGNA CTCCAGCCTG	120
GGCGACAAAG GAAGACTCAA AAAAAAAA AAAAAAAA AAAAAAAAC N	171

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GGCACGAGGC GCTGAATATC ATCGAGTGCT GGGCGATGA TGTACCTCAG GGGCAGGTGA	60
CCTCGTTCC CATGGCGTC AAGCTCAAGG AGGATGAAAC CGTGGTGTTC TCCTGGATCG	120
TCTGGCCGTC GCGGCAGGTG CGTGAACGCC GGTNATGAAG ACAAGGTGAT GGAAGACCCG	180
CGNCCTGAAG GCAGACGTCC AATTCCGATG CCGTTGATG GGCAACGGGA TGGATTCTTA	240
TGGGCGGATT TGAAGNATGG ATCCCTCCAA CACCTGAGGG CCCAGGCGTT TCATGGGACG	300
GGCGGGTTGT TAGTTCCGAT TCGNCTGTTG GCCAGGGTTA GGGACCCGAC GGATTAAACT	360
TCTGGGTGGC AAAGACCCAT TGCCGNAAAG ANTNANTTCT TAGAGCGGCC CNNGGNCCCA	420
TTCGTTTTTT TCCANCCGG GTTGGGGTTA CCAGTTAAGT NTTACCCATT TCGGCCTTTT	480
AGTGATCGAA TTTTACAATT TCATTGGC	508

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GGCACGAGGC CATGCGCAAG GACGTGCTGG CTAAGTGCTA CGGCAGGCGAT ATCTCCCGTA	60
AGCGCAACTG CTTGGAAAAG CAGAAGGCCG GCAAGAACCG CATGAAGACG CTGGGCTCCG	120
TCTCGGTGCC GCAGGAGGCN CTTCGTGGCC GCGCCTGTCT ACCGACGCCG ATGATTAACC	180
CACCCAAGCA CGCCGAACCC TTCTCGCAGC CGCGCCTTGG TTGCGAAGGT TGTCAGCTGC	240
CGGATTCCAC GGCANGCTTG AGCGNCCCG TCCGCGCAAG AGGGGTTGGG GCTGGGGCTT	300
TAGGCGAGTA NTTAGGTTGA ATCGGCCAG GGTNGGACCC AGACTATTG GTNCTGGTGT	360
TCGTTCGAGA GTTATTGTTA NAGCGGNCCG GGGGCCATT CGATTTTCC ATCCGGGTGG	420
GGGTACCAGG TNAAGNTTAC CCAATTGGNC CTTTAGTGGA TCGTTTTACA AATTNATTGG	480
CCTNGTTT	488

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GGCACGAGNA	CTGCGGCGTG	CTTCCTGTCT	CGTTTCGCCA	AGANCTTCAA	TTGGGCCAC	60
CTGGACATCG	CCGGNACCGC	CTGGTANCAG	CGGC GGCAAG	GACAAGGGCG	CCACTGGCCG	120
TCNGGTTCCA	TTGCTGACCC	AGTACCTGCT	GGAA CCGCGC	CAAAGCCTGA	AAATNAAGAT	180
TNCCGGGCGC	TTGTAAAACC	GCCC GGNNGCT	GCAGGGAAC	GCAATGTACC	CAAGTNGACT	240
TCTTATATAT	TGCC CAGCGC	CGATT CCTTC	CGCGGGCCTG	GNACTTGCC	TGCAAGCTTC	300
ACCGNAAAAA	GCCTGGCGCA	TGGGCCACCG	TATCTNACCT	GGCATTNGCA	ACGGTTGCCG	360
NCCAGNTTNA	CGGACCTTGG	ACGGNCCGTC	TGTGGGGTT	TTCAAGGGGC	GAAAGTTTC	420
GTGN NCCCAG	GGTGNCCGCC	GAATT CAGAA	CCGGAAGGGC	TGGTTGGTAC	TNGGGTTTG	480
GGCGACAAT	TGN					493

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GGCACGAGCC	CGAAGTGGTT	GCGGTACTCC	TTGAGCGAGC	TGCCTTCCGG	CGCCACATCG	60
GTGTCGTGGA	AGCTGTAGTA	GTCGATGCC	AGCTTGGAGA	AAA ACTCAA	GGCCGCGTCA	120
CCTTGCCGAT	GGCCACTTCC	ATCGGCTTNA	CCGCTGCGTT	GCCACGGCG	CTTGAAGGTG	180
CCCATGCCAA	ACATATCCGC	CCCCGGCCAC	ACAAAGGTGT	GCCAGTAACA	GGCGGCCATG	240
CGCAGGTGCT	CGCGCATCGG	TTTGC CGAGG	ATCAGNTTGT	TTGCGTCGTA	AATGGCCGGA	300
AGGCGAGGGG	AGAGTCGCTG	GCAGGGGCTT	CGAAGCGCAN	CTNATCGACA	ACGGGGGAAG	360
TACGGCATGG	GGCGTTTTC	CTNATTGTT	TC NTNGGG			396

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GGCAGAGGCC GGTTGCCGNT AATCCGCAGC GACTGGTGGG CGGCAC TGCTGCN TTACCGCCTG	60
CGNGGCACCN TGCAGNAAAA CAACCTGCAC GGCAAGACCG GCTCCATGAG CGGCGTGTG	120
TCGTTGAACG GGGTATGTCA CCGATGCCAA TGGCGCAAC TGGTGTGTTTC GATGGTGACC	180
AACAATTACG TGGTCGCAGG CGCGCGGGTC AAGGCGCTGG GAAAACGCC TGGCCACGGC	240
ACTGGCCAAC AGCACGGACT ATTGAGCACC GAAGATCAAA TTTTNGACGN GGTGGTCTCC	300
GGAAATGGGG TTGTTGACAT TCAACACATG TAANTGATTG ATCCCAGCGT TTTTCGGGN	360
AAAANCCC	368

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GGCANAGGCC AGGCCATCGC CCTCAAATAC GACGGCAAC AAGGCCGAC CCTNNNCGCC	60
AAGGGGAGCG NATGCCCTGG CGGAAGCCAT GCCTCAAGCT GGCCCGGAA GAACGANTCC	120
CGATTTACGA AAATGCCGAG CTGGTCAAAT TACTGGCACG CATGTNGTTG GGCGACACAT	180
NCCCCGAAGA NTTGTACCGC ACCGTCGCCG AGATCCATCG CGTTTGCNTG GGACGCTGAA	240
GGGCAATTCC CGGTGGGCTA CGACCCGGAA CGCGGGCCG GTGGAGCGTT TTTTGACGGG	300
AAAGAGGGCG ACGATTATT AAGGTNGGA GCCGGTTGAN NTTTCCCAAG TTTTTGGGG	360
CCNCCGN	367

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GAGCAGACAC CAAGAAGTCC CAGGCCAAAA TTTTAATTGG NCTAGANAAT GTGGCTGGGG	60
TGTNAGTNAC CAGCCTCAAG GATGGGCTCT TNAGCTTGCA TCTAAGTNAG AATGTCATCG	120
GTGGGCTCCA AGGGGGACTT CCTGCTGGTN AGCGAAGCCA TGTGAATTGA CCTGCTGACC	180
AAAATGTACC GGGCTGTGCT GGATGCNACG CNAGGCAGCT TACAGTCACC GTGAACTAAG	240
AAAGTTCTCC AGTGAAGGTT CCAAGGAGAA CAGTGTGGCT GTCNAGGTTC GTNCCAGGGC	300
CCTGCAGTGG TGNCACCAGN AAGGTTACGT TACAAAAAAA GGGGGNGTCC TTG	353

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

TNCNTNTTT TATTTAGTNC TACATAGTTT TATTGCATGG TTGGGTAAAA CTAACACCAC	60
AGGNAAGCAA TGTAAGATTG TCATGACCAC CATGGTCCCT GGTGCTNNAT TTTAAATTTT	120
TTTGGGGGAT GGCGTCTNAC TTTNTTGCCC AGGGTAGAGT GCAGTGGTGC NATCTCTG	178

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GGTGGTGAAT TTCCCCAACT ATNACCAGAC CTNAAAATC GTGGGTAANA AGCTGGTGGA	60
GGTNTCCACC ATCGNAGGCG TGACCTATGA GCGCNTAANA AGAGAANTGG CCTAAGCAGC	120
CAGGCCCGGC CCAGGGAAGC TACAAACCCA CCANTAAAAC TGAATATAAG GACAAAAAAA	180
AAAAAAANTT TTGGGGGGGG GNCCGGNTCC CN	212

(2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

CAAGGATTAC AGAGCTAGTA AGTGGCAGAN CTGGGTTTA AACCCAGGGA AGCTAGATT	60
CAAAGTTTG TNTTCTTAAC TACTAAGCTA CACTGTTGAT CACCCTTGGN GTCGTGGTT	120
AGGAAGAAAA GGAAGGGAA ACAATGAAGG TGGGAGAAGA TGAAGGACTT AGGGCTAAA	180
GCTGATGCTT CANTGAAGGT GGGAAAACCT GTGCCTGTGG GGTTTCCTC AGATTACACA	240
CACGTGGCAC AGTTTNCAT NATNCAGGTT GCTGAAAAAN AGGT	284

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GGCACGAGGC TCTGTGGAAG ACGACCACAT CCCCTTCCTC CGCAGAGGGG TACCCGTGNC	60
TCCATCTCAT CTCCACGCCC TTCCCTGCTG TNTGGCACAC CCCTGCGGAC ACCGAGGTCA	120
ATCTCCACCC ACCCACGGTA CACAACTTGT GCCGCATTCT CGCTGTGTT TCCTGGCTGAAT	180
ACCTGGGGCT CTAGCGTGCT TGGCCAATGA ACTGTGGAGA GGACTGTGAA GAGAGAAGGT	240
CCCAGCGGGG GCCAGTGAAA GCTCAGGCAG GTTACTGCCT AGGGTGTGCT GGTTTGTCC	300
TTTCANACCT TTGTTTCCN AATTGTGCTA CANTGGAAGA CNTGTTGNT TTG	353

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GGCACGAGCT CACTTCTGGA GAAATTGTT ATCTTCTGGA GAAGATAGAT ACAGATTGGT	60
ACAGAGGGAA CTGTAGAAC CAGATTGGCA TATTCCTGC CAACTATGTC AAAGTGAATT	120
GTAAGTGGGT TGTGTTGTT TTAATTGGT CATATACTCA GTGGGTTCTA TGTGACTTGT	180
AGGTTGGAAA AAATAACTAG AAACCCAGAT TCTAGTTCTC TTTCATTGAT TCATTTGGCA	240
TTTGGAAAAT TCAAAAATAA NGTTGGTCA ACTAGGTGGT GGTTAATTAT TATNTTATGG	300
GGTGTAGGA ACTTAATGCC NANANGCTGT TCTGAA	336

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GGCACGAGCC AGGCTGGTCT CGAACTCTTG GCCTCAGGTG ATCCTCCCGC CTCAACCTCC	60
CAAAGTNNTA GGATTACAGG CGTGAGTCAC TGCATCTGGC CAATTGGATA CATTCCGTCA	120
GCCAAATTTC AAATTCTTCC TATTGTGCTA TAGTATGGAT GTGCCCTTAAT GTATTTAAC	180
CACCCCTTAT TATTGGGCTT ATTATTGAAC TTATTCCAG CTTAAGTGAT AGAAACAGTG	240
CTGTACATCC TCCTAGCTAA ATCTGTGTAT ACACCCTTAG TGATTTCCCT AGCTTCAACT	300
CTTAGAAGTG GGATTTNTGG GTCAAAGGGC ATGCATCTTT TAAAGTNNTT GATGTTTATT	360
GCCAANN	367

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGCANAGTGG TAGCACCTTC AAAGAAATCC CCGTGAAC TG TCTATAGACC CACACTAAC	60
AAAGTNAAAA TTAAAGGTGA ACCTGAAATT CAAACTGATT AAAGAAGGTG NTACCAATGA	120
ACTNGAAGTG GTCCATGGAG AGCCAATTAT TAAAAAATAC ACCAAAATNC ATTGATGGAG	180
TGCCTGTGGA AATANCTGAA AAAGAAGACA CGTGAAGAAC GGNTNCATTA CAGGTCC	240
AATAAAATNAC ACT	253

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GGCACGAGCA GATTGGAAA AGCAAGGGAT AACATATGCA GTACAAAATA AGTGGTGAGA	60
TGAAAGCTAA AATGAACATC TGGAAGAAAA AAGCATGGCC AGATGGGTA AAGTCCAGAA	120
AGAAGAGTGA ACAGAGCTGG AGGTACAATG GTAAACTGTG TCTCACTAAA ATCTTCCAGC	180
TCCATGAAAA GGGCTGTGGC TTGACGTTA TAAATGTNTG GAAGGAAAGA GAAGTCTATA	240
ATAATCTACC TGTTGACACA ATATACATTG GGGAGTTAC ANCTTAAACA ATTATTTNA	300
TATCACTTCA TTTTACCCAG GTATTTCAAG GGAAATTTT AAAACGGTTA CNCTTTTCC	360
ATGTACCCN AAAGTCNTG GGCAGTNTCA TCTTNGGCC	400

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GGCAGAGNCT AACCTCATTA AACACCTGAA AGTTNACACT GGAGAAAGGC CTTATNAGTG	60
CAGTGAAATG TGGAAATCC TTTAGCCAAA GTCTAGCCT CATTCAACAC CGCAGAGTTC	120
NCACGGGNAA AAAGGCCTTA TCAGTGCCAG TCAATGTGGG AAATCCTTG GGCTGCAAAT	180
CTGTCCTCAT TGCAACACCA GAGAGTNCA CATTGGAGAA AAGCCTTAGC TGTACTGNNG	240
AATATGCAAT TTCCCTTTA GTGTAATTAT ACTGAAGGNG TAACANCTNT GAAGNGNGGA	300
CAAGTTACCT GATTTGGAA GCCCCAACAT NTAGGGTTAT ACAGTGGGGC GGTTTTCCCC	360
TTAAGTTCC CGGTTATGTG NTTAACATTT TTTNNAACAT GGCTTTTAG GAAGGGTTAN	420
GACTTTTTT NAATTG	436

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GGCAGAGTTA CAGTGGATGA TCTGAAGAAC CTTTCATAG AAGCTGGATG TTCAGTGAAG	60
GCTTTAAAT TCTTCAGAA AGATCGAAA ATGGCGCTCA TTCAATTGGG ATCTGTGGAA	120
GAAGCAATTG AGGCCCTCAT TGAGCTTCNT GAACCATGNA CCTTGGAGAA AATCACCACC	180

TCAGAGTTTC CTTCTCAAAA TCTTACAATC TGNACTTNC TGTGAATTTC TCTCCTAAAA	240
CTGGGACCAT AATTNCAGT AAAAACCTTC AGACATNGGA CTGAAGCAGC TTCAAGACCC	300
AATTTGCC C TCTTNCACA AAATAAACTC TTTNCTGAGT TTGATATTNC AAGTATATT	360
NNAAAAATCA AGGGGTTTTT TTTTTGGGA ATTCCCCC	398

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

CCCAGAGGAC AGATTATCTA CACGTGGAAA GGAGCAAATG CCACACGAGA TGAGCTGACA	60
ACATCTGCGT TCCTGACTGT TCAGTTGGAT CGGTCCCTTG GAGGACAGGC TGTGCAGATC	120
CGAGTCTCCC AAGGmAAAGA GCCTGTTCAC CTACTGAGTT TGTTCAAAGA CAAACCGCTC	180
ATTATTTACA AGAATGGAAC ATCAAAGAAA GGAGGTCAGG CACCTGCTCC CCCTACACGC	240
CTCTTTCAAG TCCGGAGAAA CCTGGyATCT ATCACCAGAA TTGTGGAGGT TGATGTTGAT	300
GCAAATTACAC TGAWTTCTAA CGATGTTkk GGTCTGAAA CTGCCACAAA AATAGTGGCT	360
ACATCTGGGG TAGGAAAAGG TGCTTAGCCC AGGAGGAGGA GGAAAGGAGC AGAGTATTGT	420
AGCAAAGTTG TCCCTAAAGG TGCAAAAACC TTAGGGATCC CAAGAAGGcG AGGAGCCAGA	480
GGGAGTTCTT GGAATTCCCC CTTGGAGGG	509

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

TTATCATAGA TTTNCCNGGT TTAGTTCAC A TCTATCTCGA TGAGTGCTCT TGCCTGCGCC	60
AGTCTTAAGC CTCCTGCTT GTTACATTG TTCAATAGAG CAGATTTGTA TTCTAAATAG	120
GCTCCAGGGA CCAACCTCAC CATCTGACAG AGCTCCTTTT CTTTTTCATT CAGCTTCTCT	180
GTGCCAGGGA GGCCAGTGAG GTTCAAGGGT GGTGCAGTCC GTCTACCTGA ATTGAGGCC	240
ATTGGAATGG AAGGACTCAG GCCGGAATCA ATGTCAGCTT GCCGGCGGAG CCACTGCTGG	300

CAAGCACTAC TGNNCTGGAT ATACTGGAGA ACTTCTGAGA GCATAGTCG TTTAAGGC	360
TCTTCCTCCC GTGTCTTCTT GAGGTGATCG TAGGTTCTGG CACTACAAA ATTGGTAATG	420
CCTGCTGTCC TGTATTCTTG GAGCCTCTTG ATTTCCCTTC GGAGTTCAAA TTCCAATGCA	480
TGGNTTCAA TGAATTGGC ATGTTCCACT GGCCCCACAA TTCTTGCAAA TCGNCTCATT	540
GTTCATACA GGTCCTGGAC CTCCCTGGGA TACCGCCGNT CCATTAATTG AAACTTCTA	600
	600

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GGCANAGACC TGNATGTAGA TGCCCATCCC AAAAGGAGCA AGATCTGCTC TTGCAGTGGG	60
TGTTGAGAGG GGCTGGGAAG GCTTTTCAG TCAAATATGG AGCTGAAAAN NTTCAGAATG	120
TGCNTATGTT GTACATTATC ANTAAGAAC CTAACAGGAG CACAGTGTGA TTTCTCTTCG	180
TAGTGGCGT ACATGGTCTT GGGTTCCAT GTGCAGCAGT GAGAGTTGGT CTCCAAAGCA	240
GAACGGTCAG CATTAACCTC AGCCAAGCAA GCATTCTGTA TGGGGTGCTC CCTTTAAAGC	300
CCAAGGGAAA GCAGGCTCTG CTGCTTTGC CCACCTTTTC AGAGGGAGAG GTGTTGCC	360
ACCANGGTG CCAGGTGTGC TGGGGGCCTG AAGNTAAAAT TAAGTTGTTT TGGGAAAAAA	420
TAATGTCTTT AAGTTCTGC CAGAGNGAAT NNGTANCCAT TTAAAATCCA TTTCATCAGG	480
GGGTTTTTTT AGTCAGT	497

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GGCAGAGCTG GTGAAGACCC AGAGGAAAGG GGAGTAAAAC TTGGATTGGG AGATTCATT	60
TTCTACAGTG TTCTGGTTGG TAAAGCCTCA GCAACAGCCA GTGGAGACTG GGAACACAAC	120
CATAGCCTGT TTCGTAGCCA TATTAATTGG TTTGTGCCTT ACATTATTAC TCCTTGCCAT	180

TTTCAAGAAA GCATTGCCAG CTCTTCCAAT CTCCATCACC TTTGGGCTTG TTTTCTACTT	240
TGCCACAGAT TATCTTGTAC AGCCTTTNA TGGGACCAAT TAGCATTCCA TCAATTCTAT	300
ATCTAGCATN NTTGCGGTTA GAATCCCAGG GATGTTCTT NTTTGACTNT AACAAATCTG	360
GGGAGGACAA GGTGGTTNC CGTGTNCCAC ATTNACAAGT CAAGNTCCCG TTGGACTTTG	420
CAGTTCCCTGC CAGTTCCGA CCANCTGCAN TTTNGGACTT GGAGGGGGNC CTAGGNAACG	480
GTGGACCA A	491

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GGCAGAGNCA GTGTATAACA TATTACATGG TATGCCATGG AATACTATGC AACAAATAAA	60
AGGAATAAAC TATTGATACA CACAACAAC TAGATGGATC TCAGGGGAAC TATGCTGAAT	120
GAAAAAGTCC AACAGAAGAA GTTACATAAA TATGAATTCC AGTTAGAAGA CATTCTGAA	180
ATGGCAAAAT TATAGAGATG GAGAATAGAT TATTGATTTG ACAAGTCTCA AGGATGGAGT	240
GGGGAGAGGG GTTGTGTAAG CCAAAGAGAG GTAGCAAGAG GGATCCTTAT GGTTGATGGA	300
TCAGTTCTGT ATTTTAAC TGTTGGTGGC CNCTATATCT ACACNNNTGGN TAAAACCTACC	360
CTAACTTTAC AAACACACAA TGGGTACTTT NAANCCGTTG AGTCGGATTA TCTCTNGACC	420
AAGTCATTTC CCATTNGTA TTNACCTTGG TTGACCGGTT TTTCCTGTAA GNATTGCCGT	480
CTGGGGGGTC CACCG	495

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

ATTTTATGTT TTCTTTTAT TAATTTTCT TCTTAAATAC CATGTCTTC TGGCTGAAAT	60
CCTTGCCAAA ACCAGGAAGG GCCAGTGTAC TGTGGGTGAA TTTTNCTAAT TCATTTCTTT	120
GTCATTTGAA GCCTTCTGTG GCTTCATGCT GCTTTATGTG TGTGTAAATA TTCAGTATCT	180

TTTCCTAGTT TGCACACTTG TCACAACTGC TAATTAAGCC ACCTATGGAC ACATTGTAAT	240
ATAAATTATT TTGGGCCACG GTGGAGTGGG AGGGAAAGAA TCCAGTTCA CAGGGGTTAA	300
ANTNTGGCAT GTNGTGGAGG TTAATATTTN ANTAAGTTG CCAAAACCAC TTC	353

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

NTTGCTGCCG TCTGCACACG GTCCGCGCGT CGNTGGAAGA CCTGGGNTGG GCCGATTGGN	60
TGCTGTCGCC ACGGGAGGTG CAAGTNAACC ATGTGCATCG GCGCGTGCC GAGCCAGTTT	120
CCGGGCGGCA AACATGCACG CNCNGATCAA GACGAGCCTG CACCGNCTGA AAGCCCGANA	180
CGGTGCCAGG GCCCTGTN	198

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GGCAGNNNTG GAACAGGACA TCCAGCCTGA TGGGCAGATG CCAAGTGACA AGACCATTGG	60
GGNGAGGAGA TGATTCCCTTC AACACCTTCT TCAGTGAAAGA CGGGGGCTGG NNNCATGTGC	120
CGAAGGCAGT GTTTGTGGGA CTTGGAACCC ACAGTNCATT GATGGAAGTT CGCACTGGGN	180
ACCTACCGCC AGCTCTTCCA CCCTGGAGGC ANCTTNATNC ACAGGCAAAG GAAGATGCTG	240
NCAATAAACT TATTGNCCCG AGGGGNACTT ACACCATTG GNCAAGGGAG GATTCAATTGG	300
AGCTGGTGGT TTGGGANCCG AA	322

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

AGCGCAAAGA	CAACTTCCAG	ACCATCCTCA	GCCTCCAGCA	GTTCCAAGGG	NCGGGCGCAC	60
AGGGACATCC	TGGTATGCAT	GACCTCGTGT	TCTGGTCGG	GGACCTGGAA	CTTACCGCAT	120
TGGAGAACGCT	NATGAACCTG	NCACTTTGGT	TCAAGTTGG	NCATGCGTAC	AGTNAGTGCA	180
GN	T					183

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAAGACCCCCA	GACATCAAGC	TCTTGAA	GTGGAGCACC	GATGAATGTG	CAGATCAATG	60
AACATTCCC	TGACAGGATT	ACATTGCAGT	GAAAGGAGTN	AGTGATGNCC	AAGTACCTGC	120
CTCTGCACAG	TGCCAGGGNC	GGTNATGGCG	CATAACGCC	TTGCCGCCAA	AGTTTCAGTT	180
GTGCCCATTA	GTGGTGGCGN	CCTGCACTTA	ACTACCATGN	NTGAATGGCA	CGG	233

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

CACCCCTGCAG	GTGGACAGCT	GGCCGGTCAA	CGAGCGGTAC	CCGGCAGGCC	GCCAGCTGAC	60
CATCTTGAAC	AGCCAGGCTG	CCATCAAGAT	CGGGGGCCGG	GAATCAGGGC	CGCCCCCTTCC	120
AGGGCCAGGT	NTCCGGCCTC	TACTAACAAAT	GGGCTCAAGG	TGCTGGCGCT	GGCCGCCGAA	180
GAAGCAACCC	CAATGTGNCG	GNACTGAGGG	TCACCTGCGN	CCTGGTGGGG	GAGGNGCCGT	240
CCGTGNTGGC	TNCAGTGCN	GGAACCACGG	CCACCACCN	GGCTGGTTGT	ACATGGGCCA	300
CCACCNTTCT	GGGAGGACTA	CCACCACCAT	GGGCCACTTA			340

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GGCACGAGAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	60
AAAAAAA AAANANANAA AAAAAAAA AAAAAAAA NAGN	104

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GGCACGAGAA GAATTGAATT TACATGAGCT CTGTGCAGTG TGCCTAGAAC ACTTCAAGCC	60
TCGAAATGAG TTGGGGATTT GCCCATGTAA GCACGCCCTTC CACAGAAAGT GCCTTATTAA	120
GTGGCTGGAG GTTCGTAAG TGTGTCCCCGT GTGCCAACAT GCCAGTTCTA CAGCTGGCCC	180
AGTTGCACAG TAAGCAGGAC CGTGGACCCC CTNCAGGGAC CCCTTCCTGG GGCAGAGAAC	240
ATTGTATAGC TTACCGCAAG GATNCAGACT GTTGCTGGAC ACGAACGTCT GTTGGAGCC	300
AGGAGGAACA CATGTGGTGT TTGTTGGTT GCTNTTNAC CTNGGGACAC CA	352

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GCNTCGNTGT CCAGCNTGGT NTCCAGTCGG TTNTTCCTC ACATGGTGGC TCCTGNCCAC	60
CCTGGCCTGC CCACCTNAGG GATCCCCAC CCTGCCATCG TTTCCCCAT CGTNAAGCAG	120
GAACCGGCAC CCCCCAGCNT GAGCCCTGCA GTGAAGCGTG AAAATCACCA GTTNACCGTG	180
AAAAAAGGAG GAGGAAAAGA AAGCCCCACG TGAAAGAACG CTCTGATTGC TTTCATGTTG	240
TATTATGAAN GGAGATGAGG GCCAAGGTGG TGGCTGAGTG CACCCCTGAAG GGAAAGTGCC	300
AGCCATTAA CCAGATAACCT TGGTAAGNAA AGTGGGCACA ACCTGTTTC GNGNAGGANC	360
AGGTCCAAGT TATTAGGAGN TTGG	384

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GGCAGAGCTC CGTCCNNGA GATTTTTTTT TTTTTTTTTT TTTTTTTTTT TTT 53

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GGCAGAGGAC CGTCGCAGTC GGACCAAATG CTGGCAGAAT CTTCGTCCGC ACGGCCAG	60
CTGGAGTTGC ACTTGCGGCC GCAACNNCNA GGGGGCGCCG CAGAGNGTGN GNCAAACGGG	120
GACGACTGTC GCTCGGNCC GGGCGNTGCT GCCGTCTGCA CACGGTCCGC NCNTCGNTGG	180
AAGACCTGGG NTGGGCCGAT TGGGTGCTGT CGCCACGGGA GGTGCAAGTN AACCATGTGC	240
ATCGGGCGCG TGCCCGAGCC ANTTTCCGGG CGGCAAAANA TGCACGNGGC NGTTTAAG	298

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGCAGAGAGA AAGGTTCGGT TACTGCCGAA GACTGCTGCC TGGAGGCAAA GGGAGCGCC	60
TTCCTGAAGT TTACTGCATT GTGAAGCCGC CTGGGAATGC TTCACCTCTT TTNAAGGGAT	120
CTTGGATGAG GTGGAAAAAA GACGAGGCAT CTCTCCTGCC CTGGTTCAAGC CACTCATGNG	180
AAAGTGTCAAT GGGAGCCCC TTTCCCAGCC CTGGGCAAA CCATCCTGT NNAAGNAACT	240
TCCTGCCAGG TTTCAGGAAC TGAGGTTGAT CAAACTGTGC CGCCCGNTGG GACTTCCCGG	300
CTTCGAGCAA GTGGGACTTT GNAGTCTTCT CTTGNTCNTN CCTTCAGGGT TCCGGCAACT	360

GGTNTNGTGT GTTTGNNTCTC CCTGNTTTT GGNAGAGGAG GGTCATCTC ATTGCAGACA	420
AGNTCAAGTA CCCGCCCTGG GTTAATTGGT GTTAAAGGGT TTTGAATGAC ANTGGTTNT	480
TGGGACCCNC	490

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GGCANAGCTG GGGGTGTCTC TGCAGGGTAC TGGCAGCCTT GCTACACTGT CCTCATTCCC	60
AGATGGAAAG ACCTGAGTGC CTCTGGCCTT CCTCCGGAA TGATTTCTC ATGAAAATGA	120
NCCAGGCCAC TTCTTCCGAG GGCCAGGCCG CCCCCCTCCCC GAGAACCTGT CCTGCCGTCC	180
GCGGGTGTNT GGCCTGTAGG GGACTGAGAA GCTGGGCTTG CTGGGCACCT CTGGAAATCT	240
GAACCCCTGTG GGGCAAAGA AAGCACC ACT GTAGTTCTG CAGACCCCCA TGCGGTTCAT	300
TGTGCATTGT TTGGTTCTT AGGATGTATG TNTTGCTAGT TTTTTTTAAT GGAAACCCGG	360
GANTAATGTA AATAGCTTT TTGGGNACGG NTTTTAATGT CAAGTATGTN CCGTGGTTGGA	420
CTATTTCAAG GTGCTGATGC ACAATAATT AACACCTGGNG GGGGCCGGNA AAAAAAAA	480
AAA	483

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GGCAGAGGNC CCGCGGTGCG CGGCCCTACG ACCTGGACCG GCGAGATGAT GCCTATTGGC	60
CGGAAGCCAA CGGGGCCGCC CTGGAATGAG CGCTACCATT CTAACCTTAA CCGCCAGTAC	120
CGCTTCCACG AACTTNAAC CACAGGAAC CGCGGCCGCT NACCCGNAC CACTCGGTG	180
GNACAGGAGA GAAGGTTCAA GGTTCAATGA ATGGGNAGAA CGNAGAAGGN ACAGCATTAA	240
CCCAGAACGC CATGGGAGGN ACCAGAGCGG CCACGGGCCG GGAATTCCCG CGAATGGGTT	300
GGGGGGGGTT ATGGCTCTGA ACAAGGGNTT TAGNCAGGG CCNGGGTTG CCTTCTTCCC	360

CCCAGGGGCA GACGTTTATT GGGGGGACCA TTGGCCNAAG AGAAGATGAC CGTCATGGC	420
AGGNAAGGNC NACGGGGGN NTNNTGGACA GGNTTACAAG AGTTGGCAAN TNGCGAANAN	480
CATTTCCGTT AATTCCGGC	499

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GCGTCGCCTT GTTCTACGAT ATGACCATT TCCATATACA CCACTCGGCT GGCGGTTTA	60
CGCGCCACTT CAACTTCGTG GNGTGACGAT CACCTGGTA ATATTCTGTT CTGCCAGCTC	120
ACGAATGAAT GCTGACGATT TGTGCCGTAA TTTCCGGTC CAGTGCGGCG GTCGGTTCAT	180
CGAACACGAG TACCTCGGT TCCATCATCA ACGCACGGC AATAGCAACA CGCTGCTGCT	240
GACCACCAGA AAGATGCAGC GGGTAACGAT CGCNATAAGG TTTGAGAACG CAGACGTTNC	300
CAGCAGTTTT TTCTGCACGG GGCCAGCGCC TGATTCTTTA ATTCAANCCC CATTACAAGG	360
GCAGGGCGGT TTCAATTCAA GGTTTGTTN GCACGGTCAA ANTGGGGCCA CAGGTTNTN	420
TT	422

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGCACGAGCA GGGCTAGGTA ACCTGTCTTG GGAGTNTGAG ACCGCCCGC CCTGCCACGC	60
CCCTCACCGC CCTGCCCGA GGCGCCAGCN NANCTCCTTG GCTTCCTTTC CTAGATAGTG	120
ANGTCCACCA ACCTTGGAGG TGCCTTTCA AAACACCCGG GAGGCCGTGC CTCAGCATTC	180
TGTTACTCGG CCTGCAGCCC CAGTGCCAGG AGCCACCCCG AACCGCGAAC CCGGCCAGGC	240
TGGTTNCAGG GAGGCCGAGG TGGCGCTGAG GTGGCTTCA GCACGCTGGG GATTGGNTTC	300
CTGCTNCACG GATGCTGTTG CATTCTGCC TGCCACTTT TGCCNGACAC CAGATNTGTT	360
TTNAA	365

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

CACAAACCTNC TCATGGGTGA CACCAAGGAG CAGCGCATCC TGTAAACCACG TNCTNCAGCA	60
TGAGGTAGCC CTGNGAACGN ACAGAGCGTG CTGGAAGGCC ATTGACACCT ACTNGCGAGT	120
CA	122

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

GGCAGAGGNN CGGGNGCTGC ATCGACGTGA ATNAGTGCTG GGCCTCGCCA GGCGNCCTG	60
TGCCAGCACA CGTGTGAGAA ACACACTCGG CTCCTACCGC TGTTCCCTGCG CCTCCGGGTT	120
CCTGNTAGCA GGGACGGCAA GCGCTGTGAA GACGTGAATN AGTGTAAAGGC CCAGCGCTGC	180
AGCCAGGAGT GTGCCAACAT CTATGGCTCC TACCAAGTGCT ACTGCCGCCA GGCTTACCA	240
CTGGCTGAGG ATGGGNACACA CCTGCACAGA CATCGACGAG TGTNCTCAAG GCGGCCGGCA	300
TCCTNTGGCA ACTTTCCGNT GTTTCAAAG TGGCCAGGGG AGGTTTACCA TTGTGCATGC	360
CCTGAGCAAG GTTACAACAT GTACGGGCCA ACGGTAGGTT CTGCAAGGTT GNGATNAAGT	420
TTTGCNANCT TNT	433

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GGCAGAGTGG GAACCTCTTT CTGGGCTGGC GANGCCTGAG GCCACTCCCT CAGCTTGCAG	60
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GGAGGTGTGG AGGGAGAGGC GCGACGGGNA ACAGGGGCTG CGTGC GGCTC TTGCGGGCCA	120
GCTGGAGTTC TGGGTGGGCA TGGGCTTGGC GGGCCCCGNA CTCGGANTNA GNCGGCTGGC	180
CCT	183

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GGCAGAGGGN AAAGTTGTNT TGGCTTGGA TTGCAACTCT TTGGCAGGAA TTCAGCGAGA	60
GAATTTCACAG AAAGCCATGG GAACTGGTGA CAATCAACTA TTCCCTCTGAA CCTGAAGAAT	120
CTGANTTTG TATTGTTGA CTGACCAAAA CAGGATGCGA GTGTAAATGA ACATCATGCC	180
CATGAATTGG TGCTCGATTT TATACTCAAT TGGATGCTGC TCAAATGAGA AATGATGTCA	240
TAGAGGAAGA CCTTGCAANG AGGTTCAAAA TGGAAAGACTG TTTAGGCTNC TAGCAAAATT	300
GGGAACATNC AATGAGAGGC CGGGTTTCAG AAGGATCCC CTTGGTCCAG AGACNGGAGA	360
CCNTTATCTG TTGNAACTCT TTAGGGGTCC NNNTTTCT CAGGTGACAG AAGCAGTGCN	420
TCCCTGGATT GACCCAGGC TATNATTCTN TGTCTTNACA GTTGGTGCTG GTNTGCCANA	480
AAATNAGCCC GNT	493

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

CTCCCACCTC GGCCTCCAA ATTGTTGTTA TTACAAGTAT GAGCTACTGT GCCCAGTCCC	60
ATTGGGGTAT TTTTCTGTGG TTCTCAAGGG TTGCCACAG AGAGACAGAC CACTTTGGG	120
ACTCAGGAAA TCTGGATGT ACCAAGACTA AATCTATATT AACCTTCTGA TCTACTGTGC	180
AGGATGGCAA AGTGTGTTAT TTCCCTGTGNA CAATTCTGGA TCTAAAAATG TAAGGGTTGA	240
AAAAAAAATG TAAGGGATGA GATCAACTAT TTGTGAANGT TGTCCGAGAG GNTGGGTTG	300
CAGGTGTGTG GGTGCAANCA GTNCCCTNCA CACTCA	336

(2) INFORMATION FOR SEQ ID NO:496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GGCANAGGNC CCTGGAGGGN TGGAGCCCAG CCTTAAAGAC CCAGGGCAAG CTGAACACCA	60
GGCCTGGNAA AGGTGATCTT CTTCTCAGAG TCTGGCTGCC ANGGCAGTGG CAGGAAGGTC	120
TGGGGAGACA TCGTTGATGC CTCAGGCTGG GCCCCCCGTAG CCTCCATAAG GGTAGTTCGA	180
GGCTGCTGGG TGCTGTACGA NGAGCCAGAG TTNCGGGTC AGAAGCTGGT CCTGCCTGAA	240
GNGGTCATGG GACTCAGANC CCCAGGGTCA AAGTGGAGTC CCCAAGGTTT CGGNTCCCTA	300
AGGNGGGTTG TCTGGGACT TACAAGCANC C	331

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GCCCAGCCCA ACTCGGGTCT GCTGCAGGCC TCGGTACATCA CCCTCTACAC CATGTTNTA	60
ACCTGGTCAG CCCTATCCAG TATCCCTGAA CAGAAATGCA ACCCCCATT GCCTAACCCAG	120
CTGGGCAACG AGACAGTTGT GGCAGGCCAG GAGGGCTATG AAGACCCAGT GGTGGGATGC	180
CCCGAGCATT GTGGGCCTCA TCATCTTCCT CCTGTGNAC CCTCTTGAT NCAGTNTGCG	240
ATCCTNCANA CCACCGGTCA GNGAAGCAGC CTGNTGCAGA CCGAGGAGTG CCCACCTATG	300
GTAAGACGCC ACACAGCCAG CAGCAGCAGC AGGTGGNCAG CNTGTGAAGG GCCGGGNNT	360
TGAACAAAGAA GNCAGGACGG NGTTCACTGA CAGTTNATTC TNTNTTTCCA TTNTTGNCNG	420
GTGNTGGCT TNATTGCAAG TTNAGGATGA GGTTCACCAA TTGTTACAAG CCCGTGGAGA	480
CCGG	484

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

ATGACAAGAG GCCCTCTATA TATCTCTTCC CACTCTAAAG CTNACCACAC CAACCTACGG	60
NATCTTAACC AC	72

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GGCAGAGCCC CCATCCAGAG CATGATGTGC CAGTACTGGC CAGAGTCCTG GTGGAGGACG	60
ATGAGATTCA TGCAGGGATT CATCAGGGCT TTCAGGCCCT GCCCAGGCAC CTATGGTACT	120
TTGCTGGACT TGAAACAGAT GGAAGAGCGT GCCGTTCTA GGTGAGCTCT GCCTGGTCCG	180
CCTCTGGCTC ACTCCGCCTT CAGAGACCAG ACTCCACCTT CACACTCANG CATGGGATTC	240
TCTGCCTTNA AGATAAACAC	259

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

GGTTACCTTG GCTACCAGTG CAAACACTAC GCNTGCNTCC GGCGAAGGGC GGCTACTGCG	60
CTGGTACCNN GGNTGGGCC CCCCCGTATAA AGCATCATT	99

(2) INFORMATION FOR SEQ ID NO:501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GGCAGAGGTN AGCTCGAAA AGCGATCGGA GCACAGTGCT ACTTGGGAAT GTTCAGCTCT	60
GACTCAGAAA GGTCTCAAAG CGGTTTTGA TGAAGCAATC CTCACCATT TCCACCCCAA	120
GAAAANGAAG AAACGCTGTT CTGAAGGGTC ACAGCTGCTG TTCAATTATC TGAGGTTGTC	180
TGGGACCTGC CTCCACCCCA TCCAGGGGAT GAGANTGGNC AGCCAATCTC TGTGCCAAG	240
CTTCCAGCCA AAAAGGAGGG CACGACCAGA AAGGAACCTCC CTTTGGCAC GGGGNNTTG	300
CCCCATTNAC CCTTCTTNAG GCCCTTNCCC NAAA	334

(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GGCAGAGGTG CTGCAGGGGG TCCTGCCGGC CCTGCCTCAG GTGGTGTGCA CTACCGCGAA	60
TGTGCGCTTC GAGTCCATCC GGCTCCCTGG GCTGCCCGCG CGGCGTGNAACCCCGTGGTG	120
CTCCTACGCC GTGGCTCTCA GCTGTNNAAAT GTGGCACTCT GCCGCCGCAG CACCACTGAA	180
CTGCGGGGGT CCCAAGGNAC CACCCCTTGA ACCTGTGAAT GACCCCNNGGT TCCAGGACTN	240
CCTNTTCCTC AAAGGNCCCT CCCCCGGAGC CTTTCCAAGT	280

(2) INFORMATION FOR SEQ ID NO:503:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GGCANAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANAAAAN CNCCNGGGGG GGGN	114

(2) INFORMATION FOR SEQ ID NO:504:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GGCANAGGAC AGGATCAAGC ATGCTTCCT TATCAAGGAG CAGAAAATCA TTGTGAAAGT	60
TTTGAAAGCA CAAGCAGGGA GTCAGAAAGC TAAATAAAAG ATGAAGCTTT TTTGNAGTAN	120
TAAAAAATTAA AAGACTTTT AAAAAAATTA GAAGGCAGGG AACCCAGATG GGNAAGTGTC	180
TTCCTGAATG CTCCTGGCC TTGGGAGGGT CCTTTCTGTG TGTTCAATTG ACAAAATCTG	240
AAAAATGCCG CTACTTGGC AAAGAGAAAT GTTTATAGGG TCTAGCTCTA GTATNCAGGN	300
AAGGGAAAGC AGNGGGAAGG GTGGGTTGG GACNGNTTAG	340

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GGCACAGGTA GAACCCACCA TGGTGCTGTC TCCTGCCGAC AAGACCAACG TTAAGGTNTG	60
TTTGGGGTAA GGTGCGGNNG GTACCTGGNG NAGTATGGTT TCGGTGGTAN CT	112

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

AAACCAAGCT GTACTTGGCA ATGAACAGTG AGGGATACTT GTACACCTCG GAACTTTCA	60
CACCTGAGTG CAAATTCAA GAATCAGTGT TTGAAAATTA TTATGTGACA TATTCACTCAA	120
TGATATACCG TNAGCAGCAG TCAGGCCGAG GGTGGTATCT GGGTCTGAAC AAAGAAGGAG	180
AGATTCACTGA AAGGGCAACC ATGTGAAGAA GGAACAAGCC TGCAGCTTCA TTTTCTGCCT	240
AAACCACTGA AGNCCCCATG TTACAAGGNG CCATCACTGC ACGTTCTCA CGGGGTTTCT	300
TCCCGTTCTT GGAAGCGGGG ACCCCCCAACC AGGGGCAGAA GTGTTTCTG GGCGTTGCTT	360
GAACGGGGGG CAAATNCCNT GGGGCCACAA TGGATCAACG TGG	403

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGCCCGAGCA CCAAACTTGG CAACACGACC ATTGTGGTGC CCAAGCCCTT CCGCCCGATA	60
CTTGGCCTGC ATCTGGACTT GGGAAATCCTG TACTATGTCT ACATGGGGNT GCTGGCAGTG	120
TTCTGTACCA ATGCCATCAA TATCCTAGCA GGAATTAAACG GCCTAGAGGC TGGCCAGTCA	180
CTAGTCATTT CTGCTTCCAT CATTGTCTTC AACCTGGTAG NGTTGGAAGG TGATTGTGGG	240
GATGATCATG TCTTTCCCT CTACTTCATG ATACCCTTTT TTTTCACCA CTTTGGGGAT	300
TGCTCTTACC ACAACTGGTA NCCCTCANGG GGTGTTTTT GGGGAGAAAA CNTCTGNTAA	360
ATTTTGCTGG GNAAGA	376

(2) INFORMATION FOR SEQ ID NO:508:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GGCACGAGGA AAAACAGTCC TGGGAAATGT ACGACACTCA TTCTGCTAAA GAAATAGGCA	60
AGTAACAATT TTTAACAAAGT GAAATATATT ACTACTTAAT TTTATTCAAA ATTCAACCAAC	120
TTAATGTGCT TTATAAATAT TTNCATACCT TTCAAGCTCT ACTGATAAAA CATAATTTAC	180
AGTTAATTAA AANGTGAAGT TAAAGTAAGT ACAAAANCAT TTTCAAGGTG ACAAAATTAG	240
GAAGGTGACA GTNCCGATTG AAACACAGAC ATATCACACC CAAGGGTCAA GTCAAGCCCT	300
TCTATTTACT TGGGGTATTT TCCCCCACTC ACATCTGGTT CAGTGGAAAGT GGGGTCTGG	360
ACCATCCTAC CAGGNGCCGT TACCTGTGG TTNCTCTGTG TTCCCNTGGG GGTGGCTTTT	420
AACTTTGCAG GTTTTGAC TGCCTCANTA GGTTGGGTT CTTTGNCCT TTGGNAATAT	480
TTTCCTTTNC CCTTAACCAC TTTT	504

(2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

GGCAGAGCAG CCCTGAGATC GAGGGAGATC TGCAGCCTGC CACACATGGC ATCCGCTTN	60
ATTCTGGAC CAAGTAAAGA TGGGTCCGTG GCCCACACTC GGTCAATGTGC TCAGACAACG	120
ACTGNTGAAA ACGCCCAGTG CATTTGCAT CGNACTGATA GTGTGTTCTT TCCGGNNNTC	180
ACAAACATTA ACAAAAAAGT TTAACCTTATG TGAACCTGGG CAGTTNATTTC TATGACCATT	240
TCCTGTGCCA TNTAAAATTT TTAAGGGATG AAAAATTNTG NAAAAAANAA AAAAAGTCTN	300
GNNGGGGGGGG CCCCCGGTG	318

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGCAGAGGTG AAACCCTACA CTTGTTGTNA ATGTGGGAAG GGTTTCAAAT ATGGCTCAGG	60
TCTCCTTAGT CATAAGAGAG TGNACACTGG CGAGAACCCA TACAGATGCC ACAGTGTGTGN	120
GAAAGGGCTA TAGTCAGAGC TCACATCTTC AAGGTCACTCA GAGGGTCCAC ACTGGTGAGG	180
AAACCCTATA AATGTGANTA GTGTGGGAAG GGCTTGGCC GCAACTCCTG TCTTCATGTT	240
CATCAGTGAG TCCACACTGG AGAGAACCCC TATTACGTNT GGTGTGTGTN GGNAAGGCTT	300
NCAGTTAATT ACCTCAGGTN TTGCGGGAAC CACCAAAGAG TGCCATTAA GGCGNAGTNA	360
CCCTTATTAA GTAGTTGTTA CCATAGGGNT TTTCCCATCT TGGGANNNCN AAGGNTTTT	420
TATTCCN	427

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GGCAGACCTC GGCCTNNATT CNTNCAAAGG CACATGGACA CAGCCCTTA ACCTGGCAAG	60
CACCAGGGAA GGAGAACTTC TATGTGGACG AGACAACNT GGTGAAGGTG CCCCCATGANN	120

GTTGCAGTCG AGCACCATCA GTTAACCTTC ATGAACTCGG AAGCTCCCCT GCCNAGCTGG	180
TGCAGATGAA ACTACGTGGG NCAATGGGAA CTNTTTCTT NATCCTTCGG GACAAGGGGA	240
AGATGAACAC AGTTCATCGC TGCAC TGAGC CGGGGACACG ATTNAACAGG TGGTCCGNAG	300
CNTTGACCCA GNAGCCAGGT GGGACCTGTT ACATTCCAA AGGTN	345

(2) INFORMATION FOR SEQ ID NO:512:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GGCANAGGAC CACTTGAGCT TCCTCAACTC CTTCAAGATG AAGATGTCCG TNATCCTGGG	60
CGTCGTGCAC ATGGCCTTG GGGTGGTCCT CGGAGTCTTC AACACAGTGT CACTTGCC	120
AGAGGCACCG GNTGCTGCTG GNAGACGCTG CCGGTAGCTN CACCTTCCTG GCTGGAACT	180
CTTCGGTTAC CTCGTGTTTC CTNAGTGCAT CTGACAAGTG GGCTGTGTGT CTGGGNTTGN	240
CAGGGGNCGA CT	252

(2) INFORMATION FOR SEQ ID NO:513:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GGCAGAGTAG AAGTCGGCG GACCCGGAAC CCAGAGGACG CGACACCAGT ACTTATGCTT	60
ATCTCTTCAA GTATATCATC ATCGGAGACA CAGGTGTGGG GAAGTNATGT CTCCTCCTGC	120
AGTTTACAGA TAAGCGGTTTC CAGCCTGTCC ACGACCTCAC AATAGGTGTG GAGTTTGGNG	180
CTCGTATGGT CAACATTGAT GGAAAACAAA TCAAACGTCA AATCTGGGAT ACGGCTGGGC	240
AAGAACCTT CCGTTCTATC ACCCGTTCCCT ACTACAGGGG AGCAGTTGGA GCACTGCTGG	300
TGTACGACAT TACAAGGCCTTCA ACCACTTGNC CTCNTGGTTA GAGGATGCC	360
GGCNACANTN T	371

(2) INFORMATION FOR SEQ ID NO:514:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GGNACGAGCA AGCACTGCTC AAACAAGGAG GTGGTGTCCCT TNGCCAAAGT CCTTATNAAA	60
AACTGGAAGC GGCTGCNAGA CTCCCCCTGGC CCCCCAAAAG GAGAAAAAGG AGAGGAAAGA	120
GAAAAGGCAA AGAAGAAGGA AAAAGGGCTT NANTGTTCAN ACTGGAAGCC AGAACGAGGC	180
NTTTNTCCAC CAAGGAA	197

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GGCAGAGNAA CATTCTAGCA GGGGTAAGTG ACCATAGCTG AATTCTTTTC TTATCAATCA	60
GGAAAATGAA AATCCTTCCT TAATCAATTCT CTCCTAAAGTC TCTGACACAT AACAAACAAC	120
CCAAAAATGC ACCTCTCTTT CCATCAAACCT CCACTGATAT GAAAAATGGG CAACCTGTTT	180
TTCCTTGCCC TGTTAGTGAA CTTGTGGGTG TACCCAGTGG CCACTCTAAG GATCTCTATA	240
ATCAACAAGA CACAGTTAAC AAGTGTGGC AAGCAAGTGG AGAAATCAGA ACACACACAC	300
ATTGCCAGTG GGGATGTAAA GTGGGAAAC AGTTTTGGAA GTTNCCTCGA AAAGTTAAA	360
CCNGGGATTT AACCTTACAA CTCCGTAAATT NCCATTTACT TCNAGGGTGA TTNTCCAAA	420
GGANNTGAAA ACGTNTGTTT AACNCCAAA NCNGTTACAC AATGTTCAC AGGGGCNTTT	480
TTCCTTATTN GCCCAGGGTN	500

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

TATATGCGTC TAACAAAAGA GTTACAAAAT ACATGAAATA AAAAGATACA GACATTAAG	60
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GAGAAATAGA CAAATCTACA ACTATAGTTG GAGACTTCAA AGTACCTTT TCAGTAATCA	120
ATAGACCAGT TAGAACACCT CAGCCAAAAA TAGCAGAATA TAAATTATTT TTGAGCTCTC	180
ACAGAACTTT GCTGAGATAC ATTATAACCT GGGCCATAAA ACAAACCTCA ACCAATTAAT	240
ACAGTTGAAA CCAGAGTGTG CTCTCTGGAC CACAGTAGGA TTCAANCTAT TAATTAGTAN	300
TNTTANTANT GG	312

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GGCAGAGTGC AAGATTGGAG AGGAAATGCT GGCAGACTTT GTGTCCCAGA CTTCTCCAAT	60
GATCCCCCTCC ATTGTTGTGC ATTGTGTAAA TGAGATTGAG CAAAGAGGTC TGACTGAGAC	120
AGGCCTGTAT AGGATCTCTG GCTGTGAACC GCACAGTAAA AGAGCTGAAG AGAAATTCCCT	180
CAGAGTGAAA ACTGTACCCC TCCTCAGCAA AGTGGATGAT ATCCATGCTA TCTGTAGCCT	240
TCTAAAAAGA CTTTCTTCGA AACCTCAAAG AACCTCTTCT GACCTTTCGC CTTAACAGAG	300
CCTTTTGGA GGCAGCAGAA ATCACAGATG AAGACAACAG CATAGCGCCC ATGTTACCAA	360
GCTGTTGGTG GAANTGCCCG AGGCCAACAG GGACACTTGG TTTTCCTCA TGTTTCATTG	420
CAGNGAGTGG TTCAGAGTNC NCNTATTAAA TGGGTGT	457

(2) INFORMATION FOR SEQ ID NO:518:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GGCAGAGCTT TTTTGTATTT TTAATTTGT ATTATTGAAA GCCTTGGAGA TCTCACAGAT	60
AGATATGCCA AATTCTATAT TTTGTAAATN CTCTATATTA GAAAACAGCT GTGCACACAG	120
GGCGGGTGTG CTCATTGTA CTGTGTGTAT GTCGGTGTAT GTACTGGTGT ATATGTGTGT	180
GTGTTCATGC TGTGGACTGG TCTCACACAG GATGTTTCC CTGATTTAG ATTGGCAGT	240
TTTGGGTTTT CCAAGGTACC ACCAGAGCAG TGGGTGTGTG CTTTTGGGGT ACNTATGCTC	300

CAGATTAAGT AGGAGGATGC ATGGGNCCAC ANTGCCCAT NTTTCNGGAC ACAGG 355

(2) INFORMATION FOR SEQ ID NO:519:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GGCANAGACG GAATTACTCC TTGTNTGTNT ACCTGGTGAG GCAGTTGACT GCAGGGAANN	60
CTTGTACANA AACTCAGAGC AAAGGGTATC CGNANCNCAG ACCACTCGGG GGNCACTGAT	120
CAAGGAGNAA TTGAACTGCT GACCCTGAAC AGTGAAGGTG GCCACTACAA GTCTCCGGGT	180
GTCACTCATG TGCCCGCTAG NAAGNNNTGCG CCTGAACTGT CCCTTGTNGT GCCCTCACCT	240
GCGNCCACCT GCAGAGCTTN GGATGCTGCC CTTTATCTAC AGATGAATGA GAAGAAGCCT	300
ACATGGACAT GTCCTGTGTG TGACAAGAAG GTTCCCTATG GAATNTTTAN TCATGANGGG	360
TTNATTATGG NGAT	374

(2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

CCANAACGCC AACGCCCTCGA CAACTATAAC CATTNACCTA ACACGCGCGA ACAAAACGCC	60
TGGATGCCTC CCACCCCCGCC GGCTGGCCGG CCGGCCTCCT ACGAACCTAC GCTGCGACTC	120
CNCCCCNGCG GCCTCGCCAC GCGAACTCTC CGACTACTNC ACACGCNCTC NACTCCCAC	179

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GGCAGAGGGN GACCGAGGCG ATGCTATAACG ANAAGTTCAAG CCCGGCCGGG CCTTATCCTC	60
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TCCATCCGGG TCTGCAGGGA ACATGATCAC CCGCCGCTCC TTGGGTTACG CGTAGTTAAA	120
CTTCCAGCAG CCGGCAGGTAC GCGGAGNGGC TNNTGGAACA CCATGAATT TGAAATGTTAT	180
TAAAGGGCAA GCCAGTTACG CATCATGTGN GTCTTCAGCG TGNATCCATT CACTTCGGC	240
AAAAGTGGGA GTAGGGCANC ATATTCATT TAAAAATCTG GGACAANTCC ATTGNTAATA	300
AAAGCACTGT ATGATACATN TTCCTGNNTT TTTGGTNACA TCCTTCCAT GTAAGTTGGT	360
TTNTAATTGN AATGGGTTNC CAAGGGNTT TGGGNTTGTA CATTGTTAGA NGTGGTGNNT	420
NTCCTTACGA TGGTNGTTNN NAAAAANTGA TTGGAATGTT CCNNAATGGA TCNCAAAGTT	480
TTTTTNGGGN	490

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GGCAGAGTNA AAGGAGGAAT TGCAGATGCC GATGGAAGAC TGATGCAGGG TGACCAGATA	60
TTAATGGTGA ATGGGGAAGA CGTCGTAAT GCCACCCAAG AAGCGGTTGC CGTTTGCTAA	120
AGTGTCCCT AGGCACAGTA ACCTGGGAA GTTGGAAAGAA TCAAAGCTGG TCCATTCCAT	180
TCAGAGAGGA GGCCATCTTC AAAGCAGCCA GGTGAGTGAA GGCAGCCTGT CCATCTTCA	240
CTTTTNCCAC TCTCTGGNTC CAGTACATCT GAGTCACTGG NAAATTAGCT TCAAAGAAGA	300
ATGCATTGGC ATCTGAAATA CAGGGGTTAA GNACATCGAN ATGANAAAGG GCCCTATTGA	360
TTCAN	365

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

NGGGNCAGTG AATCCTCCGN CCTCTTGGCA CACCAGGGAC CGCTCGTGGG ACTCCACATC	60
CTCCAGCCCC CACAATCCTN TTCAAGGGCTC CCTGACATNC CTGGGGNTGG NAGAGNCCAT	120
CCCGGGG	127

(2) INFORMATION FOR SEQ ID NO:524:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

TCCNTCCATA GGCACACTGG NTCATNTNAG AGCCCCTGGG ATCGTTTACA GGGAAAGTTCC	60
CACATGAGGG CCCATGTGTG ACNTGTTATG GTCCGATCCC GNTGNTCTGN GTGGATGGGT	120
TTTTNACC	128

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GGCACGAGTG GCAGTGGCA TGGCGACCCC CTCCATTAA AACTCTAACCC ACCTCCCCCT	60
GGCTCCAGCT CTTNATCAAT GCCCGAAACT GGACCCTGGG AAGAGAGNCT GNCTGACTGG	120
CCANNGGAGC TCACCTGGGA CCCCATGGCN TTTNAACCTA AGTGGGTCTT GCCCCCTCCC	180
CCATGAACCT TNAGGAGCAC CCCATATTAT TTCCAAAAAT ATCTTGGACA GGCAAGGNCC	240
AAAATGCCAA AATCTCAGNG GACTTGATGA TCTGCCTGCT GATGTTCTT TCTGTGGGNT	300
GTGGTCTATT TTTNAGTTNC TGCTCTT	327

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GGCAGAGTGG AGATGTTNA TTACCTGGAG TGTGAACTCN NCCTCTTNCA AACAGTATTC	60
AACTCNCTGG ACATGTCCCG CTCTGTGTCC GTAAGGCAGC AGGGNAGTGC CGCCTCGCCC	120
CGCTGATCCA GGTCATCTTG GNACTGCAGC CACCTTATG AACTACACTG TCAAGCTTCT	180

TTTCAAACTC CACTCCTGCC TCCCAGCTGA CACCCTGCAG GCCCACCGGG GACCGNTTTC	240
ATGGGNGCAG TTTTACAAAG TAAAGTGGGT TCAAGTAAAC AGGAATGGAG GTGAATTTC	300
AGGGCGTTNT AAAATNCATT TAAGGCCTGG GAGTGCAATG GGGGAATTG GGGTTCANTG	360
GNAACTGNCT TACCGGTTCA AGGG	384

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GGCAGAGCTC TGGAGAGGCA GGCACAGGGG CACCNGNCNC GTNATGCAGC TTCGCCCTGG	60
GTTACCTCTA TGGCTCGGAC CAGCTGGTGG TGAGGATCCT GCAGGCCCTG GAACCTCCCT	120
GCCAAGAACT CCAACGGCTT CTAAAACCCC TACGTCAAGT ATCTACCTGC TGCCTGACCG	180
GAAGAAAAAG TTTCAGAACCC AAGGTGCACA GGAAGACCCCT GGAACCCCGT TCTTCAATGT	240
GAACGTTTGC AATTCTGCGG TGCCCCCTGGC CGGAGCTTGG CCCAAACGNC AAAATTGCAC	300
TTTCAGCGTG TTATGAANTT TGAACCNTTT TTGGTGGTCA GGACCTCATC GGNNCAGGTG	360
GTG	363

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GGCAGAGTNT GACTTCAAAA TCAAAACTGT AGAGCTAAGA GGAAAGAAAA TTAGATTACA	60
GATCTGGGAC ACAGCAGGTC AGGAGAGATT CAACAGCATT ACCTCAGCTT ATTACAGAAG	120
TGCCAAGGGG ATCATATTAG TATATGATNA TCACTGAGGA AGGAGACATT TGAATGATTT	180
GCCGAAATGG ATGAAGATGA TTGATAAGTA TGCTTCAGAA AGATGCAGAG CTTCTCTTAG	240
TTGGGAANTA AGTTGGACTG TGAACGGGAC AGNGGAATCC ACCAGGCAGC AGGGGAAAGT	300
TTTGCACAGC AGTTCACTTG GGTGCGGTCT TTTGAGCAAG TTCCCAGGGT AACCCATG	360
TGGGNCGGGN TTTTTNGAA ACTTGTGCGGT GNCCTTCCN	399

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

NTGATTGTTC CAAGAGGTTC CGTTTTTG GGCCTTGGT NAACCTTGG GGGGGTAAA	60
CATTTTTNC CCCTGGTNGG CTTAAAGGNG CCCCCCTTAG	100

(2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GGCAGAGCCC ACGCACAGCA CTTCCACAAAG CACCAGCTGT GGCCCAGCCC CTTCCGGGCG	60
CTGAAACCCC GGCCAGGNCG NCAAAGACCG CAGAAAGNAA GGGCCAGGNG GTGTTCATGG	120
CCGCCTCGCA GTGCTGGTAC TTTGACGAGA AGACGATGCA GAAAGCCCGG AGTAAGCAGT	180
GGGATGAGCC GAGGGTGTGC TCCCAGGAGTT ACCTGAAGGT GGACTTCGCA GACATCGGCT	240
GGNATGAAAT GGTATAATNT CACCGAAATC TTTTGATGCC TACTACTGCG CGGGAGCATG	300
TNAATTCCCC ATGTCTNAAA TCGTTTCGTT CCATCCAACC ATGCCACCAT NCAGAGCATT	360
GTTCAGGNT TTGNGGCATC ATCCCTGGG	389

(2) INFORMATION FOR SEQ ID NO:531:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

ATGGTGCAGA GCAACCNAGT GCTCTATACG CCCGGCAAAG AGCCTGAACC ACTGNTAGNA	60
TNCGAAGTAT GTGCCGTAC GTGGGTNAAC AGCAAGCCCG CGCTGGAATG NGTATACCTC	120
GGAGNCTGAA TGCTGGGAGG NAACCAACAC ACTGGTGCTG CACAACACGT GTAAGGGTCT	180

CGCTGCTGGC CGCACCCATC ATGCTGGAAC CTAGCGCTGC TGAACCGAGC TGTGCAAGNG	240
AGTGAGTTT CTGNCTGA NCATGGGACC CCGAAGNCG	279

(2) INFORMATION FOR SEQ ID NO:532:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GGCANAGAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	60
AAAAAAAAAA AAAAAAAA AAAANGNCCN GGGGGGGNC CCCN	114

(2) INFORMATION FOR SEQ ID NO:533:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GGCANAGGNC TGCTCAAGGC CACGGAGCCC GGGTTATTG GCGTGTGGC GCACAATGGC	60
GAGGTGCGTA CCGCCAGTCT GCTGAGCGAG CGCAACGCAG CCAAGCAGAG GCTGGTGGTG	120
CTGGTCAAGG ACAATGGCGA GCCTCCGCNC TTNGCCACCG CCACGNTGCA CGTGCTCCTG	180
GTGGACGGTT TCTCCCAGCC CTACCTGGGG CTCCCGGAAG GCGGCCCGG GACCAGGCCA	240
ACTNCGCTCA CCGTTTTACC TGGTGGTGGC GTTNGCCTTC GGTGTCTTCG GTTCTTCCTN	300
CTTTNTNGTG CTTCCTGTT CGTGGCGGT GNNGNTTTNC ANGNAGNAGC ANGGGGNCC	360
CCGTTGGGTT TCGTTGNTTC GGTGCCTNAA GGGCCCTTTT CCAAGAAAAT TGTTGGATTT	420
TAGGGGNAAC GGAACCTATT CCANAGTTAC CATT	454

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

AATGCCGTTT TCTGTTTCGT GGGGCATCCT CCTGCTGGNA GCCTGTNCTG CCTGGTCCCT	60
NNTTCCNTGG NTGAGGATCC CCAGGGAAGA TGCTGCCAG AAGACAGATA CATCCCACCA	120
TGNATCAGGA TCACCCAACC TTTCAACAAG ATCACCCCCA ACCTGGCTGA ANTTCGCNTT	180
CAGCCTATAC CGNCANTGGN ACACCAGTTC CAACAGGACC AATAT	225

(2) INFORMATION FOR SEQ ID NO:535:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

CATCTNGAAA ATNCATGNGA AAATTAGTGN AATGAAGTTA ACTGANATT GTCAAAACAA	60
TGTGTTGCTG ATGAGTCAGC TGAAAATTGT GAACAAATCA CTTTCATACC CTTTTGGGA	120
GACAAATTAT GTCACAGTTG CAACTCTTGG TGAACCTATG GTGAAATGGC TGACTGCTGT	180
GCAAAACANG GAACCTGNGN GAAATGNANT GGTTTTGGC AACCACAAAG	230

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

AAGAAAAGAC CCAGCCTCCC TTCCAGCCCC TCTCCTGGCC TCCCAAAGGC TTCTGCCACC	60
TCAGCCACTC TGGAGCTGGA TAGACTGATG GCCTCACTCT CTGACTTCCG CGTTCAAAAC	120
CATCTTCCAG CCTCTGGGCC AACTCAGCCA CCGGTGGTGA GCTCNACAAA TNAGGGCTCC	180
CCATCCCCAC CAGAGCCGAC TGGCAAGGGC AGCCTAGACA CCATGCTGGG GCTGCTGCAG	240
TCCGACCTCA GCCGCCGGGG TGTTCACC CAGGCCAAAG GCTTCTNTTG GCTCCTGCAA	300
TAAACCTATT GCTGGGAAG TTGGTGACGG CTCTGGCCG CGNCTGGCAC CCCGAGCACT	360
TCGTTTGCAG AGGCTGTTTC CACCGCCCTG GGAGGCAGCA GTTCTCGAG AAGGATGGAG	420
CCCCCTTTG CCCCAGTGC TACTTGAGC GGTTTTGCC AAGATGTGGG TTCTGNAACC	480
AGCCCA	486

(2) INFORMATION FOR SEQ ID NO:537:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

TNAAATTTA ACCATGTGGG AAATCNTGCA CATCCAGGTC TGGNCAGTTT GGCAACCANA	60
TCGGTGCCAA GTTCTGGAA GGTGGATCAG TGATGNAACA TGGCATCGAC CCCACCGGNN	120
ACCTGACCAC GGGGACAGCG GACCTNGCAG CTNGGACCGG TATCTTGNG GTACTGACAA	180
TTGAAAGCCA CAGGNGCAA AATATGTTNC TGCCTGCCAT CCTGGGTGGA TT	232

(2) INFORMATION FOR SEQ ID NO:538:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GGCAGAGCTC GNCNTNCGN CTCAGCCTG CAGCTCACGG TGACCCAGGT AAAGACTTGG	60
TTCCAGAACCC GCCGCAACAA GTGGAAGCGG NCANTCTCGG CTGAGCTGNT AGGCGNCCAA	120
NATGGCGCAC GNNTCGGCGN AGACTNCTGG TGGAGCATGC CGCTGGTGT CCAGGGAACAG	180
TTCGCTGCTG NCCGTGCCGG TNCCGCNTTC GCTCGCCTTT CCCGCGCCGN TCTACTACCC	240
GGGGAAGCAA CCTCTNGGGC TNACCNNTCT ACAACCTATT ACAACAAGCT TCGACTAATG	300
GACCGGGCC	309

(2) INFORMATION FOR SEQ ID NO:539:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GGCAGAGAAG ACATTTCCA GCAACCCTG GTGCAGGTGG CAGCCTGGGT GCATTGGGA	60
GTATGGGGAC CTCCTGCTGG CAGGAACCTGG AAGTTGATTG AGCCCCTCA GGTGGACGAG	120
TAGGAAGTGC TGGCATTGCT GGGAAAAGGT GCTGCAGTCC CACATGTCCC TGNCCAGTTA	180

CTCGAGGGAT ATGCCCTCAN AGCCCTTCAT GTAAGCTTCA GCACCTCGCC TCTTTGGGGG	240
ACAACAACCG GCATCCGCCA GTGGNTGTTC CATCTACGGG AAGCTGNTTT GGGACGTGGA	300
GCTGTCANCA NCGGTGCTTT GGGAGTTNGG ACACAATTAA TCCGGAA	347

(2) INFORMATION FOR SEQ ID NO:540:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GCTTAATAAA ACACATCCGG TAATTTATAA CGTCTGCAAT TATCAGAAAC CCGCTGCCGG	60
TGAGCCTGCG TTGTTACTCT GGGATGATGT CATAACCTTA TTCCATGAAT TTGGTGATAC	120
GCTGCACGGC CTTTTGGCC GTNCAGNNTT ATGCCACGCT TTCCGGCAC ACCACGCCGC	180
GNGTTTTTTT CGAATTTCGG TCGCAAATGC AACGAACACT GGGGCAACGC ATCCGCAGTA	240
TTTCGCTCGC TACGCCCGGC ATTATCAGAG CGGGGCAGCA NTGNCTGACG AACTGCAACA	300
GAAAATGCGT NATGNCAGCC TGTCAACAA GGGTATN	337

(2) INFORMATION FOR SEQ ID NO:541:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GGCANAGGGN ACCATGGAGG GTGTAGAAGA GAAGAAGAAG GAGGNTCCCTG CCTGTNCCAG	60
AAACCCTTAA GNAAAAGCGA NGATTTTCGC AGAGCTGNAA GATCAAGCGC CTGAGAAAAG	120
AAGTTT	126

(2) INFORMATION FOR SEQ ID NO:542:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

TTAAATCCAN NTCCATACAA CGCTCCGCCG CCGNTCCTGC CGNGAACCG GAACTGCCCG	60
CCACNCGCC CCCTGCCGAC AGCTCCGTNA CTATGGAGGA TATGNANCAGA ANTACAGCAA	120
TATAGAAGGG AATTGCCAG AGGGGATCCA AGATCAACGC GAGCAAAGAT TCAGCAGGAT	180
GGACGGTGAA AATNTTTATT GGAGGCTTGA GCTGGGNTAC AAGCAAANAA GATCTGGACA	240
GAGTACTTTG TNTCGTTTG GGGGAGTTNT AGACTTGCAC ATTTA	285

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

CTGGGGCCGA CGCTCTGNCC GGNTGCTGCC CTGAAGGAAA GCCGGGACGC GGNCCCCCGC	60
CGAGAAAGCTT CTTTGCTCCG GAACGCCCT GGACGTGGCG GGCAGCCGGA AGNNNTAACCC	120
ACCATGAATC CCCTGGGTGC TCCTGGCCTG TGNCCCTCCC CTGTGNCTGC TGACCCACTG	180
CTTGGCGCCT TTGATTGCA GGGACTTCCG GAAAGGGTCC CCTCAACTGG TCTGCAGCCT	240
GCNTGGCCCC CAGGGCCCAC CCGGNCCCCN AGGAGCCCCA GGGNCCTTAA GAATGATGGG	300
ACGAATGGGG TTTTCCTGG GAAAAAAGGG TCCAAATTGG ACNAAGAANG GGGAACCGGG	360
GGGGACAAAC GNGNAGGAAG AAATTTTTT TTTCNAAC	397

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

AGCACGAGCT GGCATGTNAC AACCCAGGGC TGCCTGAAAA TGGATACCAA ATCCTGTACA	60
AGCNACTCTA CCTGCCAGGA GAGTCCCTCA CCTTCATGTG CTACGAAGGC TTTGAGCTCA	120
TGGGTGAAGT GACCATTNNNT TGCATCCTGG GAACAGCCAT CCNACTGGAA CGGGNCCNNT	180
GCCGTNTTGT ANAAGTAGGC AGAAGCGGCA CAGAGACGTC GCTGGAAGGG GGGGAAACAT	240
GGCCCTGGNT ATCTTCATC CCGGTCCCTNA TCATNTNCTT TANTGTTGGG AGGAGG	296

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

ATGNTTGTC CCGCTGAGCA GTACACACCC AAGGCCAAGT ACCATGGCAA CGTGATGCTA	60
NTGCNCGCCA AGACGGGTGG NGCCTACGGC AGGTNCCTGG GCGCGGACTA CAACCTNTCC	120
CAGGTATGCA ACGGGAAAGT ATCCGTCCAC GTGCATCGNG AGGTGACCAC CGCACGCTGC	180
TGGTAGGGCA GGGNCCTNGT AGTTCCATCA TCAGCATCAT CCACAGNTCC CTNG	234

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GGCAGAGGTT TTAANATCTT CTTCAAGAGA CGTCTGATGA ACCTCATGCG GGATGTGGAG	60
CGGGAGGGCC TGGACTGGGA ACCTCATCTA TGTGGGCCGG AAGCGGATGC AGGTGGAGCA	120
CNCCGAGAAC GCTGTGCCTC GCGTGAAGGT AACCTGGTGG AGGCCGACTA TTCCTACTGG	180
ACCCTGGCCT ACGTGAATCT CCCTGCAAGC GGCCCGAAA CTGCTGGCTG CTGAGCCGCT	240
CTCCAAGATG CTGCCTGTGG ACGAGTTCCCT GCCCGTTAAT GTTCGACAAA CACCCAGTGT	300
CCGAGTTACA AGGCCCACTT CTCCCCTCCGC AACCTGCATG TTTCTCTGTG GAGCCGTTGT	360
TCATTTTACCCACACATTA CACAGGAGAC GATGGGTATN TGAAGTTAAC ANCGAGACTT	420
CATCGTATGG AACAAATGAGC AAGTTAAGAC CGATTGGAAC NGGCCANTTC CAAAGTTTNG	480
GGGNAGCAGG ATT	493

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

CCTCAAAAAG TCCGGGAAGC TGAAATCCCC GAATGGNTGG TATAACCGTCA NGCTGGNCAA	60
GCACAAAGAG CTTGACTNCC TNACGATGAA GGAACCTGGTT TCTACACCGCG AATCT	115

(2) INFORMATION FOR SEQ ID NO:548:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GGCANAGGN NC ATTTTNCTG GCTATAAAGC GGGGTCTCCG GAACCAAAGG NNGCACACAG	60
CTCTT	65

(2) INFORMATION FOR SEQ ID NO:549:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GGCACAGCTC GGCGAGANAN AGCTTACTCA AATTGGCCAA CATACCCCTCA GCTGTATGTG	60
AAAGGGGAGC TNGTGGGAGG ATTGGATATT GTGAAGGAAC TAGAAGNAAA TGGTGAATTN	120
CTGCCTATAC TGGAGAGGNG AAAATTNAAT AAATCTTAAA CTTGGTGCCC AACTATTGTA	180
AGAAATATTT GAATTNACAT TGGGAAGCAG TTTCATGATT TTAGTCCTCA GAAATGGGTT	240
CTAGGGNNTT AGGAAAATTT CCTGNCTTTN CT	272

(2) INFORMATION FOR SEQ ID NO:550:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

TACAAC TGAA ACCTCCAGTA CCTTAGAGGT AAGANCTCAG GGCCCTATCC TCACAGCAAG	60
TGGCAAAAC CCTGTAATGG AGCTCATTGA AAAAAGAAGA GGTCTCAAGT TATGANCTCA	120
TCTCAGAGAC TGGTGGNAAG CCATGNACAA GCGCCTTGT GAATGGAGGT AGCAAGTAGA	180

TGGACAGAAA	TTCAGAGGCG	CAGGTCCAAA	TNAAGAAAGT	GGCAAAGGCG	AGTGCCAGCT	240
TTTGGCTCCT	TGNGNAGTAA	ACTTTTTTTT	GGGACCCAAT	GCGGGCAAAT	TAATTAAGGA	300
AAAAGNAAGA	TTTATTCCCT	TCAGGGCAA	GGGGNCGTTT	GTGGAATTAC	AGCTNGTTT	360
CTNNCAGCAG	TCCCAAG					377

(2) INFORMATION FOR SEQ ID NO:551:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GGCAGAGCCC	TGATCGACCC	CAACATCTTG	TNTCTNAACA	TCCTCTCTTC	CGGATAACATC	60
CACCCAGCCC	AAGATGACCG	GACCTTTAC	CAATTAAAGG	CTGCGTGGGA	CAGCTCCATG	120
CACAACTTN	TCCTGCTGAA	CCGGGTCAACC	CCTTATCGAG	AGAAAATCTA	CATGACACTC	180
TCCGCTTATA	TCGAGATGGA	GAAC TG CACC	CAGCCGGCTG	TTGTNACCAA	GGAACTTCTG	240
CATGGTCTTC	TATTCCCCTG	AATGCCAACG	TTGCCAGCCT	CGGGGTNCCA	TCCGCAACCT	300
CTTTGGGCAG	TGGGAGCCTT	CGGGCCTNCA	NAGGAGTNAA	CCGTGTGAAC	TGGTGTNTTA	360
						360

(2) INFORMATION FOR SEQ ID NO:552:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GGCANAGNAT	TTTNACTTT	AGCAACGTGA	TCTTCCTTTA	AGGGGAAGTA	TGTCCCCTCC	60
TAGAAACACT	CCCGCCTTGG	AGAAGGGTT	GAGTCGCAA	CTCCACTTAC	AGACTACGGA	120
GGGAACCCCA	GGGTCAAACC	AAACCAAACC	AATTCTGGCC	AGTTGCTTAG	CGCATTCAAG	180
TTACTTAGTG	CGCTGGAAGG	GCATTTTCAG	GCAATCCAAC	TTCTGGCTCG	AACCTTCTCG	240
GAGTATTCCA	AGGGATGGGA	ATACTCTNCA	CTTGAGGCGC	TTGCCGAGGG	TGGCCGCTTT	300
GAGGNAAAAC	GTGANNTNT	TGAAAGAAAT	GTGTTGTTNG	CCAGATTACA	GTTCACCA	360
TTCTNACATN	AAGTATGTGG	GAAAACAGGA	NGTTATCCCT	TTTGGGTTCC	NGGGGTCTTC	420

CAGAACCAATT AGGGGGCAAA CATCCAATT TGNTTNTGGG CACTTCCAAG AGNC 474

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

ATGAAGATGG GTGGNCTGCC GCGTACAACA CCTCCAAC	TC AAAAGCCCC TAGTCCCCCT	60
ATGTNAGGGA AAAGGGACAC TTGGGCGGCA CTCCCCCTAT CGCACACTGG AGCCAGTNCG		120
TGCCTCCAGT GGTACCAAAT GAATTACNTA CCTAGCCAA CCNGTAAATA TGGCTCCCTC		180
GCAGCAAAGC CCTGTGAAGG ACAGTTCTT TGAAATCAAA GAAATCGAAC TTACAGCAGC		240
ANTGGGNGTA NTGGAGGGAA GCCACCCAAN TAGTCGGAGC ANCAATCGAG AGAACATTGG		300
AATGGGTTAT TTGGGGG		317

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

ACTNGGCCG TTCCCGGCCA GCAGTTCCCC TATGAACCGC AAGCTNNNTT CCACTGCNTT	60
TTTGGCAAAC AGCGAANGGG ACTTCTATTATGAGTGGGGC AGTTTCGGG GGGCAAAGTG	120
GCCAGGGTAT ATGATTTAC TAGGGGCTGC CACATGCCA TCCTGGNGGA CAAGGCCATG	180
GGCATCATGG NTGCNTGGNG GGGNNG	206

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

ANATGGCCCC CGGGAAACAC AGCAAGANTG CCAGCTTCCT GTTTGGNATG CGGAACAGTG	60
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NCAGCCAGTN AATGAGGACT CAAGCTGGC TACCTTATC CNAGGGNCAG CCCCTGCCTA	120
ATGGNTCCCC AAAGGACACA GAATTCCCTTC TGAAACCCC AACGCCTTCA AGAACGGATT	180
CCAACCTGCC GGTTGGATGG TTGAGGGTCC AGGACACCTC AGGGACCTAT TNACTGGCAC	240
ATTCCCAACA GGGGACCACC CAGTGGGGAA CCCCCCGGGC CGGGNTNTCC NNTTTAAAGG	300
GG	302

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

NAAGCCCATA GCTCAGCAGG CGGCACGGCG GCCTGACCTT NAGGGCAGCN AGCTCCCTCC	60
CGGTTTCGCN TTCCCTCGCG GTCAGCATGA AAGCTTCAN TCCC GTGANG TNCCGTAAAG	120
AAAAANAGCC TGTGGGAACC ACAGCCTGGG NATCTTCCCG GTGGCAAANN NCCTNTGGGA	180
CGACCCGNTG AGCCTGCTAT TACAACATGA ACGANTGTTA NTCCAAGTTC AGGAGTTGGT	240
GCCCAGCATC CCCCAGAACCA GGAGGTGAGC AAGNTGGAA TTNCTGCAGC ACGTCATCGA	300
TTACATTTNG GACNTGCAGT TCGCCTGGGA TTGGNTTCCA TTTTGTT	347

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GGCAGAGGGN CGGGGCCTAG TAATGGAAGG GGTGANATGT GGGCGGGGCG AGCTGTGGGT	60
GGGGCCTAGC CATGGGAAGA GGTGAGCTGT GAATGGGCT AGCTATGGGT GGGGTAAGCT	120
GTGGACAGGG CCTAGCCATG GGAAAAGGTG AGCTNTGGC GGGGCCTAGT CACGGGAAGA	180
GGTGAGCTGT GGGCGNGGCC TAGTCATGGG AAGGGGTGAG CTGTGGATGG GGCCTAGCCA	240
TGGGAAGGGG TGAGCTGTGA GTNGGGCTGA GCCATGGAA GCAGCAAGCT NGTGGAGTNG	300
GCTNGGCCGG ACTGTGGN	318

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

TGAACCAGCA GTATATGTAA TATNNNTNATG CCCAGGACAC AGAGACTTTA TCAAAAACAT	60
GATTACAGGA CATCTCAGGT GACTGTTCTG TCCTGATTGT NGTGTGGTGT TGGTGANTTA	120
AGTGGTATCT CCAGANGGGC AGACCCGAGG CAGCCNTCTG GTTACACACN GGGNAACAAC	180
TATTGTCGTG TTACAAANGG TTCCATGNCC ACNACANCAA NGATNGGGAA TTGTTAGGAG	240
TCACATTACA TAGNATTGGT ACACCCGACA CATAGCATT NCCANTNCTG GTGGATGTGC	300
ACNGTGGNCC AGTGNACAG CTTGNTCAGG GTGGAAGTCA CNTAGGTGGC ATGCCATGGA	360
CCNGTTGTTG GGCNTGGATG CNTCTACCAAC CACTGTCCAC TGACAGCCTT GGGCTGCNTT	420
CCAGGTGTTT CAAATTGGTG GTTTGGTANG TTCC	454

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GGCANAAAAG ACGCAANCCC ATGAAGCTNA GGTCTTGAAG CAGCTGGCTG AGAAAACGAG	60
AGCACGAGAA AGAAGTGCTT CAAAAGGCAA TAGAAAGAGA ACAACACAAC TCAGTGAAAA	120
TGGCAGANGA GAAAATGAA CCCACAAANT GGGAGGCTAA TTAAGNNGAA CCGAGAGGCA	180
CAANTGGCTG CC	192

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTCCCCCCT NNAGGGNCCC CC	52
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(2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TGAAGGGCCA TGGCTATGCT TCCCTGGCTC CAAGGGCCA TTTCCCTCTA GATGCCCTT	60
TGGCCTTNT GAGGGAGCGA GGAACAGGCT CGAAGGCTCC GGGGTATCTG CCTTCTGCTG	120
GGCTCCTGTG AACAGGCCCTT CTGTGCCAG CGTTTGACT TGCCCTCCCC AACAGTGGGC	180
CTGTTCTNN CCGTGCCAGG CCCCAGGAGA GCCGCAGGGG CCTGNACAC ACTCCCAGCT	240
CACCCTCACC CCAGCCTTTT TCCCCACATT NAGGGGTTTT TTGGGAAGCT GGTTCTCAA	300
TCCCTTCAA CCTCAGNTAG AGGTTAGGGT TNTCCCTGAT TTCCTGGGGG TTNCCAGCCT	360
TAAAAANTNA ATTGGCTTTC CCCAAGGGGC CCCTTAAGG GAGGGTTTG GGGG	414

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

TTTCCAAACA TTCTATAGAA ACTCACAGTG TATATAAATA TAATACATTC TGCTTTACC	60
TTTTTNACCA GATTCTTCAT TTTCTGATG GAGAAAGGTA TAAAAATGTC AATATCATGA	120
TTCTTGATGA TGACATTCCA GAAGGAGATG AAAAATTCA NCTGATTTA ACAAATCCTT	180
CTCCTGGACT AGAGCTAGGG AAAAATACAA TAGGTAATTA ATAATTNCTT ATAAACAGCT	240
TCCTCTCCTT CATGCTGGGT TCCTTAATAT GGGGAAAGAT GTAAAAGGGN TGAGGAAAGT	300
CTTGGTGGTT TTNCTGTGGN TTAAAATGGG GAATGATTT TAAGTCNNG GCATTTCCAG	360
AATTTCCCGT GNTCNGGTGT AACATGGNCC CTTTCCACGG GTGTAATGTT GGGNGGTATA	420
TATGCCAGTT ATGTNAAAG GCCAAGGTAG GGTGGTTACC CCCGG	465

(2) INFORMATION FOR SEQ ID NO:563:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GGCACGAGGT CCTGAAAAG NGTTGTGGGA AAAGCTTCTA TGTCTGCAG AGGCTNAAGG	60
TGCACATAAG GNNCCACAAT GGAGAGAACGC CCTTNATGTG CCATGAGTCT GGCTGTGGTA	120
AGCAGTTTAC TACAGNTGGA AACCTGGAAG AACCAACCGGC GCATNCACAC AGGAGNGGAA	180
ACCTTTCCTT TNT	193

(2) INFORMATION FOR SEQ ID NO:564:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GGCANAGGGA AAGGTGCGTN TGGGGCTGGG TCTCGGAGTG GGAGACGTGG AGTNCAGGGT	60
GGAATGTAGC AAAGCCCATC CACCAGCCAT GTACTACCCC CCAACCCGGN CAGGCTGGAG	120
CAACCGTTN TGGGGAGCCG AGCCCCGTT CTNGCTGCAG TGAGCCCGGA CTGGGGCACG	180
NACTGGCCAN ACT	193

(2) INFORMATION FOR SEQ ID NO:565:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

AGCCAGANTT CGTCTCTTGT CCTGCACTAT AGATTTCACA CTGGAGAGAA ACCCTACAAA	60
TGTAATGAAT GTGGACGAGC CTTGGTCAC ACTTCATCCC TTATTAAGCA TCAGAGGACT	120
CATACTGGAG AAAAGCCCTA TGAAATGCCG GGTAATGTGG GAGAACCTTG AGCCAGAGCT	180
NCATTCACTG CATTGTGCAT TACAGATTTC ATACTGGNAG AGNAAACCTT CACAAATGTA	240
ATAAAATGTGG GAGAGCCTTC AGCCAGAGTT CCATCTCTTC ATTCAACATT TACAGNTTTT	300
CACACTGGGA GAGAAACCT ACAAAATGTAA TGAGTGTGGG AAGGGCCTTT GCNTCCTAAT	360
GTATNCCTT GTTAAACATC CGGTGAAGTC NTGTTGGGA AAAAAAACCC TATAAATTCC	420

469

AGTGGATTTC AGNAGGGGNT TTCAAGTGGG NGTGCAGAC CTTCAATTGG

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GGCACCGAGTG CCACCTGACT GGANGAGAGC ATCCTTCAA CAGGGCAGTC AGGCCAGCCC	60
TGATTAAAG CCAAGTCCAC AAAATGGAGC CACGTTCCCG TCCTCTGGAG GATATGCCA	120
GGGAATCACT GATAGCCGAT GAGGAGTCCC AGGAGTTGA ATGATTAAAT ATTTGCATTA	180
AAAACGGTG CTGGTCTCAG TGTCAGTGAA TANTGAAATC TGGTCAAGGC AGCCAGGAGG	240
GGGGCACCTT GGACTGACTC CCAGATCGTG GAGCTCCAGG AGGATACCCA TCGCCGACAC	300
TCACCTGTAG CACCTTCACT TAACCATTTC GACTGAGGCA CATTTCAT ATTGTATTTC	360
AGCTTTTGT GGTAAAAAT CTCTAAGTNA CATCCACCTG TGTAATTAGG AACCNGTGGA	420
ATTGTTACTG GGTGGTTAA TACCAAACGT GGTTTGTGN TATTGGNGT ATAAATTACT	480
GGNTTGT	487

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GGCAGAGTGC CACTGNCCAC CCGGTTCCA AGGCTCAAAC TGTNAGAAGA GGGTGGACCG	60
GTGCAGCCTG CAGCCATGCC GCAATGGTGA GGCCTGGAGG CTGNANCAGC GAGGGNTGGG	120
GTGGGGTCC TGGATGGCTC ANACAGTNCA GGGTTGGAA TCCTGGCTTT GAACTCTTCT	180
GAACCCTAGG GCCTGGGAC CTGACCTTCT ACCTGCAAGC CTGTAAAATG GGCAAGGAGA	240
CATCCCTAT CTNATAACTA TTAATATTCA CTGAGGAATT ACTGTGTGNC CAGGCCCTAT	300
TTTTAGGCAC TGNGGTTACA GCAGGGAATG AAACCGACAA AGTCCCTGGG CCTGCCTGTT	360
AGAGNTNAGG TGCCCGGTNT	380

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNTNGGGG 60
65
GCCCN

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

CTAGATGAAA TGGCCAAACA AGCTCGAAAT CTCATCACTG ATATTTNCAC AGANCAGTGT 60
ACCCTTAGTG ACCAGTTGCT ACCCAAGCNT TGTCCCAAAN CTATCAGTCA AGCAGTGNA 120
TAAGAAATCA AAAAACGAGA CTGGTAAGAA AGGGGAACCT GNAAAGGNAG NAAACCAGGT 180
GTTGAGAGCA TGAGGAAAAA CAGGCTGGTT GTGNACCAAC CTTGNATAAA TTGCACACTG 240
CACTTTNTGN AGTTATGCTT CTNTATGATT T 271

(2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GGCACGAGCN ACAATCCGGC CAGTGCCCAG GCTGCCATCC AGGCCATGAA TGGNTTCCAG 60
ATCGGCATGA AGCGCCTCAA AGTCCAGCTA AAGCGGCCTA AGGATGCCAA CCGGCCCTAC 120
TGAGGGCCCC CAGGTCTGGA GATCCCANAG GAAGGGCGC CTCANACCCT CTTCCCACGA 180
CTGGCCNCGG CCATCTCCGC ACACCTGCC TGGGCCTTGA CTGGGTTCTG GGGCAAACGA 240
TGCTTACGTG GCCCCGGGG CGCAAGANNA CCGGCCNTTC CCACNCCCCT GNCTGTTGA 300
AAGGGCCATG GGTGATGATT TCCCTGGGT 329

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

GGCACGAGGN ACACCAAAGG CTTGGTGAGA NCGCTCGGGG AGGAAGCCCT GCTGAGAATA	60
CGTTCTCTCC ATAAATNAAG AAGGGCTAAG GCGATGCGAN GAGAATACAA AAGTNTTGG	120
TCGGCCTATC AGCTCATGGA CCTGCCTGGT GGACTTGAA GGGCTGAACA TGCGCCACTT	180
NTGGAGNCCT TGTGTNAAA GCGCTNCTGC GGTATNCATC G	221

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

CTCCTACCTG CNGGCTNCCC TAGNGGTNAAC TCCCTCCCTT AGTGGCCAAN GACATCAAGA	60
AGATCTTGGAA CAGCGTGGGT ATCGAGGCAG ACGGACGACC GGTNCAACAA GGTTATNCAG	120
TGAGCTNGAA TGTGGGNAAA ACA	143

(2) INFORMATION FOR SEQ ID NO:573:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

GGCAGAGGTG CTCACTGGAG CTGTGAAAAA TGGGCTTGCC CTGGTGAGGC CTCCCGGGCA	60
CCATGGTCAG AGGGCGGCTG CCAACGGGTT CTGTGTGTT ANCAGCGTGT CCATAGCAGC	120
TGCACATGCC AAGCAGTAAC ACGGGCTACA CAGGATCCTC GTCTGGANT GGGATGTGGA	180
CCATGNNCAG GGGATCCAGT ATCTCTTGA GGATGACCCNN AGCGTCCTTT ACTTCTCCTG	240
GGCACCGTTA TGAGGCATGGG CGCTTNTGGC NTTCTGCGA GAGTCAGNTG CAGCGCATNG	300

323

GGCGGGGACA GGGCTCGGCT TNA

(2) INFORMATION FOR SEQ ID NO:574:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

AGTAGAGCCA CTTCATCTCT GGNATGGTNT TACAAAGTCA GNCAGNAAAG CAGAGCAGGA	60
CANGGAGGGC CTTTTGTCCC TGGTAATGTG TTTGGGATCT ANTCCCGAT GCTGCGATGC	120
TGCGGGAAGC CTTGGGAGGG CTTTAAAGCA GGGGCGTGGC TTGCCTGTAT TTATTNCAGC	180
TGTGTNGGAG AATGATTGT AATACAGCAA ANGNTTNAAA GGAAGGGCAG	230

(2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GGCCATAAAA CAAGGCTTCC AGTTTCGCCG AGTTTGGNAG GGTGTTTCC GGCAACGNCA	60
GTANCCAGAT TGGTCACATC ATCGTAAATA CCAACCGTAA AGCGCGCTTT CGGTTTAGCC	120
GCGTTGAGCT CGGCAAATAC CGCCAGTACA CAGTCTGGC CAAATTCTTT GGATGAANGA	180
CCATAGCGCC CACCAATGAA CACGGGGCAG AGTTTCGCGC TCGCNATTAT TGAAAGGCTT	240
CTGCCAGTG AGGGTACATT TACATCCAGA TAGAGCGGTT TTGCNTGGGG GCACCGGGGT	300
TNCCTTGGGT TCTGTCCAGT TACCGTCANG GTTGGGTACG GGNTNCCGGG CAGAA	355

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

TCGCCAGACG GCAGCAAACG GGCATTCGCN TTGTCGAAAA CCGGTAGTNT GAACCTNTAC	60
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GTAATGGATT TGGCTTCTGG TCAGATCCGC CAGTGAAC TG ATGGTCGCAG TAACAATACC	120
GAACCGACCT GGTCCCCGGA TAGCCAGAAC CTGGCATTAA CTTCTAACCA GGCGGACCGC	180
GTGNGCANTN TAAAGCCGGG CGTGGCTTGC GCCANTGCCGG GCTGACGGTG GAGCAACTGG	240
CCAGACAGGT GGAGCCGGAA TACACACCGG CGCGAAAAGT TCATTTTAC CATTGCGAAC	300
CACCGGGGCC TGNCGTTGGG GGTTCATCAG CNAAGACGGG CATTACGGCG TGGCGCGGGG	360
GTATTTNAT TGANTGGGGC AACCAGTTA ATGAGGNGAA CCCGTTTCAC TTGCAACAGC	420
GTACCTTN CCAAGGG	437

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

ATCAGCAGGC GGTTACGGTT AAAC TGCTGA ACCTGGAACN NCGGGNANAC CGGTTGNNGT	60
CGCGGCTTGT GTGCAGCGTT ANNCACCGA GATGATGAAC GTNATTNGG CCGGTNTGGA	120
TNGATCTGCC ACTGACGNCG CGANCAGTCG ACCGATCATT CGAGTTCCAC CTTCTTATTC	180
AGCAANGAG AAGCGGCCA TAAAGGGCA ACATCAGGCC CATNACGNTA NCAGCGTAAT	240
GCTTGTAGC TGCANCCAAA CGGGCAGTCA CGNTTTAA GGGACTGGGG CCTTGGTG	298

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

NNTANAAGGN GGCCCAGTG GCACAAATGC AGNAAACTCC CTCTGGTGAT GATTTCAGCC	60
TCTCCTTGGC AGATACTAAA TCTACCATCC GGAAGTGGAG CCAGAGCTNC GCATTTGCAT	120
TGCTAAAGCG TCTTCAAGA GGTGCAGTCT TTGAAGGGCT GGGTANNGTN GCATCTGTGG	180
GANCTGAAAA TTCC	194

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GCTGGCTGAT GAAACGCCGG AAGCCGNCAG TATTGTAATC CTCGCCAAGC AGCGTTTAN	60
CCTNCGCGAC CCAATGTGCA GTCGCTCCAT GCCACCTTT	99

(2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAGGAAGCCA ACACCTTTAA ATTCAACCGT TGCGGGCCAG CTGCGGTGCC CAGCATATAG	60
TGCGCGGTTT CGTAACTACC GGACCAGTCG CGCNGCCTCG TTACAGGCAT CTTTNAGCGT	120
CGCGAAACCG TATGCACCGG GATCACTTCC GCACCCATTA AGCGCATAACG AAAAACGTTA	180
GGCGACTGGC GTTCAACGTC TTTGGCACCC ATATGAAATA CGGCATTTNA GGCGGAGCAG	240
GGCGCTGGCA AGGGCCGACG CCACGCCATG CTGACCGGCA CCGGTTTCGG CGATGATTTC	300
GGTTTTACCC ATCCGTTTCG CCAGNAAAGG CTGNCCCCAG CACTTGTAA TTTTATGNNG	360
GNCGNCGTGC AGCAAATTTT CAGGTTT	387

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

AACATCAACG AAACATACGCC GCGTTTNAA GATGCNTTTA TTGATTTCTT GGGCGGTGCC	60
GGAACCTCGG AATCGCCGNT GGGNGCAATA TTACATACGG TAGAAGGCAC ACCCGGCGAG	120
ACGGTGATCG AAGCGAAAGA NCTGACCAAG AAATTGAGGG ATTTTNCCGC CACCGATCAC	180
GTCAACTTTN CCGTTAACG TCGGGAGATT TNTGGTTGC TGGGGCCAAA CGGCGCGGGT	240
AAATCGACCA CCTTTAAAGA TGATGTNCGG TTTGCTGGTG CCGACTTCCG GCCAGGCGCT	300

GGTGCTGGGG ATGGATCTGA AAGAGAAGTT NCCGGTTAAA GCGCGCCAGC ATCTTCGGGC	360
TATTATGGCG GCAAAAATT TTGCTTTA CGGTNAACCT GGACGGTCGA ACAGAATTAA	420
CGGTTTTCC TCTGGTGTGT ATTGGCTTAC N	451

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GGCACGAGTA AGGCTGGGT ATCCTGGTGA NAACTGGAGA GGATCTACTC GGNTCCCTGC	60
CTGGCCAGTG GGGAAACACC GGTCCCCAG GCACCTTCAC CTAACCAAAG CGATAGATT	120
CCACCGCCCC TNATGCCGCC CTTTGGAGGN AAAGTAAAAA GTGAAAAGGA AGGAAGAGGA	180
GGCTTCATGG CTGAGGGAGGT CGCAGCGCCA TGAAAGTCCC TGTTTCTGCC TCCTCGCTGT	240
GGCTTTGGGT GAGCNAACCC CGCGAACTCA TCGCCCAAGA AACTAGAGGG AAGCGGAGGG	300
GAGGTGGCCC CACTGGGAGC CGATGCCANG NTTGGGGAGT GGGGCAGGTT CACCAGACAT	360
ACAAACCGTT TCTTNATTNG TTTCCTATN AGGCAAG	397

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GGCACGAGAA CGGAGACTGC ATTGACATAG ACGAGTGCNC CAACGACACC ATGTTGGTA	60
GCCNCGGCTT CTNTAACAAAC ACTNATGGCT CCTTCCGCTG CCTCTTTAAC CAGGGCTTCG	120
AGATCTCTCC CTCAGGCTGG GACTGTTGG ATGTAACNA NTGTAAGCTT ATNCTGGCGG	180
TATGTGGGGC CGCGCTCTGT NAGAACGTGG AGGNCTNCTT CCTGTGCCTC TTTGCCAGTA	240
ACCTGGAGGN GTACGATGCC CAGGAGGGC ACTGCCGCC ACGGGGGCT TGAGGTCAGA	300
GTATGTTGA GGGCNCAAC GGGGGGACCA TGCCCCGGCC CCCACCCGGT TGGACTGCNA	360
TTCCGGGNAG AAGGGNCATG CGCCCTGCTC CAGTNTCCTG GGCCGGAACA NCACANAGGC	420
TGAATNNNTG TTGCACCCAG GGCGTTAGTT GGGGAGTGCT NTAAACCTGT GCCCGTTTA	480

502

GGAATTAGTT GAATTCAAGGG AG

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

CCAGCCATTT CCTGCTCTAC GTACGTAATT CCNCCGCCGG ATGGCAGGGT GACATGGATT	60
TACCGCCGCA GCCGCTGATA CCTTACGCCG ACTGGTAAGT TTTCAGANAG CGCCTCTTT	120
AATGCCGCTG CGATCGGGTA TACTCGGGCG GCAATCTGGG ATTTCGGGG GGAGACAATT	180
TGCGCGTAAG TCGCTCGTTA ACAATCAAGC AGATGCCAGC NCTGCCAGA ATNAGCGCGT	240
CGGTGAAAAA AACAGCCGCA TNAATTGAGC ATCGAACAGG GTGCCGCCAG CATTGCGCCA	300
AACAGAGGTT TCAGGACTTC TCTACGNTGT GAAAAGAAAG CTGGCGACTG CTTCCAGGAA	360
GAATGAAAAA TAGCAAGCCG ATTTCAGGAT GCCCGGCAGC CCGNAAAGCG NCTTNATGT	420
GCGTCGCCAG AAAAAGGCAC ACCACATTGA AGGGGGACAA AAANCAGCAG GTTTGCCCGC	480
GGCCCAACGT T	491

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GGCACGAGCN AGNCCGACG CCGCCGACGC CCCTACGACC CCAACAGCGT CCGCATCANC	60
TTNGCCAAGG GCTGGGGGCC CTGCTACTCC CGGCAGTTCA TCACCTCCTG CCCCTGCTNN	120
ACTGGAGATC CTCCTGCAAC AACCCCCAGAT AGTGGCGGCC CCGGCGGGAA GGGGCGGGTG	180
GGAAGGCCGN GGCCACCGNC ACCTGCCGGC CTCGAGAAGG GGCGATGCC CAGAGNACAC	240
AGCCCCCACG GACAAAACCC CCCNGATTAT CATNTTACCT AGATTNAAT NTAAAATT	300
ATATATTATA TGGGAAATTA TNTGATTATA ATTTGTT	337

(2) INFORMATION FOR SEQ ID NO:586:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GT	TTTTTTTAC TGGCAACCCC NACGCTGTGG CNGTTTNCG CNTGGGGCGG TAATGCAGTC	60
AG	CGTAACGG TACTGGTGGC GCTGCTGGTC TGTNTNATCC CAACCACTAT TGGCGGCCTG	120
TN	GTCAAGCGA TCGGNNTCGC CGGGATGAGC CGGATGCTAG GCGCGAATGT AATTGNCACC	180
AG	CGGACGTG CAGTTNAAGC GGCAGGTGAC GTTNACGTT TGCTACTGGA TAAAACCGGC	240
AC	CATCACAC TCGGTAACCG TCAGGCGTCG GAGTTTATCC CCGCGCAGGG CGTGGNTGAA	300
AA	AAACGCTGG CTTGACGCCG CACAACCTGGG CTTCGCTGGC TGATGAAACG CCGGAAGGCC	360
GC	AGTTATTG TGAATCCTCG CCAAGCAGCG TTTTTAACCT GCGGCGGACG CGATTNTGCA	420
GT	CGTTCCAT GCCACTTTT ACCGTTTANT GCGNAAGCCG GTTNAGCGGG GTCAACATCG	480
GC	ACCGNAT GNTCCGTA	498

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GG	CAGAGCNA ACGGCGNGGC AGCGCACNGC AGGCGGNATT CATTCCACTT AAAACCTGAA	60
AAC	ATTGGAC CACACAAAGT CTTACTGATT TCAGGTAAAA ACAATAATTG AAGATGTCCA	120
GCA	AAAACAGC AAGCACCAAC AATATAGCCC AGGCAAGGAG AACTGTGCAG CNTTTAAGAA	180
TTA	GAAGCCT CCATTGAAAG AATAAAGGTT TCGAAGGCAT CAGCGGACCT CATGCTTAC	240
TGT	GAAGGAA CATGCCAGGA GTGACCCTTT GCTGATAGGA ATACCAACTT CAGAAAACCC	300
TTT	CAAGGA TAAAAAAATT GCATCATCTT ATAGTGGATA GAGAAACAGT TCTTGGCTCT	360
TCC	CAACAAG GCAATTGAGC GCGNTCCCTTG NAGNGTTAC CTCAGTTATT TGGTAACCNN	420
GTT	TATAATTAA A	431

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GGCTGCGGTC AGGGCTTCAA ACATGAGTCC TTTGCCCTGC CATTGGGCC CAATCGAATA	60
ACCGAGATAG CAGGCATGAA AAGAGCCACG AACAAACATTG GAAAATTGG CAACGCATGA	120
AATCTCTTT TCGTCCGGGT CGAATAAGCC AAAGTAGAAA GCTGNAACCT TGTTTATGAA	180
AATTGGTTAA ATCATCCCCA GCCTGGCCTG CCAACCTGAT GGATAAACAG TGGGCTTGCG	240
GTCGCGGCAC TGGCTTCCA GGGCTTGAG GGAAATGGC GNTTTCTNCT GCGTGAATAA	300
NTCCGCAAGN ACGGCCAGGC ATTACGNNTT CATGCACCA	339

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

AATTGTCTC ANCCGATGCC GGCTACCAAG GGGGCCACA GCCGNAGGNG CTGGTCCGAG	60
GTGGATGTGG ACTGGCTGAT CGCCGAGCGC GCCGGCAAGG TAAGAACCTT GAAACAGCAT	120
CCACGCAAGA NCAAAACGGC CATCAACATC GANTACATGA AAGCCAGCAT CGGGGCCAGG	180
GTGGAGCACC CATTTCGCAT CATCAAGCGA CAGTTCCGGG CTTCGTGAAA GCCAGATTAC	240
AAGGGGTTGC TGAAAAACGG TAAACCAACT GGTCGATGTT ATTCACGNT GGTCAACCTN	300
TTTCGGGNG GNACCAAATG ATTACGTCAT GGGGGAGAGN	340

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

CGCCTTAATG GTCCGACGNG CCTAAAGTTA ATTNAGGATT TAAGTAAGCG GAAAACGCGT	60
NATCGAATGG GTACGCCATT TATGCGTGAN CTGGAAGAGA AACGCAATCN NTTAATGGTA	120
AATCGGGGGC GTTTCTGCGC CCCCAGCTG CCAACATTG CAAATNCTTT NCACCTCCCT	180

GCACATCCG ACACGTAC CATCCATAAT TNAGGCTTAT NTGTTGTTA NCAGTAACCT	240
TATGTTT	247

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

AACAACACCG GTATTACGCA AAACTTATCG TACATTGGCG GCTAAAACGN CAAAAGGAGA	60
GATCAGATGA GTCAGGTAAG CACTGAATTT ATCCCGACCC GTATTGGCTA TTCTNACGGT	120
TTCNAATCGN CGCGGTGAAG AAGACGATAC CTCCGGTCAC TATCTGCGCC GATTGGCGN	180
AAGGAAGCGG GCCATCACGT TGTCGATAAA GCCATTGTGA AAGAAAACCG NTGACGCTAT	240
TNGGGCTCNA NGTATCT	257

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

AACCTGGTCA CAGTNAGCGA TCCACAAGAC CTGGCAGGCG ACGGAGTGTN CCTTGATCAT	60
AGCGAGCCCT ACGAACGCTC GGCGGAATT ACCCAGGTNT GGCGGCGTTT ATTGCAGAGA	120
AGAAACCGTC GNATTTAAC AC GGTAAACATA TTCATGTGCC GCGGAGCAAT AACTNCTCTT	180
CCCAGGCAAT TTCAACAGCC GTATCCGCTC ACTTTANCTT TGGCGGATCG TNNAGATGTN	240
GCCCAGNAGC TGGCGGCAGG AACAGGTTGA TCTCTAA	277

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

TGCCAGAGN CGGGGGTTAA AGAGGAGGAA GATGGCAGAT AAGGTTCTAC CTCACCNAAT	60
CCGGGAGCTT GTTCCANAGT NTCAGGCGTA CATGGNTCTT TTGGCTTTG AAGCGGAAC	120
GGTACCAAGAC CATTGCTNCG CAAGCGGGAT GGAGATCCAN GTAGGCCATC AAAAAGCCTC	180
TGNNCACAAA AGCGAAGTTT CGGGATCTGA CATTTCCAA TAAGTTCATT CCCAGCAAGG	240
AGGNAAGGNG	250

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

ACGTTTNAG CGGAGGCCA GCTAATGTTT NAGTATTAC CCGAACTNAT GAAAGGGCTA	60
CACACNAGCC TGACGCTAAC CGTNGCCTCG CTGATTGTGG CACTNATTCT GGCATTNATT	120
TTAACCATCA TCCTGACGCT GAAAACGCCG GTNCTGGTGT GGCTGGTGCG GGGTTATATC	180
ACGCTGTTA CCGGTACGCC GCTGCTGGTG CAGATCNTNC TNNTTTATTA CGGGGCCGGG	240
CCAGTTCCG ACTTTNCAGG AGTATCCGG	269

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

AAAGAACGGA TTAGCATNAA ACAGGTTCTA TCGGTTCTC NGGTTTNCAC AGCTTCACGC	60
CACCGGAANGA TTACGCGGTG CATCAGGCAC AGNTTTNCG GCGGTGTAGA AGTATCANCC	120
TGCGGTTNAT TCAGCAAGCT GCTGGCTTTC ACCAGCNTAA TGTCTGGCGG CAGGTTATAA	180
ACCATCTTTT GCAACACGCG TACCGTTGCC AGGGTGAGGA TGCCCAATGG NAATGGTTCG	240
ANCCGTTGCG AACGCGGCCA GGTTCAATTG NGCCGATTGA AATTGACACA CGGNTGTCCC	300
GTTCATTTT GCGGAANC GT TCGAGGGATG ACCTTCCCGT TTNGGTCCNA CC	352

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

AATAACGCGG GTAAACGGAA TCATCCATAC AAGCANGATA ATGANCGGA ATGGAACGGA	60
AAATNTTCAC AATCGCAGAA ACGGTANNAT ACAGCTTCGC NTTNACAATG AATTGCC	120
GGAACGCGTG AACATAAAGC AGAACGCCAA CCGGCAGNAC CAATGCACAA AGCCAAAAAA	180
ACCGGATACG AAAGGTGCAT TGCCAGCTTT TCCCATTACG GCCACGGAAC CAGCAGCCAC	240
ATGCTNCGGC TTCAGAACAT TAACCCAGTT ACCTCTGATT TTTAACATGG TGTTCCCTGG	300
CAGCCCAGGC AATGGGGGGN TTGCGNTNAT NCT	333

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

CAGCAATGGC GTCAAGTTGG GCAAAANTAA CATTNTCCCTG ATCGGNCCGA CCGGTTCCGG	60
TAAAACCCTG CTGGCTGAAA CCCTGGCCGC CCTCCNGGAT GTCCCGTTNA CCATGGACCG	120
ACGNGAACTN ACACTGAACC GAAGCCGGTT ATGTGGGTGA AAGACGTTGA AAAACATGCA	180
TTNNAGAAAG CTGTTGCAGN TAATGCGAAC TGNGAATGTC CCAGAAAGCN CAGGTGGTTA	240
TTGTCTTACA TGGGTGAATG GACCAAGATT TCTC	274

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

ACAGACCCTC CTTNNNTCCGT TTNTGGGAA TACTTCCCTC GGGTGAACTG AAAGTAAATT	60
TTTTTTTTTT CCCAAACA	78

(2) INFORMATION FOR SEQ ID NO:599:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GTNAAAAAG GGCTCGGTGT ATTCAAAAT AGCGGCGGA ATTACCTGAA NCGCAATTGG	60
TGGTGGTTCT CCACAGGN TA CTTGTAAAAG CNAATTGGGA ATTATCAGCA ACAACCCGGA	120
AGTTTGCCGA TGTGCCGTAC CTGGGAAGGG CTTTCCCCGA CCAATAAACCC CAGTGTACCG	180
ATTCTGGCAA TTCCTAACCA CAGCAGGT TA CTGGNCCAAA GGTGAACC AT TAAACTTACG	240
TGAATNCACT GNACGGAGAA GGAAACGGGC GCCAATTTT GTTTGCTTN ATGGATNCCG	300
CATGATATTC CCCGNCGGTG	320

(2) INFORMATION FOR SEQ ID NO:600:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GGCAGAGGTA AAATGGACAT TTTAGGGGAA ANTCTGTGG AAAGATAGCC CCTCCTCCTG	60
TTGTGTCTTC AGGGCCATT TTTTTATCA AATTGTCTC TGAAC TACGA AAACACATGG	120
TGCAGGGTTT NCCATACGTT AATGAAATT TCAAGANAGG TCCTGAATGT NCCCAGTAAC	180
TACACAACAC CTNAGTGGGA GTGAATGAAA GTCCCCGGG ATTNCCTGA ANAAAATAAT	240
GCCCAACAGC CTTGGAATGT CACTTNATNA TTGGTNCTTT TNCGCNAAA GAATGTCCAG	300
AGAATT TATT CCTGGGAATT TGAAAAGGTT TTG	333

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

TGTAACCCTC CCAAAGGNGC AGCTGGCCAN AAAACCATCG NTGCCCTCT CNGTTGCCTT	60
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CTGGTGAAAG GANTGATGAG CCACCGTGAA CGGAAGTTCC GTGCCCTCAG CATTANCACC	120
	123
CTT	

(2) INFORMATION FOR SEQ ID NO:602:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GGCTACGTAA AGAATAAAAT CAATCTCCCT NCNCAACGGT GGTAATTACN TTTAAATGAT	60
GGCCTCAAGT CGGTAAGCCG CTATGGNTGA TCCNGTTTG AACACATTATG GCATGAAGGC	120
GAACGGCNTT TATTGTTACC TCANGCATCA AACGTCACCC GCAGAAGTGG AACCCAAAAT	180
CGCNGCAATT TATGAANC GT TTNTAACGTT AACGGAAATT CGCGAATGTA TTTGATTCC	240
CAGTCACCAT ACCCCTTTT TNCCATCGG GGTTAGGTGG GTTATGCGGN NGACCCNTAN	300
	306

TTACTG

(2) INFORMATION FOR SEQ ID NO:603:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

CTGCACTGGG NNCATGAACT AGGCCTGGCC TTCACCAAGA ACCGANTGAN CTATACCAAC	60
AAATTCCCTGC TGATCCCAGA NTCGGGAGAC TACTTCATTT ACTCCCAGGT CACATTCCGT	120
GGGAATGAAC CTCTGAANTG CCAGTGAAAA TCAGNCAAGC AGGCCGACCA AACAAAGCCAG	180
ANTCCATNCA CTGTGGTCAT CACCAAGGTA ACAGACAGCT ACCCTGAGCC AACCCAGCTC	240
CTTCATGGGG ACCAAGTTTG TTTGCGAANT AGGTTAGCAA CTGGTTCCAG CCCATTTAC	300
CTTGGGGGCC AGTTCTNCTT GNCAAGAAGG GGACAAGCTT ATGGTGGAAC GTTCATANCA	360
TCNTTTTGG GTGGNTTTAC ACAAAAGG	388

(2) INFORMATION FOR SEQ ID NO:604:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

AAGCTTTACT GGTGCGCGAA AAAGTTGAAG CCGCGCGCAG AGCANTGCTG CTGTATCCGC	60
AAGGTTTAAG CTGGGAATTG GTGGGATGAC GTCACCGTAG AGATCCGTTT CTGGCTTCCG	120
GCGGGTAGTT TTGCAACCAG CGTTGTCAGG GNAACTTATC AACACAACAG GTGATTATGC	180
CGCATATTGC TGAGTAATGA TGACGGGTA CATGCACCCG GTATTNGAAA CGCTGGCGAA	240
GCTTGCCTGA GTTTTNCTGA CGTTCCAAGT GGTCGCCCGG GTTCGNTAAC CGCAGGGCGN	300
TTCAAATTCT TCTGNCATGG GATTCCCTCCC TGCGNACGTT TTACCTTTGG AAATGGGGGN	360
TTATT	365

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

TTACAGANNT AAGCCGCCGT GCCCAGNCAC AAACTTCTTT AATNACAACC ACGNAAGGGG	60
CACACATGGG TCCTGTCTCT GGTATGGATT CACACACACG TGCACAAATT GAAGTCCAAT	120
AAAAAGCATN TGCCCCACAGA CCCACCATGT GCCATTAAG ANCTTCTCTN CCAGCACAGA	180
CTNGTTGGTG TTGTTCCCTNG TGCTTGNAGC TCTTCAACAA AGAGCTTTG CCGT	234

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

TCTCTNCGAC TCATTGAGCC AGATGCTGAG GAAAAATGTA GAAAAGCGAG CACANCCAAG	60
NACAGCGGCA CTACCGGNCA CGNGACTCGC TTGTATAAAA GGTTTTTN	108

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

TGGTGGAGCT CNGCATCCAC GAACAACCGC ATCCGCAAGT GCCCAAGGAA GTTTTCAGCG	60
GGCTCCGGAA CATGAACTGC ATCGAAATGG GCGGGAAACC CACTGGAGAA CAGTGGCTTT	120
NAAACCNGGA GCCTTCNAAT GGCTGAAAGC TCNGCTACCT GCGCCATCTC AAAGGNCAAG	180
CTGGACTGGC ATCCCCAAAN ACCTCNCTNA GAACCCGTGAT TGAAACTCCA CCTAGACCAC	240
AACAAAATNC AGG	253

(2) INFORMATION FOR SEQ ID NO:608:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GGCACGAGGN CCCTCAAAAG NAGNAATCAG CTNCANTGAC AATAAAGATG GGACATGCAC	60
AGTGACCTAC CTGCCGAGTC TGCCAGGCAG CTACAGCATG CTNGTCAAGT ACAATGACAN	120
NNACATCCCT NGCAGCCCCT TTA	143

(2) INFORMATION FOR SEQ ID NO:609:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

CCCNNTNCTCA TGGGGNTGTT TCCTACTAAC CCCAAAGNGA AGACCCAGGA GGAACCCCT	60
GGNCCAGAGC AGGGCCCCCTG TTTTGACCGT GGTGTCCAAG TTCAAGGCCT CACTNGAGCA	120
GNTTGTGCAG GTCCTNNACA GNACCACGCC CCACTNCATT CGCNGCATCA ACCCAACAGC	180
CAAGGNCAGG CGCAGACCTT TTTCCAANAG GAGGTCTAA GCCAGCTCGA GGGCTGTGGN	240
TT	242

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

CCCCCTCCATG TACAGCCGCT CCATCCAGGG NCACCATGTC TGNCTCCTGG TGAAAAAGGG	60
TGAGANCTCT N	71

(2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

AGTACACTGG TNCCCGTACC GGGCAATGTA CCANTACAGG CCCCAANCAGA AGACGAGCTG	60
GAGCTGCGCN AGGGGGACAG GGTGGATGTA ATGCNGCAGT GTNACGATGG CTGGTTGTG	120
	120

(2) INFORMATION FOR SEQ ID NO:612:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

CGTGNGCCCC NCAGAAANATG GNCCCGGGTG CAGAACCGGC AGAGCGGGTC TGCTACTGGT	60
CCCNTAAGCC AGAGTAGCCA AGACTGAAGT CACTGCTCAT CCGGAATGGA AATCCCGCCG	120
ACCAAATACC CAGCCTCCAG GGCGGCCTTG GTGGCACAGA ACTACATCAA CTACCAGCAG	180
GGGACCCGCA CAGGTGTTN AGGTGCAGAA GGTCAACAAG CCAGCATGGA GGATATTCCA	240
GGAAGAGGAC ATAAGTATCA CCTTTAAATT TGCTGTTGAA GAATTATACA AAAACAANTA	300
AGGTGAACTG CACAGNTGAA GTACTTTACC CTTCAACGGG ACAGAACTGA CCAGAGTCAC	360
TTCACATTTG AAGGGGAACG GGAAGATNCA GATGAGAGAC ACACTTNTNC AAGCTTAGTC	420
CTGAGGACGT AGAGACAATT TCNGCATTG GATNN	455

(2) INFORMATION FOR SEQ ID NO:613:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GGCACGAGCT ATGCCAGCA GTGCCAGTNA CTTTGGGGAC CTGGAGCCA GCCCGCTGCG	60
CCACTTTGCC TCCAGACAGC TAATACTCGG GGAAATGCTT TTGGGAGCTG TGGGCGCAAC	120
CCCAGTGGCA GTTATGTGTC CTGCACCCCT AGAGATGGCA TTTGTGGCA GCTCCAGTGC	180
CAGACAGGTA GGACCCAGCC TCTGCTGGNC TNCCATCCGG GGATCTACTC TGGGAGACAA	240
TAGATGTGAA TGGGACTGNG CTGAAGTGCA GCTGGGTGCA CCTGGGACCT GGGCAGTGAT	300
GTGGCCCAGN CCCTCCTGAC TTTGGCCTGG CACAANCTGT GCCCCTGGNC TGGNNNTGTA	360
TAGACC	366

(2) INFORMATION FOR SEQ ID NO:614:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

TTAAGGTTTC GCTGACCGGG ACATAATGGC TTACACCTTC TCCAGTTGA CCGCGCACTT	60
CTTGAAGTCC GTCTCTTCG AGAGCGGATC GGTCGCATCC AGCGTCAGTT TGTTAACCAA	120
CTGTGCCGGC GTCGAAGAAC GGCAATGTACA CCAGGCCCTG TGGCGGACGG TTANNACCGG	180
CCGTTCAAC AATCGAGATC ACTTCGCCAC GGCGAGAAC CACTTTNACT TTGTCGCCAC	240
GGCGCAGATC GCGCGCTTTC GNATCCAGCG GGTGGAATAA AACAGGACCG CTTCCGGGGA	300
AGGCGCGGTG CANTTCTGGT NACACGGCGA GTTCATAATT GCCGGTTNTG NCCAGTGGTT	360
CCAGAACGTG TTCCGGTTAG AGAGCCACAA GTTCGTAATT CTTCATCCGG TGGTTCCGC	420
CGNCGGTTTC NATGGGNATT CGGAAGATCA NC GTTTGCC ATTCCGTTT ACCTTAGAAT	480
TTTAGCTTT GGCCC	495

(2) INFORMATION FOR SEQ ID NO:615:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GGACTGCACC GGCACAGAGG CCCACATCTC CAGCTGCAAN NGTTNCCCCA GGTGTCAGT	60
GACCCCATGA AGAATGTCAC CTGCNAGAAT GGGCTACCGG CCGTGGTGAG TTGTGTGCCT	120
GGGCAGGTCT TCAGCCCTNA CGGACCCCTCG ANATTCCCGA AAGCGTACAA GCCAGAGCAA	180
CCCCTGGTGC GACTNAAAGG CGGTGCCTAC ATCGGGGAGG GCCGCGTGGA GGTGCTAAA	240
AATGGAGAGT GGGGGACCGT CTGCNACGAC AAAGTGGGTA CCTGGTNTCG GNCAGTNATG	300
GTCTTGCAGA GAGCTTGGGG CTTTTGGGAA GTNCAAAAAA GGCAGTTNAC TNGNTTCCG	360
ACTTAGGGTA AAGGGTTTCG GACCNATTCC AACTGGAACG GAGTTCCA	409

(2) INFORMATION FOR SEQ ID NO:616:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GGCAGAGCNC GANTTNAAAA AAGGAAGGCA ATCATTGGAT TATACAACTA TGCCCATGAA	60
ATAACTCATG GAGCAAGTGN ACAGAGAAAT ACCCACGCCT TGGCCAGATG ATTGTGGATT	120
ATGAAAAAACC CTTTAAAGAA GATGATGGNA AGATTTNNNTN NCCCCATNAG CAAGTNTCTT	180
TNAGATGCAC TAATTTCCCT TCCAAATGGT ATATCCTCGA AAGGAAATCT TTTCACCTGG	240
ACCAGTGGAG AAATGNCCAG TTATTGAGNC TCATCAGTGN NACCTTNGT	289

(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GCCCGAGGAA AACCGTGTNC NATNAGCCAT GAGTCAACNC CACCGTGTTC TNCNANATTG	60
CCGTCAACGG GAAGNCCCTT GGGCCGCGAT NTNCCTTAA CCTGTTGCA GACAAGGTCC	120

CAAAGACAGC AGAAAATTC CGTGCCTCTG AAGCACTGGN NGAGAANGGA ATTTGGTTAT	180
AAGGGTTCCT GCCTTNCAC AGGATTCA TT CCAGGGTTA TGTGTCAGTG TGGTGGANTT	240
CACACGCCAT AATGGCACTG GTGGGCAAGT CCTTTNTGGG GGGGAATTG AAGGTGNGNN	300
TTT	303

(2) INFORMATION FOR SEQ ID NO:618:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

CCCATTANN TCGGATANTT GCCGNGAAAT CGGCCGGATT AATGGCGAGT ATTTGGCACA	60
TCCNTTGGCA ATGCTGAAGG TGGTCAGGAA GCCACGGGTC ATCAGGTTTN N	111

(2) INFORMATION FOR SEQ ID NO:619:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GGCAGAGNCA GAAAACTGCC CCAGGGGATG CAGCTGGATT NTTGGAAGAA ACGAGAGTTT	60
TGGGAAACCG TCCTGGCATC CTGGAAGGGG CCTGAAAGCA GCCCCTTATT CAGAACAGA	120
GCCGGCNCCA CAAAAAGGAA GCCCCCAAGA AACTAGGNGA GCTTGAAATT AAAAACATGA	180
GTAAAAATNT CATAAAANCA GGGAAAGCTTC AAAGACACAG GGNACATTGC CAGAACCCAG	240
AGAAGGTGTA AGNAGAAAGC CGTGAACCTC CCAGGGCTGT NTGTGGAGTC TNGCAGGGC	300
TGCCTGGTTT GCCGAGTCCC ACGTTTCGN CAGTGTGGTG GTNCCGNTGG GGAGG	355

(2) INFORMATION FOR SEQ ID NO:620:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GGCAGAGGGA AGACACAAGA TAAAATTAAC ACCAAAAATA AAGAAATACT TAGGTATAAN	60
TCCAAGAAAG CATGCATAAG ANCTGTATGA AGAAAGCTAC AAAACTCTTA TAAAAGACAT	120
AACATTTCAG CGATAATAAG TACAAAGTTG GAGGGATGAC TTCGAGACTT ATTAGAAAGG	180
TACTGTGAAT GAAGACAGTN TTGTATTGGT CCAAAAANTC GGCCAATAGA ACACATGGG	240
AAGCCAGAA AATAGACTCA GTGCCAGGCC GGGCGTGATG GTCAAGCGT GTAAATCCTA	300
GCACCTTGGG GAGGTCCGAG GCGGGCGGGT TCACAAGGTT CAGGAGNTCG AGACCNTCCT	360
GGGCCAACN GTTAAAACC CCCTGTTNTA NTAAAATTAC CAAANNATT AGCTGGCGT	420
GGTGGCAGTG CCCGTAGTNC CCGCAANTTG GGNGGTTGG GCAGGCGATT GGGGTGACCC	480
GGGGGTTGGA GTTTTCATTN NGGGGGTTTG	510

(2) INFORMATION FOR SEQ ID NO:621:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

CAGCGGATCG GTCTGCCCT GTANNCAGTT AGCTCTTCAT GCACCCGCAG CATAAAACGG	60
TGNAAGTGCA GGCNCTGTTT CCGGTCTCCC GGCAGGCTTT GATAGAAAAG GTCCATCAGC	120
CAGGTTTCC CGCGTCCTAC ACCGCCCCAN ATATATAAGC CACGCCTGG CGTNATGCTT	180
TGTGTCTTCG CGTTTACCCC ACAGCTTACC GACCCGGGCC ATTAGCCCAC TCGTCCTGGG	240
GGCTGGTGGC GTGCTATTGA TGAGTTCTG ATAAATAAAAT TTCCAGGCAG CTGACGGCCT	300
CTTTTTGAA CGTNGTCGGG TTGATGGCTG NCNTTCATTA AAGCGNCTTC AGGTATTGCG	360
ATGTTGGGT AACGGTTGC ANGATCNTAA TGTTANTCCN TGGATAAAATC GGTGNGCCTT	420
TGTTCAAGGT NNAGGAAAAA AAGGCCGTTT ACATTACGGG TATNCATCGG GGTTCCATT	480
TTGGNTTAAC GGTAAAGGGG GA	502

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

ATTGAAACGTN GCCCAGGAAT CAAAAGTCGC CGTTTTCCA GACAAGCCGG GNACGGTTT	60
TTGGTGGTG GATTGTACA CCAGAAACTC ACGCCACATT CGCCAATTCT CACGGAGAAC	120
AGGCCTTCCT GCTGCNTNGA GTCTATCGGA CAGTCAGAAA TGAATCATAT CCAGTTATG	180
CTGACTTAAT TGCTCCAGCA GNATTCGTG GGTGGNTTCG AAGCAGNGGA AGATGAATGG	240
GCTCGTCTTC TACCACTGCG GCGTTAAGTA CGCTACTGAC CAGGCGTTG GTAAAGTCA	300
TCAGGCCACGN CAACGTCAAN CAATGAATTG GATTCTTGC GATAGTTCAC AATATCCCAG	360
CCATTCCGG GNTNAGGTGA ACATTTTTT CGGCTTAGNG TTAGNCCATT TTT	413

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GNCACGAGTG GGTNATNATA CCCCTGNCAT TGACAGACAT CTAGGNGAAC CACATAAATT	60
TAAAANAGAG TGGTCCAGTG TAATGCGGTG TGTAGCAGTG CTTTGTGTTGGT ATAAATCATG	120
NCAGTNCTAA AGTGGATTTCA NATAACAACA TACAGTTGTC TCTNACACTG GCTGCACTAT	180
CCATTGGACT GTGGTGGNCT TTTGNTAAGA TCTAGANGTG GTTTGGCCT TGGAGTAGGA	240
ATTGCCNTC TTGGCAACTG TGGTCACTGC AACTGCTAAG TNTATAATGG TGTTTACCA	300
ATATGACCTN CTCCAAGATN TCCCNGTGAT GGTT	334

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GGCAGAGNCC GANCCACCAT CTNCTNGAAC GTCAACGGCA NACAAAGTAA ACAGGACCAA	60
GATCCACAGC GNAGTCCTGA GCACCCCTGGA NTNTCCTCGT AAACCCGGC NGCTGTTNGA	120
GANANGTNGT TGAATNCACG GCCCTCCNAN CGACCTGGGT CAAAAACACC AGCATCCTCT	180
TCCTGGAGCT GGTCAATTTC ACCACCNTC ACACNAGACT CTCACATAAC CACTGGACTC	240
AGCACTTCCA NTGNCAGTCC CGNATA	266

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GGCAGAGCTC ATAGCTTGT	TT GGTTACCTCC ATGGGGCACA TAAAGCTGAC AGATTTGGA	60
TTATCTAAGG TGGGACTAAT GAGCATGACT ACCAACCTTT ACGAGGGTCA TATTGAGAAG		120
GATGCTAGAN AGTCCTGGA TAAACAGGTC TGTGGCACNC TGGAATACAT TGCACCAGAA		180
GTGAATTCTG AAGGCAGGGT TATGGAAAGC CGGTGGACT GGTGGGGCCA TGGGGATT		240
TCCTTNATG ANATTCCTG GTTGGGATGC GTGCCATTCT TTTGGGGATA ANTCCANGGG		300
NCTATTTGG GACAAGTTCA TCATGATGAG ATCAATGGGC CTA		343

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

CTGCGGNGCA AAAGCGGTTC GCCAGATCTT GCCCAGTCTG CGANGATA	GT TGTCAGCAA	60
CACCAAGCGGC AGGCCTTTAT CCATAATCCC GTGAAAAAT TCCGCTGCAC CCGGTAGNCG		120
NACGTTATCG TGCATCAGCG NCGCGTNCGC ATATCGAAA TTACATTTT GAATGGTCAT		180
GGACTACCCA GAATATTGAC AACAAATTAG CGCCACTTAT TAAAAGCACA TTAAATTTC		240
CAGCAAATGC TGGAGCAAA TACCGTTGAG CATGGCGCGT TTTTACCA	GG GCAGCAGN	300
CCGTTTGCG AGCGGTTGAT TCCAGCTTCA GAACGTNACC ACCGGNCAGN TTTAGTGCGN		360
AAA		363

(2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GGCAGAGGGC ACCCTNTCCG CGCGAANC GG TGCGCGCGA CTCGTCCCGG CCCTGGCCCC	60
CCGCAAACAA GGATCCGCTG CGCTCGGGGA ACGAACNNN CGNCTCGTGG CCCCGGACCT	120
GAAAGACCCT TCCAGCATGC NAAAGGAAAG TTCCCCCAGG CGGACCCCGC AGAGCATTCC	180
CTACCAGGAC CTCCCTGCAC CTGGTNAATG CAGACGGACA GTAACCTNTT CTGGCAGGTA	240
CTGGGAAACC CACAGGCACA CCCAAGGCC TCATCTTTT TTTCCCATGG AGCCGGAGAG	300
CACATGGGCC GTTATGAAGA GNTGGNTTCG GATGNNTGAT GGGGCTTGGA NCTG	354

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

TANNCGTAGT GGTGGTTAAC CACTATACT GGGAAAGATG ATGCCCGGCC GNCGACGCCG	60
TGGGGCAGCA CCATCATTNA TAAAGCCCAT GTNAAAGGAT TAATGTACTT GCCNCCCGA	120
GATCCCGGTC AAAATCCGTG GCACTTATNA AAGCCCTCGG GCATCCGGTG AATGNTCGCT	180
ATTTGAAACA TTTGGGCCAT TACCGNGCTG GGAAC TGCTG CCATGGCGCA TTTTGCCAGT	240
NAAACCAAGTT TGNAAAAGCNT GGGGGGTNAG TAACTTATTG GGGTTTACAA CCCG	294

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AAAATCGTTA CCACGTAGG CCCAGCAACA GATCGCGATA ATAATCTTGN AAAAAGTTAT	60
CGCGGGGGT GCCAACGTTG TACGTATGAN CTTTTCTCAC GGCTCGCCTG TAAGATCACA	120
AAATGCGCGC GGTATGAAAG TTCGTGNAGA TTGNCCGCAA AACTGGGGCG TCATGTGGCT	180
ATTCTGGGTG ACCTCCAGGG GCCCAAAATC CGTGTATCCA CCTTTGAAAG AAGGCAAAGT	240
TTTCCTCAAT ATTGGGGATA AATTCTGGC TTGACGGCA NCCTGGGTG AAAGGTTGTA	300
AGGCGNCAA GTAAAAGTTG GTGTTCGTTN ACAAAAGGNC TGNCGGCTGA ACGT	354

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

CTGGCTTTGT GTTTGGTCA TTAATGGGT GAGTGTGCGG NTCACCGCTG CCATGTATT	60
CTGAGCTTTC GCTTTCGCGG CTTTTGCTN TGGCCCTGG ATGGGTAGCC AGGTCA	120
AATGCTTTG AATTTTNAAG GTACCGCGCT CCAGCTGTTA GNAAGCATA	180
TAATTTACT TGCAGCACGA GTGAAGATTG GCTTGTCGG GACTGCTGTC GATGGCACGA	240
AATTGTTCC AGTGGCAGGC TGGGATTCTG GCTGTTAAAG TCTTCTCGAA ACTGGCTGAT	300
GGAGAGATCG AANTNNGGGC TTTAGCCAGC AGATAAGGCG CGGTNNNTTG CC	352

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GGCAGAGCGC ATGTGTGNAG GCGCTAACAA TGAAATTCAA GGCGAAGTG CAGAGCAACC	60
GGGGCCTGAC CAAGGAGAAC CTCGTGTTCC TGGCGCAGAA ACTGTTAAC AACAGCAGCA	120
GCCACCTGGA GGNACTACAC TGGCCTGTCC GTGTCTGGT CCCANTTCAA CAGGGAGNAC	180
TTTNCCGGGG CTGGNAACTA CACCTTCTGG CANTTGGTT TTACGGGGTG ATGGGAGGTT	240
GTTGAAGAAG CACCACAAGC CCCACTTGGG ATNNATGGGG GCCATCCTAG GGTTTTGTG	300
AATTAAGCAA CCAGTCCCCA NGNNCTGGTT	330

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GGCAGAGAGC ATACCATCTT TGGACGGGTT GTTGGGGCT TTGACGTACT GACAGCCATG	60
GAGAATGTGG AGAGTGACCC CAAAAGTGCAC CGCCCTAAGG AGGAGATCCG CATTGATGCC	120
ACTACAGTNT TCGTGGACCC CTATGAAGGA GGCGATGCC CAGATTGCGC AGTAGCGGNA	180
AGNACACAGC TCAAGGTAGC CCCGGAGACC AAAGTGTAAAG AGCAGCCAGC CCCAGGCAGG	240
GAGCCAGGGC CCCCAGACCT TTCCGCCAGG GTGTGGCAA GTTACATCAA CCCAGCAGCC	300
ACGANNCGAG CAGCAGAGGT AAGGAGNCCT TTAACCATTG GCCATTTTC CCCNNTTNCA	360
AGAAGAAGNC CATTGGGGT TTTGGGGAT TTCAGTTCTG GTTAGCAGCA NAATTTTAG	420
GTGTTACT	428

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

TTTGCAGCTC ACGGGAAAT TTNTGCGCCA CTACCGCATC ACCAACATG ACCGGAATAA	60
TGGCGTGATC GGNTCCCGCC AGGNTAAAGC CCGNCGNCGA CATTGCTCA CGGAACGTGAC	120
GCGCGTTCGC CCACAGACGG TNACGNAGTT CGCTGCCCGC TTGACCATC TCCAGTACTT	180
TNATGGACGC GGCAACAATG GCCGGTGCCA GCNAAGTTGG AGAACAGGTA CGGACGAGAA	240
CGCTGGCGCA CACTNCAACC ACTTCTTGC GCGCCCGGT ATTAACCACC AGAAGCCCCG	300
CCCAGCGCTT TTACCAAGCG TACCGGTGGN TAATATTGCA CCCGGCCCAT CACATTGCA	360
GTATTTCATG GGGGAACAC GGACCATTT TNAACGGACA AAACCGACCG GNTGGGGAGT	420
TCGTNTTACC TTCANCAGGG NA	442

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

TGCCGCTCTT TATGTGGGCC GCGCGTCACT GTCAGCCCC AGGTAATCAG CGGCGCGGCC	60
ATCTTCCGGC CAGCAGGTCA TAATGGGAAT GCNATTGANA TCGNCGTCAT CGCCAGANAC	120

GATTTTTGT TGGCAGGGCG CACCACGCAG CCGCTTGTC GGCATGTTCA ATACTTGCTT	180
AAACTGCGGC AGTTTATCAA ACAGGTCGCG GAAACCTTTT GGCGGCTCCG GCTCTTCAG	240
AAACGCCAAT AATTACCAA CTTCACGCAG CGCCGNAAAC ATCTTCCTGC CCCATGCCA	300
TCGCCACGCG CTTGGCGTT ACCGAACAGG TTGCACAGCA CGGGCATTGN GTAGCNTNA	360
GGGTTTTCG GAACANCAGC GGCAGGCCA CGGGGAAGGC AAATGCGGTT CAGCAATT	420
CATGGTTTN CAGATGGGG ATNCCACCGG GAGNGTNGTA AGTTTTAGG	470

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GGCACGAGCG CTCACTGGGG GACCGAATCC GGGATCTTGC TCAGCTAAA AATCTCTATC	60
CCAAGAACCC CAAGGATGAG GCTTCCGGA GCCACTACAA GCCTGAACAG ATGGGTAAGG	120
ATGGCAGGGG TTATGTCCA GCTACCATCA AGATGACCGT GGAAAGGGAC CAACCACTTC	180
CTACCCCAGA GCTCCAGATG CCTACCATGG TGCCCTCTTA TGACCTTGGA ATGGCCCTG	240
NATTCCCTCA TGAAGCCCCC TTTNNNTTNT	270

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GGCANGAGCT GGACCCCCCA ATGCGGGCAA GAGCAGCCTA GTGAACCTGC TCAGTCGGAA	60
GCCTGTGTCC ATCGTGTCCC CGGAGCCAGG GACCACCCGT GAACGTGCTG GAGACCCCAG	120
TCGACCTGGN CCGGATTTC TGTGNCTGCT GAGCGACACG GCTGGGTTGC GGGNAGGGCG	180
TGGGGCCNN GGAGCAGGAG GGCAGCAGG GCGCCCGTGA AGTAGGCTTA GAGCAGGCTG	240
ACCTCATTCT GGCCATGNTG GGATGCTTTC TGAACCTGGC CTCTCCCTCC ANTTGGCAAN	300
TTCCCTGGTC CACCGTNGTT AGNCTCT	327

(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GGCAGAGCTG AGCCTTGGAG ATTATCATCA AGCCAGACCC CTCAGCAGCA AGTGGAGCTG	60
TTTGACTTGG AGAATAACNN AGAGTACGTN TCCAGCGGAG GGGGCTTG ACCGGTTGCT	120
GATGACGGCT ATGGTGTGTC GTACATCCTT GTGGGAGGAG AACCTCATCA ATTTCCACAT	180
TTCTTCCAAG TTCTTCTTGC CCTGAGACGG ATTCTCATCG CTTTGGGAAG GCACCTGAAA	240
NNAAGCAATG ACTGACATCA TCACCTTGTG TGGNTCTTCA GTTCTNAATT TCCAAAGTA	300
ATTCCACTGG AGCTGCTGGG GAAGGTAAAA CGAGCTCTTT NTGATGCAA CCAATGNAAA	360
ATTAGGCATT AATCCNGGNC CTNAGTTCGG GA	392

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

ACTTTGCCGG AACATCCTGC TGGGGCTTGA TCCACGTCGC AGTTGCTTCT CGCATGACTG	60
CNTCGGTGGG CAGTTGCAA AACTTGCCA GCTTCATCTG CGCCTCTTT GCGCCGATCA	120
TTACTGGTTT TATTGTTGAT ACCACCCACT CATTCCGTCT GGCACTA	167

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

AGAGCNGAGC AGTCAAGATG TGTGAACCTCC ACCGAAGACC AGACCGNAGA GTTCAAGGAG	60
GCCTTCCAGC TNTNNNTAACCC GAACAGGTGT ATGGCAAGAC CCTGTTACAG NCA	113

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

AGATAGCAGC CTTGTAACCT ATGANCTACA TTNTCGGCCT GAGCAGGACA AGTTCTCTCA	60
AGCTGCCAAA GTCGCAGAAC TTGAAAAGCG CCTGANAGAG CTGGAGACAC TGTNACGTTG	120
TGAATCAGGA ATGCTCAGAA ATCCCCTTT TGNCAGGTNT ACAGGGAAGC CTGTNCTCAT	180
GGAGACTGTA GGAGCTGTTG CAAAGCAAAA GGTGGAGCGC CCTAGAACCT TGCAGTTTG	240
GGATCAAGTG GGAGGCTCGG CTTACAGAGT GTNCCTGGGG AAAGGTTGAA CGAGATTGCG	300
CCAAGCTTAA AAGCCTCTNT TAGGAAGTTG CAGTTCCNC AAAGCAAAGT TGCNCCNGTT	360
TTTGGNAAC TTTT	374

(2) INFORMATION FOR SEQ ID NO:641:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GGCAGAGGAT GACATTNGNN TNANCTACAA GATTGGAGAG ANGTGGGACC ATCAGGTGCN	60
AANTGGNCAT ATGATANGNT GNACATGTTT TGGGAACGGA AAAGGCGAAT TCAAGTNTGA	120
ACCCCTTCATG GAGGTCAACG TGTATGNAT GTTGGGTAAG ACATACCACN TAGGCNGTAA	180
CAGTGGNCAG AAGGGA	196

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GGCAGAGCTG AGATCAAGGG CCACAGGGGA CCTACGTGGG CGCNATGCCG GGAAAGATCA	60
TCCAGTGTAA AGAGAAGACC AAGACGGAGA ACCCCCTGAA TCCTNATCGA CGAGGTGGAA	120

CAANATCGGC CGAGGCTACC AGGGGGACCG TGCCTCGGNC ACTGCTGGAG CTGCTGGTAC	180
CCAGAGCAGA ATGCCAACCTT TCCTGGNACC ACTACCTGGN ACGTGNCCCG TGGGANTTGT	240
TCCAAGGTAG CTGTTTNATC TGGCACGGGC CAANGTTCAC GGGACACTTA TTCGCCNAGC	300
CGTTGGAAGG ACCGTTATGG NGGTTGATTAC AACGTGTCGG GGTTANTTGG NCCCAGG	357

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

GGCACGAGGT GGCAGGGNNNT GTGTGTGCTG AGGCGGCTGA GCGGCGGACA TGCACACTAC	60
AGTGCCTGGC GATGGAACAG TAACCAGGGTT TGTNAGAGGG CTCTGCAGTA TAAACTAGGA	120
GACAAGATCC ATGGATTACAC CGTAAACCAG GTGACATCTG TTCCCGAGCT GTTCCTGACT	180
GCAGTGGAGC TCACCCATGA TGACACAGGA GCNAGGTTTT TACACCTGGC CAGNGAAGAC	240
ACGAATAATC TGTTCAGCGT GCAGTTTCGT ACCACTTCCA TNGACAGTNG TGGTTGTTCC	300
TCAAAATTCT TGAGGCATAC CGTNCTTTNT GGGTTTCAG AAATATTCTG GNAGAGACC	359

(2) INFORMATION FOR SEQ ID NO:644:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GGGGCAAAAA TGCCGAAGAT GCGGTGCATA ACGCCATCGT GCTGGAAGAG GTCGCTTATA	60
TGGGGATATT CTGCCGTCAAG TTAGCGCCGC AGTTACCGGC ATATGCAGCA AACGCTGCTG	120
GATAAACACT ATCTGCGTAA NATGGNCAGC TNGGCATATT ACGGGCAGTA ATGNCTGTAT	180
AAAACCACAG CCAATNCAAA CGNAACCAGG CTATACTTCA AGCCTGGTTT TTTGNTGGNT	240
TTTCCAGCGN GGCGCAGGTC AGGTTTATC TTAACCCGNA CACTGGCGGG GACACCCCG	299

(2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

CGGCCGCGCT GCTGGACAAG CTGTATGCTC TCGGCTTGGT GCCCACGCGC GGTCGCTGG	60
AGCTCTGCAC TTTCGTCACG GCCTCGTCCT TCTGCCGCCG CCGCCTCCCC ACCGTGCTCC	120
TCAAGCTGCG CATGGCGCAA GCCTTNCAGG CTGCCGTGGC CTTTGTGGAG CAAGGGCAGC	180
TACGCNTGGG CCCTGACGTG GTTACCGACC CCGNCTTCCT TGTNACGCGC ACATGGNAGG	240
ACTTTGTNAC TTGGGTGGAC TCGTCCAAGA TCAAGCGGCA GTGCTTAGAG TNACAATGAA	300
GGAGCGCGAT GATTGNTCT GGAAGCCTAG CGGATTCCC ATTTGCAATG TTGTNTTTN	360
ACAGTGGAA AATTGAGGCC TGATGTTGGA GATTTTANGA GGGTGTTCCT CTCAAGGGTT	420
NTNAAACGGT TGTAGGTTTT TAAGAATTG ATTCACTCATT GGCANGCCAG NATAGAGCCA	480
GGG	483

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

TCAGCTGCC C TGGGGCTGC TTTCCNTGGG CACGGGCTCC AGGGATCATN TNTGGGCACT	60
CCCTTCCTGC CCCAGGNCTT GGNTCTGCC TTCCTGGGG GGTGGAGCAG GGTCCAGGTT	120
TNAAACTTGC NACCTCCTGG AGGTCAAGAA GAGCAGAGTC CCCGTCCCTG NT	172

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GGCACGAGGG GATTACAGGC GTNAGCACCA CACCCGGCTT CATTAAACC ATTTAAAGT	60
GGCATGAAGT ACATTCAAAT TGTNGTGCCA CCATCCATCA CCCAAACCGA AATCCATAAC	120
CATTAACCA TAACTCCTCA TTCCTACAGT NTGTTCTTT TCATTACGGG ATAATATTCC	180

ATTGTNTGGA TGGGCCACAG TTTGTTTATC CACTCACCTA TTGANGGACA NCTTGGTTCT	240
TCCCCACATCT TGCCAATNAT AAATNANGCT GCTATAAATA TTTGTNTGCA GGTTTTGTG	300
TGCACATAAG TTTTCANGTC ATTTGGGTAA ACACAAGGGG TGTGATTGCC GGGCCTCTGT	360
CTGACTTTAT TTCCATCAAC CGCNTCAAGC ACCTGGNGTG NGGGCAGGAG CCANGCCAA	420
CANNTATGTT TGTAAACCTA TTTAATTAAC AGNCCACAAT ACAGNCCAGG CACATGGGTT	480
CNGCNGAAA AACTTGGGAC TTTTGGGAGG CCCAGGCG	518

(2) INFORMATION FOR SEQ ID NO:648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GGCAGAGCAA ACTGTGACTC AGTGGATATT TGTATGCCCTT CCAAAAACAT TTTAAAGCTG	60
AGCAATTTT AATAAAGATG TATAAATAAT TTTGNATTAT TCTCATTGTA GTTAAGTTAC	120
TGTTAGTTG GTGCAATACA TTCTTCCTT CCTCATCCTT TAAATTTAA ATATATAAGA	180
NGTATGTTT GTTTTATTAC ATTAAGTGCT ATTTTTAAAA AATTCAATTGT GTGTATATGN	240
AGNCTAATAC TTGATTTGTT TCTGTATAGC ATGATTAAG GTAATTGGAA ATTTGCCAC	300
CNATTTAGGN CCNTGGGAAA TT	322

(2) INFORMATION FOR SEQ ID NO:649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

AACCGCTTCA CCGCGCGANT GGTACCAGTC AATCAGGCGG TTAGCGACAT CCACCGTACT	60
GTCACCTTCC GGCACGGCGN AGCGCGCCAC CAGCACAGAA ATCATTGTT AAATCGACCA	120
GTAACAGGGC GCGAGGGGGC ATTACAGTNT CCTTAATCAT CCGCGTAAG TTCGCCGCGC	180
AGGTTTGCGC TCATGGCCTT GCGAATGGTT TCAGTATCCA GTTCCTGGC TAAAGCAGGT	240
AAATGCAGTT TGGTTAGCTT GGGCTTCTT ACAGTCATAT CTGCACCGGN GAATNACGCT	300
GGTATGGGGC GAGGGGGTTN ACCGGTTGGG GATAACCANC CATGTTCAN TTTAACGGGA	360

CATACATTGT GTCAGGTTN ACCACCACAA TAACCGGGGN TCGCTGGTT TTTTGTAAAT	420
TTNCTGNCAG GAAAGGTTTT TTTTTTTGG GNG	453

(2) INFORMATION FOR SEQ ID NO:650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GGCAGAGGGA GAGGCGCTGA GGTGTGCTGG GTGCACTGGA GCCACCGGGGA CCCCTTGAGG	60
ACATCGCCAG GNTCNGTGGC TTNTTCCCGA GCGGGAGAGG TGGAGATGCT TATAGCAGTT	120
ACGCNTTAGG AAGGGGACAA CCAGGNCCCCG CCACACGCTT CACACACAAA CCTGCTCACG	180
CAA CTGTGAA TGCTTGGCAC GGGGTGGCCA GTNCAGATGG AGCCCAAGGC CCCNTCGGNC	240
TCTGGGGCA ACTTGGGTA CACAGGATAAC TNGGGGTGCC CGTTCCCTTAC TTAAACCCCA	300
GCTAAGGGTT ACAACTGACC CAGTTGGNCT TGGGCCCGGG GCACTTGGG TTGGTTCNNT	360
TGGGGCCCTT GNACGTTGGG CCCATTGTTG GNAAGGGTTN TTCTT	405

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GTTGGGCATG TNCAGGTGGC ACAGGTNCCA GGNCGAGGGG AGCCCAGCAG CCCCGGAGAG	60
CTGAATTTC CCTATCTGTT TCAACTGCTG GNAAGNTGAA GGCTACAAAG GTTTCGTGGG	120
NTGTGAAGTA TCAGNCTCGA GGAGACACAG TAGAGGGCTT GATTTGGCTA CGTTCATACT	180
GGGNATAGGC GGGGCCACCC AGAGGCTGGC CAGTGAAGGG CCCGCACACC ACCCACGTGC	240
CTNCAGNCAG NGAAGTGAAC ATNGCCAT	268

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

TCTTCCTTT NACCTACAAG GGATCTGTTT ACTTCACTTG CACCCATATT CATAGCTTAT	60
CCCCTTGGTG TGCCACCAGA GCCGTGTACA ACGGCCAGTG GGAAGTACTG CCAGAGTGAA	120
AGATTACCCA CGCTGTATCT TCCCTTGNA TCTATCGAGG AAAGGCTTAT NAACAGCTGC	180
ATCTCCCAGG GNAGCTTCTT AGGCAGTCTG TGGTGCTCAG TCACCTCTGT TTTCGATGGG	240
GAAACAGCAG TGGGAAATTC TTGTGAAACG GAATGAAGTA TGGGGGGAAA TTCTTCTTCA	300
GGNAAGGCC C TGGCATCTTN CCCCTCCATN TTACAGGAAA TAATGTGGGT CTNN	354

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

AATGGAAATC GGTCCAGTAA GGCTGTNATC TGGANGGTGC TCGCGCAAGTN GGGGCTGCC	60
CTGGGAATAC ATCATTNACT NTTTGGGGAC GTGAAGAAC TCATCACTGA ATGGTTTGTG	120
AAAGCAGAAA GTNCCTGGGN CTATGNCCNG NNTCCCCANT AGCAATCCCC CTGATTATGA	180
NGTTCTTCTG GGGCCTGCGC TTCTTACTAT GAGANCCNGC CAAGNTGAAA GTCCTACAAG	240
TTTGCCTGC AAG	253

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CCATAGTCCT GGACAAGCTG GAACGNAGGG NCTTCCTTTT CCTGAGCATG ANGGGGGTGG	60
GCCAAACGCT GGTNTGGTGT NTGCACAAGG AGTGAACCTT TT	102

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

CCACTGGTGC TGTGCTGTAC GGTGCAAGGA ATGCAGAANT ACTNTGGACG TCCATACTTG	60
CAAGCCCCCA AGANGGCAGA NTGGCTGGNC CAAACCTGAA NCACNCAGAT ACCTCATTTC	120
TTCCTTCAA TTCANGNNTC TNAACTCNAA AGCACNAGGT CCTTTGTTG NACANTTTT	180
TNCACCCTTC ACCCTGGGGT TGTTACNTTT TTTTTTTAAG GGTTNTTGGG GGGTTATTCC	240
TTGGGGGCC C TGGGGTTC	258

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TTCAAAC TTG CNTCCNATCC TGCCTGCAGA AAACCCAGAC TGCATTCA GTGTCAGTG	60
TAGCCACCAC TTTGNNTCCC AAGGTGGCTG AGCAACANAT TCCCAAGTNT AAGANCCATC	120
A	121

(2) INFORMATION FOR SEQ ID NO:657:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GGNTTTTCG CTCGGTTAG CTAATCN CAGCCCTTC CGGGCNTCGC GGTAATCTTC	60
CAGCGCTTTA TCCAGAACT TGCATCGGT TTTCTTCC ACCAATGGNA AGCAATGCAC	120
GCAGAGTCGG ACTTGATATC GCCGACCAGT GCCATATCCA CCTTGCCTGT GAAGCGCCCG	180
ATGCTGGCTG GNTGAATAT CCAATCTGNA ATGAATTTG GGCATCGGTC GGGTAGNAAG	240
GCGCGGTAGG GGAAATTGCC GTTGCAGAG TTAGCCACTA AACGTNTTCG GGCGGTTCA	300
TCATGGGTAT GGGAAACCTG NACGGNG	327

(2) INFORMATION FOR SEQ ID NO:658:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

CTCCTCCTCC TCCCTCCTAC AAGTCCAGTG GCCTTGGNCT TGGAAACTAA AGGANGAAGG	60
TCTGGCCCCC AGGGTGGGGC TCTCCTTCC CTCCCANCAN CCCCCGCGTN AGCACTGCC	120
CCTCTGTGAG GTTCGCTAAC TTN	143

(2) INFORMATION FOR SEQ ID NO:659:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

ANCGGCCCTT TGGAAAGGTGC NTCCCGCAAG ANGAACGGAC GCCACTTAAT CCTCCGTGAA	60
AATTCCAAGA CCAGNAANAA CATCCAGAAA TCCCTGGTTG GNAGCTCCAG GCCCCGGGGC	120
TTCNAGCGGC ACCANCGGTG AACCACGGTN AAGCTCGTGG AACCGGTTTG CAAGTTGGA	180
AGTGGNG	187

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GGCACGAGAA AAAGTAGAGC ACAAAATAGTA CAATGGCGAA TATAGACCCA AGCACATCAG	60
TAGTTACATG GAGGANGACT GTNTACTNAA AGANTTAAAT GTAGGCTAGA TTAAAAAAAAA	120
AAAAAAAAAA CCNCG	135

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

AGGCAGAAAAG TTTCCACGGC AACTAAAACA CTTAGACGCT GTAGTACAGC TCAAACCTCA	60
CCGGATGCGG AGTCATACGC ACGCGGTACAT CTTCTTCGCG ACGCAGAGNA TGTACGCATC	120
ANTTGCTTCG TCAGTGAAAC ACGCCACCGG CTTTNAGGA ACTCGCGTC CAGATCCAGT	180
TCGTTCACTG CTTCTTCCAG AGACCTGCA ACCTGTGGGA TCTCTTNGC TTCTTCTGGC	240
GGCAGGTCAT ACAGGTTTT NTCCATGGTT TCGCCCGGTA TGGGATCTTG TTCTTGAATA	300
ACCCNNCAGGA CCGGGCCNTC AGCCAGGGCA GNCAAAGCAC AGGTTACGGG TTAAGATTGC	360
CGGGTTCCGG GAAAACGTNA CTTGNTTAN GACGTGNTTT TCGGNGGAAG NAAACCACCG	420
GNATTACGGN TTAGANGCGG AACGGTTAA GNGNCNNNNT NAGGCCAGCT TTACCGTGT	480
TCTAGCCGGG AC	492

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

ACCACCCCCC GCCCCATACA CACACACACA CATGCATACA CAAAGAAAAG CTAATAAAAAA	60
TTGCATATAG AAATTTTTT TTTTTTNGG GGGGGGGTNT CGTTNTNTNA CCCAGGT	117

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GGCAGAGAAAT TAGGTTTAGC ATAGCCTATC TTTCTCCATC CNTTTACTTT NAATCTGTCT	60
TCATCTTAT ATTTAGAGTG GGATTGGTGT AGACATCATA TAGTAGGGTC TTGTCGTTG	120
ATTTGCTCTC GGACAGCATG TGTCTTTAA ACTGGGTAT TTAGACCACA GATGTTAAA	180
GTAATTATTG ATATAGTTGG ATTAATGTCT ACTGTATTTA TAACTGTTTT CTACTCCATT	240

GTCCCTTGTT CCTTNCTTT TTCGNCTTT GNACTTG TG CTCTGCCTTC TCCATTNGNA	300
	304
ATTG	

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

NTTCCATTCC ATTNGATTCC ATTCCATTCA AATNAATTCC ATTCCATTCA TCTCCATTCC	60
ATTCCATTCC ATTCCATTCC ATTCCATTCC ATCCAATTAC ACTNGCTTG AATCCATTCA	120
ATTCCATTCC ATTCCATTCC TTTCNGTTCC TTGCAATTCC ATTCCATTCA ATTCCATTCC	180
ACTGGGGTNG TTTCGAATTCC ATTCTATTCC ATNCCATTCA ATTGNA	226

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GGCAGAGTTT TCCAGACGCA GGTAAAGCCC CATGAAAGGC TGCCCTCTTC TCCCCTGCCA	60
GGAGGGCACC TGGGCAGGCT AGGAGCAGCC TGGGCAAGG GCACCCCAAGG GACCAGCCCC	120
AAGAGGCACT GCTGCTGACT CCCTGTTCCCT GTTTTTTTTT TGTTTGTTT TTTGAGANAG	180
GGTNTCGNAN TGTNCCCCCA GGTTAGAGTG	210

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GGCANAGCAA ACTTTTCCT GTTGAGTGCC CTAAGACAGT GGAAACCTTC TGTTTCACA	60
NCAGAAATGG TTATTATAAT GGGCATACAT NTCACCGTAT AATTAAGGGC TTTATGATTC	120

AAACTGGAGA TCCAACAGGT ACTGTNATGG GAAGGAGAAA GCATATGGGG AGGAGAATT	180
GAAAGATGAA TTTCCATTNC AACATTACGN ACATGACAGG CCGTACACAC TTCAGNCATG	240
GGCTNAACGC GGGGTTCAAA TACTAATGGG ATCCCAGTTT TTCCATNAAC GGTNGTTACC	300
CAACGGCCTT TGGGCTTTGG ATTAATTNAG GCCTTTACCA GTTATTTTG GGGACCGGAG	360
TTGGACTTAA AAGGGGAATT TGGGGGGNNN N	391

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GGCANAGTGG CCATTTTCGT TGGTGGTGTT CANTTGCNGC GGTTNCTGGT CAGTAACAGC	60
CAAGANGCTG CGGGAANCTG CTGGNTCTTC GTCAGATTGG GCAGAGGACG ATAAGGACTT	120
GCTTCCCGCA GCATTTAAA AATAAAGTTC CGGTAGGAAG CAAAAACTGT TCCAGGAGGA	180
TGATGAAATC CACTGTTATC TAAAGGGTGG GGTTAGCTAA TGNCCTCCTG TTATAGNGCC	240
ACCANGNTT TTACAAGTTG GGTTGTAACA TCNTTA	276

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GGCANAGTCA TATTTCTACA GTATGCCAGT ACTGAGGTTG ATGGAGAGCG TTACATGACC	60
CCAGAAGACT TTNTTCAGCG CTATCTTGGA CTGTATAATG ATCCAAATAG TAACQCAAAG	120
ATCGTGNCACT CTCTTGGCAG GGAGTAGCTG ATCAAACCAA GGATGGGTGA AGTATCTTCA	180
TGTCATTTNC TGNAAAACTN AATGTTCCTG GGAATATATT GTTGAAAAT TTNAAAAACC	240
AGCTGGGNCA CAGTGGGCTG CATGCCTGTN AATCCCAGCG CTTTGGAAG GCTTGAGGCG	300
GGCGGTNTCA CCTGGTGGGT CGGGGNGTTT TTNAGA	336

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GGCACGAGAG AAACTCTATC TAGTTAAAAA GGCAGANGAAG AAAGATAATC ATGCTCCTGT	60
TCCCCATAAAAG AAAGGGCAAG GAGTTGGGAA GGAGNAAGGG ACCCTCCTGG NTCCTGCAGC	120
CTGAATCTCC ACTTGTGCC C TCTGTCTTCC CCACTAGACT CT	162

(2) INFORMATION FOR SEQ ID NO:670:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

GGCAGAGNCT CTGAAAAAAC TCGCCAAGAA AAAAGTAAGA AATTGACTTT ACAGAAAGTAA	60
AACCACACCG GGCTAAGTAC AAATACCTTC TAGTACTAGT AGACACCTTC TCCAGATGGA	120
CTAAGGCATT TGCTACTGAA AACGAAACTA CCAACACAGT AGTTAAGTTT TTACGCAATG	180
AAATCAACCC CCAATATACG CTGCCTGCTG CTATTAAGT CTGATNAATA GAGGCAGCCT	240
TTACCTCGNC TATGAGCTCC AGTTCAAGTC AGTTAAGGCG TTNAAACATT TCAATAGGAG	300
GCTCCATTGT GGCCTATNCA ACCCCAGAGG TTCCAGGTCA AGTTGGAACG CATGGAACCA	360
CACCCCTNAAA AAAAATTGCGN GGGGGGGNCC GNTACCCATT T	401

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GGACAGTGCC ATTATCCACA CCAGCATGGG AGACATTAC ACCAAACTTT TTCCTGTTGA	60
GTGCCCTAAG ACAGTGGAAA ACTTCTGTNT TCACAGCAGA AATGGTTATT ATAATGGGCA	120
TACATTTCAC CGTATAATTA AGGGCTTTAT GATTCAGACT GGAGATCAA CAGGTACTGG	180
TNATGGGAGG AGAAAGCATA TGGGGAGGAG AATTTGNAGA TGAATTTCAT TCAACATTAC	240

GACATGACAG GCCGTACACA CTCAGCATGG CTAACGCGGG NTCAANTACT AATGGATCCC	300
ATTTTCATA ACGGTAGTAC CAACGCCTTG GCTTGNTAAT NAGGCTNACA GTNTTGGAC	360
GAGTGANTAA AGGATGGTAG TTGTTACANG GTTNTCCAAG TCAAGTTCAT TCCCAAAACN	420
GTTAGCCNTT TGAGGGTGT CAGCTNCTTA AATTTTACTG TTCAGTTAAA TTAGGTTNT	480
TTTNATGT	488

(2) INFORMATION FOR SEQ ID NO:672:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GGCACGAGAA AATATCAACT CCCCAAGTTG ATCTGTAGAT TTAACAGAGT TTCAGACAAA	60
ATCACAGCAT AATTGTTAT AGATATAAAC AGGCTGATTC TAAGATGGAT AAGGAAATGC	120
AAAGGAACTA GAATAGGCAA ACAATTAA AAAAATAAAG TTGAAGGAAT CACTATCAA	180
TTTATGACA GTATAAACT ACAGTAATAA AGNTAGTATG TTAATAGGAA CTGTGTAAAC	240
ACCAAAAGCA GTGGTACAGA ATAGGCAAGT CTAGTAATAG ACCCATATAC ATNTGGCCTT	300
TTGACAAGGT GCACNGGGAA TTTATGGGG AAGAACCTTT ATAATNAGT NTCGGACCAT	360
TGACCTNCCT TTTAANACCA AAAACTCGGG GGGGGCCC	398

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GGCAGAGNCA GAGGCCAGGC ACGGTGGCTT ATGCCGTGTA ATCCCAGCAC TTTGGGAGGC	60
TGAGGCAGGC GGATCATGAG GTCAGGAGAT CGAGACCATC CTGGCTAACCA CAGTGAAACC	120
CCATCTCTAC TAAAAATACA AAAAATTAGC CGGGTGTGGT GGCGGGTGCC TGTAGTCCCA	180
GCTACTCGGG AGCCTGAGGC AGGAGAATGG TGTGAACCTG GGAGGCAGGAG TTGCAGTNAG	240
CCGAGATCAG GCCCCTGCAC TCCAGCCTNG GAGACAGAGG GAGATTCCAT CTCAAAAAAA	300
AAAAAAAAAA AAAAAAAAN AAAAAAAATT TNTNGGGGGG GCCCCCCNTA	349

(2) INFORMATION FOR SEQ ID NO:674:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GGCAGAGCTT TCCATTCCAT TCCATTTCAT TCCAGTTGAT TCCATTGGAT TCCATTCCGA	60
TCCATTCCAT TTCTGTTCCAT TCCATTCCAT TCTATTCCAT TCCATTCCAT TCCACTGGGG	120
TTGATTCCAC TTCATCCCAT TGCAATTACAT TCCATTTCAT TCCACTNNNG GTTAATTANN	180
ATTCCGTTCC ATTCCATTG	199

(2) INFORMATION FOR SEQ ID NO:675:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GGGAGATCGT TGCCGGAATA TCCTCCAACG ACGCTCGACG GCGGGGTTTG TTTAACAGGC	60
CTTGTGCGGC AAGGTGAAGA TTACGCGCAT CAGCAAGGGN GAGGTGCGGC ACGACATTCA	120
TGACTCCATC AATCGAACGC TGCCGCGGCG TAACTAGTTG CCAGAAGCCA GCAAGGTTAG	180
TTGCGTAAGA GTTTCGCTGG TTCATCACCT GAAAGCTGTG CGTCTACAGG CAAATACCAC	240
CAATTTNTT CTGCAAAGNC CCGGCATTN ACCGCATCTT TPTCAGTCCA TTACCAAGCGT	300
TTGCCCGGCG CTTTACCAAC GGCACTTGAC ATCCGNATGG TTNCAGGAT TGATGGTTCG	360
GCCCAGGGGT TACACNTTT TNNCGGTTGT ACGGCCACAC ATNTTCAGC GTGGCAAAA	420
AAGCGCGGCG GATGCCCAT TNCCCCGCCT TGGCATTACA TGTTCAAGTT GAGCAACGTC	480
ACAANGGTAC CGTACGTAAT	500

(2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

AANTAATGCG CCGTCAAACA TACTGCTCAT AATGCGGGAG GTGTTGTNAT CAAGCACGAN	60
ACGCTGGCGA ACAGGAAGGT AAACATGATT AATCAATTGA TCTACTGGGT ACTCTCGACC	120
CAGTGAAATA ATTCTCGCGC GTAGTTGGC AGGATTAGCC ATGCGAAGAA TTGACATCAT	180
CTCTTCTTGC AGGCGGCTCC AGTCATCTTC CGTATCCTGG CTGGTGGTTT CCAGTAATGC	240
TTTAACCTTG CCTACAGGGN CGCCATTACT TATCCAACGC TTGATCTCTT CGATGCGTTG	300
TATGTCTTCT TCATCAAAGA GTNGGTGTT CGCCTTAATN GNGTNGGGT TTTAAACAAA	360
CCGTGGGNNGG T	371

(2) INFORMATION FOR SEQ ID NO:677:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GGCAGAGCCA GTTTTAAAAG TATCTAAAAA ATTTTNAATA AGACTTTTG CCAAATATAT	60
TTAAGGATCA AAGTACTTCT TGATGAATCA CTTTTTATCG TATTGATGCC TTTGAECTCA	120
TCTTAGTTG TCTGCATGTN GTTATTACCA ATTCGTGAGG AATGGCCATT TCAAAGTTA	180
CCATAAAATGA NGTAAAACGT CTTCACTGCA CACTGCTTGG CTTTGAATTTC CTTACTCTAC	240
TCTTCTTAC TGTNGTGAAC ATATGGCAAG TTAACCTTAG CTTCTGCAC TCCCTGTTGT	300
GGTTTTCCCC TTTATTGGGT GGTNATAAAC AGTCTCTGTC NTCCTAGGGA TCTNCCCNNGG	360
TTGTTGTGGG NGTT	374

(2) INFORMATION FOR SEQ ID NO:678:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

GGCANAGGNA CAGTGCCTT ATCCACACCA GCATGGGNGA CATTACACCC AAACCTTTTC	60
CTGTTGAGTG CCCTANGACA GTGGAAAACT TCTGTTTCA CAGCAGAAAT GGTTATTATA	120
ATGGGNCATA CATTTCACCG TATAATTGAA GGGCTTATG GTTCAGACTG GGAGATCCAA	180

CAGGTACTGT TATGGGGAGG AGAAAGCATA TGGGGGAGGA GGATTGNNG GATGAATTTC	240
CATTCAACAT TACGGACATG ACAGGCCGTA CACACTCAGC ATGGGTTAAC CGGGGATCA	300
AATACTNATT GGGTCCCCAN TTTTTCTATA ACGGGTNGTA CCCACGGNCT TTGGGTTGN	360
	361

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(2) INFORMATION FOR SEQ ID NO:679:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

CTCAGTTGG TATATTCTCC TGTNAATGCT TGCAATTNCA TTATCAAATT TTTGTAGTGT	60
GTTTTTAAGN TCTATCAGGT CAGTNACATT CTTTCCTATA CTGGCTATT NGTGTGTTAA	120
GTNCCTATAT CATTATTG TNAATTCTAA GCTTNCTGG ATTGAGCCTT CAATGTTCTC	180
CTGCATCTNA ATGGTCTNNA TTCCCTACCC ATATTCTAA TTCTGACTCC TGTGNATTTC	240
CAGCTATCTG CAGCCTAGTT AAGGAACCTT TGGCCTGGTT NAGGAACCCT TGNTAGNGGA	300
ATTACTGTGA CAGTTTAGAG GAAGGAATNC ANTGGGCTT TTGGAGTTGT CCAGGGTTCT	360
	365

TGCGG

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GGCACAGGGA ATAGCTCTGG CTAAGCGGTG GCCAAGGATG TGGGCAGAAAG ACAACCCCTCC	60
AGGGTNGCNA ATCAACCAGG CCCCCATACT CATAGAATT AAGCCTGGGG CCCAGCCAGT	120
NCAGGCCAAA TCAGTACCCG GTCCCCAGNG AAAGTTNTTG AAGGTATCCA GGTCCATCTC	180
AAGTGCCCTG AGGGCCTTTG GAATTAATAG TTCCTTGTCT AGTTTCCATG GAACACTCCC	240
CTCCTGCCTG TTCCCCAAGC CTGGNNCCA AGGACTACAG GCCGGTAACA GGTTTGCGC	300
TTGTTCCAT CCAGGCTACA GTGAACCTTA ACATCCAGGA GTGACCTAAC CGGTNANACA	360
	376

TTGTNGGGGT TNGNTG

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GGCANAGGGA TCTTTGGAAG TTTGATTAGA AAATGCCTTG AGGTAGTCTT CTTTGGGTTA	60
AACCTGCTTG ATGTTCTATA AGCTTCTTGT ACTTGAAATA TTGATAACTT TCCCTAGGTT	120
TGGGANCATT CTGTNATTAT CCCTTGGA TAAACTTTCT ACGGCTATCT TCTTCTCTAT	180
CTCCTCTGTA AGGCCAANAA CTCTNAGTTT TGCCCTTTA AGGCTATTTC CTGTATCTTG	240
TAGGTATGTT TCATTCCCTT TTAAATCTTN TTNCCTTNG TATCCCCTGG ACTATACATT	300
NNCAAGTAGC CGTCTTCAGA CTCACTAATT CTTTCCTCCG GTTTGGAACC AGTTC	355

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GGCANAGTGT AAGCTCAGAG AGGAGTGAAG CTCGCCGAA ACTTCGGGAA TGTAATGGTT	60
TAGTTAATGC CCTCATTTN ATTGTTCAGG CTGAGAATTG GGCAGAAGGA TTCAAACAGC	120
AAGCTTGTAG AGAACTGTNT TTGCCTCTN CGGAACCTAT CATATCAAGT TCACCGGGAG	180
ATCCCACAGG CAGAGCGTTA CCAAGAGGCA GCTCCCCAAT GTGCCAACAA ATACTGGGCC	240
ACATGCTGCC AGTTGCTTG GGGCCAAGAA GGGCAAGGGA AAAAACCTAT AGAGGNTCCA	300
GCAAACGATT ACATGGGTTT TCCCTTAAAA GNACGGGTTCC CCAATTNGGGG GGGGGCCCCG	360
TTANCCCAATT TGGNCCTTTA GT	382

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GGCANANAAG TAGCTGTAAC TACACTCCCC ANATGTNAGT AATTACTGCA GTGGTTTTAA	60
CACAGGGCCA CACATCCTTG GCTCTCCTCT CCCCAGGAGG TGAAGCTTCC TTTTCTCTTT	120
GCCATGTGNG TCTNCAGCTA GTAAAGCAAA AGCTATACT TGAAACAGTGG GAGTCAGGC	180
AGACACTTCC TGCCCCAGTG AACCAAGGTT GTCCCCGGGC AAGCCATGGG CCATCAGGGN	240
ACCCATGTNT TTCAGCATGG ACTCCGGGAT GACAGGATGA GNAACCTCAT TCTGTGGGGT	300
TTTTTCCNA AAACCCATCA NCCCCAGTTT TTAANCTGNG GAAATTTCG GGGCAAACCC	360
AACCTG	366

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GGCAGAGCGG CANGAGTTCT CAGGAGCCAC TCATCTGCTG GCAGAGGTAG CAGAAGAATG	60
CCCTTAGTGT AAGTCCTCTA CAACCATAACA CCAAATGTGC TCCCTGCATT TCAAATTCCA	120
TTGTAGAAAG TCTCTGNATA ATCTCACTTA TACTATGAGC CATTCTCAG TATCTGTGCC	180
TCTTCCTGTT AGTGTCTAC AATTCCCTTC TCCTTAATTT TTCTCCGCTT TACAAAATGT	240
CACACAGAGA AGTGCATAAT ACTTAANGCA AGCTTTGAA AAATAATGCT CCATNAAATA	300
GCTTGGTTC TGGTNCATGA TNATTGCGTN TTTATGAAAC ATTTTAAGGT GCATT	355

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GGCAGAAAGC AGAGGCAGGG NACGGNTCTN AAACCTCCAG TNTGGAGGGC CCTGGGAAAN	60
TGGCCTCAA TGTTTCCTTG TNCTCANTGG ATAGGCCTGG TCCGCCATCT GCAGTCCTCC	120
TCCCAGGCCA AGCCTGGTCA TCTCCAAGCC TAAGGACACA CAGCACAGG NGCACTTNTN	180
CCGGTTGGTC AGCTCAGGTT GCCTCATGCT NCAGAGACCT CGCAGGGGAA TGGCTTAAAG	240

GAGAGAGTNA ACAGGTTGT TAGAATTGGT ACCAGGNCCA NGTTTTNTN TTCTTCCCCC	300
AGCTATAAAA CA	312

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GGCAGAGGTG CAGAANANTA ANTNTCCAAG NAAGTNTGCC AACGGAGTCT TTCTTACGGN	60
CAAAGCTTT TAGCCCATTT CNTCACTGTG GTCTTGTCTT GGGTACAAAG TAAAGGCACA	120
ATGGGCCCCC TGGCCTTCCT GTTGNAAT CCCCTTCCC GGCTGTCTAA TCATNGTAGA	180
TCTTTCCNN GAGGAAGCAT ATCCTNTTGG TCTTGT	216

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

CTGCAGTTAT CCCAGGGCTT AAAATTAAAT TAAATTAAAA ACAAAAGACCC AAATCAAAAC	60
AAAATTAAA AAAAGCCAAC CAACCAAATA AACAAAGAAA AAGNACTGCA GTTAANCCAA	120
TCAGGTTCA CTAGTAGGGA AAAGGAAAAN TTATTAAAGA TATTGGGTCT TTTTATTCC	180
TTGCGGGATT AAATTAACCTT CCCCTAGGGC TGTGCCAAGT CCTGGANCTG AACATATTAG	240
GNGGTTTTN TTNAAACTCC AGNGNGGTGT AATTATNTTT CCCCTTAGTG TGATTGGTGG	300
ATTTTAAGGG TTTCCNTCTG NCCGGGTTT AACCCACCAC CTGGGGGAC NTGGNGGGC	360
CTTTTTTGN GGGGGGT	377

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GGCACGAGGA AAATNATGAT TCCTGTCCCA ATGCACAATC TCAGGAGTGG TTATTGCCTT	60
AAAGACTTAA TCAGTATCGT TCATGATATC CTTTTTTTTT TTTTTTTTT TTNNNNNGN	118

(2) INFORMATION FOR SEQ ID NO:689:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GGCAGAGCNG AGAACACCAA GGCAGAGATGT CTGCTCATGC CTTCCCTGTG CAGACGTGCG	60
GGGAGGAAGA TCAGAAGAAA ACCCCACAAG TTCCTATCAA TTTCACAGAA CTTTCCAAGT	120
GCTCTTAGAG TTGAAAGATA ATGTCTGGGG AAAGAGNAAG TCTAAATCTG NATGAAAGGA	180
CAAAGGTGGA TAAAGTAGGC TGTGGGGGAA AAATGAAAGG ATGATGGACC AGCTTAAGGG	240
AGGCAAGGAG AAGGCCCTA AATGCCCCCC CAAAGACCAC TGCCTGTTCT GTTCANGATT	300
CCCCAGCATH NAATTCCCTT AGNCCNTNGG GG	332

(2) INFORMATION FOR SEQ ID NO:690:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GGCACGAGNA TTACAGCGGC ATAGAGACAT ATTGCAGGAT TATACACATG ANTTCCATAA	60
AACCAAAGCA AACTTTATGG CAATACGGGA AAGGGAGAAT CTTATGGGAT CAGTACGAAA	120
AGATATTGAG TCATATAAAA GTGGGTCTGG AGTAAACAAC AGAAGANCTG AGCTATTTT	180
GAAAGANCAT GACCACCTNC GAAACTCAGA TCGTCTGATT AGAAGAGACA ATAAGCATTG	240
CTATGGCAAC AAAAGAAAAT ATGGACTTCA CAGAGAGGAA TGTTGAAGTC AATTCACAG	300
CAAANTGGAA CACTTGGGC CATTGTTT NCCTGCTGTA AAACCGTNCG GNTCCAGAGG	360
GTCAACCTGA GGAAGNGGCG GGACTCGTTC CTTCTAGGGG GTGTTATNG GGTCTGTTAC	420
CTTCNGTTGC TGGTTGTATG CGTTCCNTTG NTGGGCCTC TTCCGGGACT NTGACAGNCA	480
CCGTTTTCA CACCTGGTTT G	501

(2) INFORMATION FOR SEQ ID NO:691:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GGCAGAGGTC ATATCCAATN AATGTCCCCT GGTAAATTNTT GAAAGTNATT TAATGTTTTC	60
AGTTGATCCC TACATATGGT TACTTCTGT GGCACAATGA TAGTGTCAATT TACTGAAGTC	120
TCCAAGTAGG AGTAAAGGAG TAGCAGTCTG AATTTGTCA GGAGCTATNA ATTAAACCAG	180
CATGAGAAAT CAANTTTGC AAGT	204

(2) INFORMATION FOR SEQ ID NO:692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GGCAGAAAGT CATTCTATAG TAAACATCATC CCAGACTGCC TTCTGTATTC CCCTGTGTAC	60
AGTCTCCCTTC TGTTTCTAGG TTTAGAAGTT CAGAGGTGAC TGTTTTTTC CATTCCACA	120
GCCAAATGGG GGAAGAGGTG AGGCTAGGGG AGTGCTGTGC TGATTCTCCA GCCATGGTNA	180
GACAGGTACAC CCAGGNAGCC TCGAGGAAAG CCCTGGAGGG GAATCACATG TGTACTTTT	240
NNATGGAAGC TTTTTGCAAA GCACATCTGT GATTACACTT AGTTTATTGG AACTAATGTC	300
CCAGGAGTAG ACATGGATTG GTGGGCCAAG TTATTNGGG GACACCTAAA CNGNTCATGG	360
ACCCGANNGA CTTTTTCAAA CCTTTAT	387

(2) INFORMATION FOR SEQ ID NO:693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GGCANAGGGA AAACTGTGCC AGTTTCCAGG AGGAAGTCAGA TTTCATGGCC CTCAATGGTT	60
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AAATATACTT GGGGCTCAGT GAAGGGTGAT GACATGAGTT GGTGCTGCC CTGGCACCC	120
TCAGTCCTGT TGTTGAGTCA TCTGGTTGGG GGCTTCTGGC CCAGAGGAAC CTTTGTCCCTC	180
TGGGGCAGTG CACCTTCCAG TGATTGTCTC TGCATAGCGG TTAATGGGGT GAGGGGGCAA	240
TTTTTTCTTT GTTTGGACAA NNCNTTTTA AGGTGTCNT TGNAACCAC ACTTGTAAAC	300
AAAGCTTACC CGGG	314

(2) INFORMATION FOR SEQ ID NO:694:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

AGTCGGTAAA GTAGAGCGGC GACACGAAC TCTNCANCCG CTCCANNGTG GTACGCCAGT	60
CCTTCAAGGC CGGCGCACNC ATACGTGCGG GNNTCTCGCT CCTCTTCCG NNAAGGCC	120
TTGCGACTAC CGTTCCGCTC CACGGNCAGG AAACCAAAGG TTCCGGCGTC CAGAGGGCGT	180
CTNCCAGTCC CGGGNCANCT TTTCTTGGGA ACACCGNCAGG CTGTTGGTAA GCC	233

(2) INFORMATION FOR SEQ ID NO:695:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

TGAGNTGTTCA ATGGAGTTT TAATCAGTAT GTCTNAAACC ATTAAATNTA NTNNGATGA	60
TCATANAACGT GTGTTCTAA AANCACTAAA TNAACAAACGC CTGGGAGGGG NNATTTGTG	120
ATGATNGCTA TTGTGGTTGA GGATGTGANA ATTCAAGAGCA CNCAGNTGTG TTCTTGCCTG	180
CCTGCAGACC TACTTGAAA AAGCTTTGC ANGAAGCTTG TGGTTGNTAG TTCTCGGGT	240
TCATAGTNAT TTAGGTTTCC TTCGTTCTGG GTGTGTTGA TAGAGGGTCC TGGAACTNNC	300
	300

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

CTNCTCTGGG NATGCAGCGT CTGTTGNCTC CAGTGAAAGN CNATTCTGCA ACTGACAAGA	60
GCGGTGCAGG AAACCTCCCTCACACCTGCT CGCCTGCTCC CAGTAGCCCA CCAAAGGTTT	120
TCTACAGCCT CTGCTGTGCC CCCTGGCCAA AACAGATACT TGGCCAAAGG ACGTGGGGCA	180
TCCTGGGCC TGGGAGGTTC TACTTNCCAG CCCAATNTGT GGGNCCAAAN TTGNCTGGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GGCAGAGTTG CAACATCTCG GAGGGGAATT GTCCGGAGAG AATCATCACC TGACCGGCC	60
CACCAATGCC ATCTTAAGG CTTTCGCTAT GAATCATCGA CAAGCTGGAG GAAGATATCA	120
ACAGCTCCAT GTACCAACAG TTACCGNGGG CCAGCAGGNC CCCGGTTCAC CCTGAAGGCT	180
GGTGGTGCCG GCCACCCAGT GCGGCTNCCC TGNATTGGGA AAAGGCGGGT GTTAAGATCC	240
AAAGAGATCC GCGNAGAGTN AGGGGGCGCA GGTTCCAGGT GGCGGGGGGA TATGCTGCC	300
AAATTCCACC GAGCGGGGCC ATTCAACCATC GNTNGGNGT	339

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GGGCANNGAG GTGAATTGAG GGNNGGAGCAC GTAAGNGGTT TTCCCAGAAC AACAAATGACC	60
TAACAAGTTG CTGCTTCTCA NATGCCAAGA CTATGTATGA GGTTTTCCAA AGAGGACTCG	120
CTGTGTCTGA ACAATTGGCC CTGCTTGGGA ATNATAGTAA AACCAAACCA GCCCTACAAA	180
TGGCTATCTT TACAAACAGG TGTTCTGNTA GAGNCAGAGT ACCTGGGGTT CCCGTCTCTT	240

GNCATAAAGG TGTGTNAAAN CATTACCCCA GGACCCAGTT TTNTTCGGGG GATCTTTTG	300
GTTCCAGAAT AGGNGCCAT AGGT	324

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GGCAGAGNCA GAGATGGCCC TCCCCTCCGT GGATCCAACA TGGNATTAA AAGANCCCAC	60
AGAACAGGGT NGAGCACAGA GACCACGAAC TCCAGNTAA ACCTCGAAAC ANTCGTGAAC	120
GCCCCTNCAT TGNAAGTAGC CAATCCNAAC TCTGCCATAAT GCTTCCGGGG GTGCCCA	177

(2) INFORMATION FOR SEQ ID NO:700:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GGCAGANAAT GGGCCCTNCT TGGAATATAG TGAACCAAAT AANCTCTNCA NATGGCTATC	60
TTACAAACAG GTGTCTAATA GGGCAGAGNN CCTGGNTTCC TGTCTCTTGG CATAANGTT	120
ATGAAATCAT GCACCAGNCC AGTTTGTGCG GACATCTTNG CTTCAGCAAT AGGCCAGAGT	180
GGGATCCANC TCCNAAATTG GCCTTGTAA NACGTG	216

(2) INFORMATION FOR SEQ ID NO:701:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GNAGGCAGGG TCTTNCTGTT CCTAATGTNC ATAACCCCTCC TTAACTTTAA CGCCAACCTTC	60
TTTCCTATNG TCCAGAACAT TGTGAGCACA GCTCTAATGA TTTNGAGTGG NCATTGGTTT	120
TAAAAACCAA GCTGGCTTC NTTGAACCTCT NGT	153

(2) INFORMATION FOR SEQ ID NO:702:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GGCACGAGGA GACTGCAGTG NGTGTCCGTG TCTATCAAAT ACCTAAGGAG TCCCCAGGAG	60
CTNGCTGGCC ATCGTAATAG GATNTNTCTG TCCTGTAAAC TGTGCCAATT NA	112

(2) INFORMATION FOR SEQ ID NO:703:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GGCACAGGNT TTTNGGGATC ATGTCTGGTG GCTCCCCGGA TTATAAACACC AGAAAACATG	60
GCGGTCCAAA GG	72

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

AGCTCCACCA GCATCAAATG AAACAATAGT NCAGTTNTNC TGCTCANAGA TATTCTCCCT	60
TATCCACTTC AGGNACACCT GGCTCTGCAT GACAGATAGT CCACTGGGTT ATCAAAAAAG	120
CCCTGNNATT TNAGAAGNAT GTAGGTCCAT GGTGATAAT	159

(2) INFORMATION FOR SEQ ID NO:705:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GGCANAGCAG GAATACCAAGA GCAAGAAACT GATGTCTGAC AACGGANNNG NAGTTCAAAG	60
ATTCTTTGTA GCAGACACTG CAAATGAA	88

(2) INFORMATION FOR SEQ ID NO:706:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

CAAATCTCTN AACGAATCAT GTAATTAATA AATATTAA GCACTCATCA GTATTCTCCA	60
ATGTAACCTT CTNATTGGAG TACACAGANG GAAAGCAAAG AAGAGCATCT AACTTCTAGC	120
TCTGGCTTNN AGCCTCTCTA CCAGGCCGAN GCAAG	155

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

NCTNAGGCTA TCCCCTTGTA AGNGTTTGT ATCGGCTCGG AACCCCAAGT AACATACCAA	60
CAGACANCAC GNGGGCAGTG TGGGAGCAAC ATGCTGGTTT TAATNAGTGG CCTGGGANGC	120
AGNTA.	125

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GGCANAGGNA CGGTGGGCAC TCTGTCCCAG CGGATCACAA ACCAGGTCCA TGGTTTGAAG	60
GGACTGAGAC TCCAAGCTTC TGGATATNAG GNGCTACCTG GNAAAAAGTC GCCACAGGCA	120
AGCTGCCCAT CAACCACCAAG ATCATCTACC AGCTGCAGGA ACGTCTTCAA CCTGCTGCCA	180

GATGTGCAGC CTGCAGGAGT TCGTCAAGGC CTTTTAACCT GGAAGACCAA TGAACCAGAT	240
GGTGGTAGTG TACTTGGCCT CGCTGAATCC GTTCCGTGGT CGCCCTGCAC AACCTTCATC	300
ANCAACAAGN TTGCCAACCG GATGCAGAGA GGAAGNANGG CAGGGAAAGN AGTGAGCAAA	360
AAG	363

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GGNAGAGGTA AAAAATGGCG CCACCCAGTA CCCGGGAAGC CCAGGGTCCT GTCGGCAACC	60
AGCNCAACCA AATCCATCGG AGAAGAATGG TGNTGANAGC TTCCCGGACG CCNACN	116

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TTTTCGCGA AATTTCCTGN NGGAAAGGTC CCAGCATTTA AGGGTGAATG ATGGATTCTT	60
TGTGNTTAAN AGNAACGCCA TTGCTCTACT ATGTGAGAAA TGAGG	105

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

ATTCGGGCAA GTCCACCACT ACTGGCCATC TAACCTATAA NTCGGGTGGC NTCGACAAAA	60
GACCCNTTGA AAATTTAGA AGGNGGGTNC TGAGATGGGA AAGGCTTCT	109

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

CGCNAAAATC CCAAATTTT GGGTAACANC ATTTGNAAAA CCATCCACAA GTGTCTGNCC	60
TGCTTGGGA GGAAGATGAA GAGGCATGCN TTATTTGAAC CGAGTTGAAG TGAACGATT	120
TGANGTNTTG AATCCGGTTT CCGN	144

(2) INFORMATION FOR SEQ ID NO:713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

TAACTGGGG AAAACCCAGA GGGCATTGGA NAACAGGNTT NCGTAGAAGA ATTCAAGGGC	60
CAGATTTNA ATGCCCAANA TTGGTTTATG GGAAGCAACA AAAAAANAAA GCACATGTTG	120
CCCANTGGGT TTCCGGNAAG TTCCCT	146

(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GGNAGAGGCC CAGGTTCAAG AAATTCTCCT GCCTCACCCCT ACCANGNAGC TGGAATTNCA	60
GGTGTGTGGN A	71

(2) INFORMATION FOR SEQ ID NO:715:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GGAANACCGG TNCCAAGTGC CTGCCCTCTT TCCCCGGGGC TGGNTCTCGT NTGCCCCGGT	60
TCCTGGG	67

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

TGCTGCTGGG AAAGATCTGG AGGTCCAAGT CCTGCAAGGN CATCTCTGGA AAGAGCCAGA	60
TCCTGTTNC CCTCGTCTTC ACCACCAGGT ACCTGGACCT GTNCACCAAC TTAATCTCCA	120
TCTACAACAC AGTAATGANG GTGGTTTCN TCCTCTGTNC CTATGTNACA GTGTACAT	178

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GAGCAATATG GGATCAAACA CAAAATCACT AGATAACAAC TATTCCACAC CAAATGAAGA	60
GNGGAGACCA CAATAGAACCA CTGGATCGAT CGGGGGATCT AGGGCACATN GAAGCCATTN	120
ANAGGGAAAC AACACCCTTG AATGCAGAAG AATTTAGCCA CCACATATCTC CGTNCCATCT	180
GGGCTTATAT GNGACT	196

(2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

ATTGTNATGG GNTGCCATT GAAATAAAAG TATTATCAGA ACTTGGTAGA GAAGCTCAGA	60
ATCTTNANC TNTGGAAATT AGAAAGAAAG CTAGATCATT TGCTAAAGCA GCCATTGNGT	120
ANCAGTAATC AGCATTAT	139

(2) INFORMATION FOR SEQ ID NO:719:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GNAAGACCTG TAATGGTGGC TATCCTCCTN AAGCTTGGNA ACTCCTGGNC AAGAAAAGGC	60
CTGGTTNCTG GTGGCCTCTA TGAA	84

(2) INFORMATION FOR SEQ ID NO:720:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GGNAGAGGNA GCCCACTCCT AATGATGTGG CCATATCCNA CCTCCCTCTG GCTCAAATGT	60
TTAANAGGAT TGTNCAGGCT GTTGTGTACA GCTGTGGAGC CAGAGTTGGA ATTCTTCCA	120
AGGGGATATT CGGTTGCTGG CTGTACGNNA TGGAAGNCTT TGAAAGCCN NATTGTTC	180
CG	182

(2) INFORMATION FOR SEQ ID NO:721:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

TTGGGGAGGA GATGAAGAGG CATGAAATTA TTNGACCAA GTTGAAGTGA ACAAANTTTA	60
ANGGTATTAA ATNCGGTTAC GGATTGNTTT TAAATTAAAT GGAAATCCTT TATTT	115

(2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GGCAGNGAAG CAGTTGATCC TAAGACACGT TTACTTATGN ATAAAATGGT CAACTCTGGA	60
ATGTTGGAGA CAATCACTGG CTGTATTAGT ACAGGAAAGG AGTCTGTTGT CTTTCATGCA	120
TATGGGAGGG AGCATGGNGG ATNAAAAGGA AAGATAGTAA AGTTATACCT ACAGAATGTG	180
CCCATCAAGG TATTAAAAC AACCTTGAA TGNAATTAA AGGAATCGTG ACAAAATATNT	240
TGAAAGGTGG ATTCAGGTT TTAAAGATCG CTTTCAGTTA AACTTANATC CACGTAAGGT	300
CCATCCGCAT GTGGGGGCAG NAAAAGGAAT TGGCACANTT TNGTCAAGTA TTGGCNGTG	359

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GGCAGAGNAT TTAATGTAAG TATTATGGGA ACCTTCATAA GGAAATNAAG ATTNCNGAGAA	60
ACAGGTAAAC TCTGGTCTTT CTAAAACAGA CCTGATGAAG AGTAGAGAGT CATGGAGAGT	120
TNTAATAGAG CAAAAAGAGT GTGNATCTCA TGGTAATATA GTAGGGGAAC TTAGCAAGGC	180
CTGTTTATTC CAGATTCTTC CCTGGGGATC CTGTGTCTTC AGAGATAAGG ATACTCGTTT	240
TCCCTCTGGGG TATGGGGGGT TGGGGGGGTA CCTCTNCACC TGAGGGCCTT TTNGACCGNC	300
TTNGGAGGAA GGTCCAGAAA ATCCTTNCCG GGGNGNTTAT GAACCCGCTT TCATGGGGGG	360
GAAGGTCAGA GGNAAGGTTC AGAGAGGAAC TTTNTGCAC ATGCNGTTCT CAAATTNCCT	420
TTCCGGTTTC ATGGCAATNT	440

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GGCANAGGAA ATGCCCTGA AAAAAGACAG GGAAAGCATG GGAACACCGG TACATTGAGG	60
TGTTCAAGTC CCACAGAACCC GAGATGGGAT TGGGTGTTGA AGCACAGTGG TCCCAACAGT	120

GCCCCACAGC GCCAACAAATG GCTTCGTGCG GCTTCGAGGA CTCCCATTG GNATGCACAA	180
AGGGAAAGAAA TTGTTCCAGT TCTTCTCAGG GTTGGAAATT NTGCCAACG GGGTCACAT	240
TGCCTGTGGG ACCCCGAAGN CAAGATTACA GGGGAAGCGT TTCGTGCCAT TTGCCTCGCA	300
GGAGTTTAGC TGGAGNAAGG CTCTAGGGGA AACACAAGGT GAGGTTGGG GCACCAGGTT	360
ACATTTGAGN TGTTTTAAG AGNCAGCCC AAGGGAGNTT AAGNTCATAN TCAGATTCCC	420
	420

(2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GGCAGAGCTC ACCCACAGTA ACCACACCCA CGGTGACCAC GCCCTCACTA CCCGCAGAGG	60
TGGGCTCNCC GCACTCAACC GAGGTGGACG AGTCCCTGTC GGTGTCCCTT GAAGCAGGTG	120
AGNNCCGCCA TCCGCCGCCA CCAGTGAAGG CTGGGNCTGA AGCCTCCCGC TGCCTGGCCC	180
CCGGGCGACG GCGCTCGGTT TTCCCCACAC GAATGTGGAA CCTGTGNCCCT GGTGTNACCC	240
TGTAAATTN AAGCATCGCA AGGNGGTGCC AATGNGCACC AANNCTGATN TTCCCCCGGN	300
AGCTTCGNAAGTGAANAGCAN TTGCCCGGTT CACAGGAAAC GGGCANGTTN GGCTNGGGC	360
CCNAGGNGAC GGNCANCCAC ATNCGGTTCA NGAAGTTCCT TGNNCCAANC TGTTTNATT	420
TGGAATTCCG TGNCCCTGGG GCCCCGGTTN CGGGCAAATT CAAACGGNGA CACAAAGGGT	480
TTTGGN	486

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GGCANAGCGT GNATGAGGAG CTCNTCTACC ACAAAAGTGAC GGCAGCCGAG CTCAGNACCT	60
TGTGTACCCG CCATGCAACT GGTTGCTTT TNTCAACACC ATCTTCTACC CCGTGGAGAT	120
CAATGAAATC CNAGCCTATT GTGGTCTATG AACAAAGGGAA TACCTTGAGC AGATCTCCAC	180

TCTCATCAAC ACCACCGACA GATGCCTGCT CCAACAACTA CATGATCTGG AACCTGGTGC	240
GGAAAACAAG CTCCTTCCTT GGACCAGCGC TTTCAGGACG CCGATGAGAA GTTCATNGAA	300
GTCATGTACG GGGACCAAGN NGACCTGTTT TTCCTGCGCT GGGAAANTTTT GGGTTGATGA	360
ACACAGGAAA ACAACNTGGG TTTTGNTTTG GGGGCCCAT GTTTTTTCA AAGGAAACCT	420
TTGGNNCG	428

(2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GGCANAGTCA AATGNGAAGT GGTCACTGAA TCTAAAGGGA AAAAGGNGAT GAATGTCTTT	60
AATGGAGTCA TGGTTTGCAC TGGNCCATCA CACCAATNCT CATTACCTC TGGGAAAGCT	120
TGCCTGGGAA TTNGGAAAGT NTCAAAGGGN CAGT	154

(2) INFORMATION FOR SEQ ID NO:728:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

AACATTCCCTC TTCTCTGCCA CCATGACCAA GAAGGTTCAA AAACCTCAGC GAGCAGCTCT	60
GNAAGAATCC TGTGAAAATG TGCCGTTCC TCTGAAATAC CAGACAGTTG GAAAAATTAC	120
AGCAATATTG ATGATTTTG ATTCCCTCTG AAATTCAAGG NTACCTNACC TGGTTTATGA	180
TTCTGAAATG NAATTGGCTG GNAAACTCCT TTATGGATAT TCTGCAGCAC CTGTGAATAA	240
TACCCAGTNG ANCAGCTTTG CTNACTGCGN AAATCTGGG CTTGCAGTGG CCATGCC	300
TTCCATGGGN GCAA	314

(2) INFORMATION FOR SEQ ID NO:729:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GGCANAGCAA CTTGGTGACC TTTGTGGTAA TGGTGGTTCT CTATGCTCAC ATCTTGCGT	60
ATGTNCGCCA TAGGNCTATG AGNATGTCTC GGCATAGTTC TGGACCCCGG CGGAATCNNA	120
NNTACCATGN ATGAGTCTTC TGAAGACTGT GGTCATTGTG CCTTGGGGCC TTTATCATCT	180
GCTGGACTCC TGGATTGGTT TTGTTACTTC TAGACGTGTG CTGTCCACAG TGNGACGTGC	240
TGGNCCTNAT GAGAAAATTT CTTCCCTTGC TGCCTTGGNT GAANTTCANC TCTGGNCATG	300
AACCCCATCC GTTTTACTGC TAANGTGGA CAAAGTTAAT GGAGCGGCCA CTTTT	355

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GGCAGAGCGG GAAAGGCGGG ATCGAGGTGG GCCTGAGCCC NNGGATTTGG AGCGAACATA	60
GATGAGAAAC ACTTCCCGAG GTCTCCAGGT NTTNTGGGA GCCAGGAGGG AAGTAGGGGA	120
TGAGTCCATC TTCCAAACGG AGGGGAAAGG TCTCCCTTT TTTGGCTGG GAACCCGGGG	180
GAAGGCAGTG GGCGGNCTT CTGGAAAGGT CGGCCTGGGA AGGTCTGCCT GGGGTCTGGG	240
GGATGTTCCC GTGGGTTAGA CCCGGCGCGG CCCATGTTTC CTCCANTTAN CTAAGATTT	300
GCCGGCCTTN AAACGTTGTG CTTTCNGTCA AAGANCCAGG GGGTCCCCA AGGTTAC	357

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GGCACGAGCT GTACTCTGGG GCTCTTGGCG GCTGGTTCT GCCCTGCTGT GCTCTGCCAT	60
TTAACAGCCC ANTTGACGAG GAGAATCTAA CCCAGGAGAA CNATGATCGA GGGACANACG	120
TNGACCTCGN ATTNAGTCCT GCGNCCAACG TGGNACTTCG CTTTCAGCCT GTACAAGCAG	180
TTAGTCCTGA AGGCCCCCTGA ATAAGAAATG TNNATCTTCT CCCCCACTGAG CATCTCCACC	240

GTTCTTGGCC TTCCTGTCTC TGGGGGNCCA TNAN

274

(2) INFORMATION FOR SEQ ID NO:732:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GGCANAGGNT GGGTTTNTGA ACTNCTGNGT TTTTGCTTGC TNCTCTGGAN ATGCAGCGTC	60
TCTTGNCCTCC AGTGAAAGCG CATTCTGCAA CTGNACAAGA GNGGTGCAGG GAAACCTCCC	120
TTCACANCTG CTCGCCTGNT CCCAGTCAGC CCACCAAAGG TTTTCTACAG NATCTGNTGT	180
GCCCCCTGGC CAAAACAGAT ACTTGGCCAA AGGACGTGGG CATCCTNGCC CTGGGAGGTC	240
TACTTNCCAG CCCAATATGT GGACCAAACG GACCTGGAGA NGTATAACAA TGTGGGAAGC	300
AGGTAAAGTA TACAGTGGGG TTGGGNCCAA ACCCGTATTG GGCTTTCTTG TTCCAATCCC	360
AAGAGGNCCA TCAAATNNCC TGTGGNC	387

(2) INFORMATION FOR SEQ ID NO:733:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GGCAGANACT GGGTTGGTGA AGATTCCACA TACAAATTTT TTAAGGTTAT CCTCATTAAT	60
CCATTCCATA AAGCTATCAG AAAGAAATCC TGACACCCAG TGGGATCACC AANCAGTGCC	120
ACANGNCAG GGAGTTNCGT GGGCTGACAT CTGCANG	157

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

CTCTCNTNTT CACCACCAAGG TACCTGGACC TNNTCACCAA CTTNATCTCC ATCTACAACA	60
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CAGTAATGGA AGGTGGTTT CNTCCTCTGT GCCCTATGAG AACAGTGTAC ATGAATGTNA	120
TGGGAAAATT CCGTGAAAAN TTTTGAGCAG TGAGGAATGA GCACATTCCG CCTGGNGTTT	180
CTNCTGGTCC CAGTGNATTG GCCTTGCCT TCCTTGGAAA CTACAGTTTC ACTCTGCTGG	240
GGATCCGTGG GAATTTNN	258

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

GGCAGAGCCC ATGCATCATG CCTCTGGTCA TGACACTCGT GGCCCTTCCT CACATGAAAT	60
GAGGGGAGGG CCATTAGGAG ATCCCAGACT GCTAATTGGA GAGCCCAGAG GCCCCATGNA	120
TAGATCAAAG GGGTCTACCT ATGGNTGGTA GAGGTGGTAG AGATTNTCGA GCGAATGGAG	180
ACTCGTGCCA TGGAAACTGA AGGTCTTAGA GACACGTGTA ATGGAGAGGA GAGGAATGGA	240
GACCTGTNCG ATGGAAACCA GAGGGATGGA AGCAAGGGC ATGGTTGCAA GAGGATTGGA	300
GNTGAGGGGC CCTGTCCCCA GTTCAAGAGG CCCTATGATT GGTGGAAATT TCANGGTCT	360
GGTCCCCATTA TTTTAGGGGC AGTTGGCCCT CCTTCAGGGA NCCCGACAGT TCCCCGGCAT	420
TTTAAGGGTT GGGGNATCTT GGAGGTGGTA TGCAGGTTAC AGGNTNACAG GNACCGTTT	480
TTAGGGGGCA GTTTTACAAG N	501

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

AANCCAACAN TAAAATCCCT TCCCTCCAAC ATATGCAAAG ACGTTNTNAC CGNACCTGGT	60
GATATGCTG	69

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GGCAGAGACG GTNCTCACAT TCTCCCCANA GGCGANATG CGGGTAATGG CGCCCCGAGC	60
CCTCCTCCTG CTGCTCTCGG GANGGCCTGG CCCTGAACCG AACACTGGC CCTGGCTCCC	120
CACTNATNTG AGGTATTCA ACACCGCCGT TCCCAGGCCG GTNCGCGGAG AGCCCCGCTT	180
NATCTNANTG GGCTACGTGG ACGACAGTCA TTTGTGCGGT TTCGACAGGA ACGCCGNGAG	240
TTCCGAGAAG GGGAGCCGCG GGTCTCGTTG GGTGGGAGCA GGAGGGGNCG GAGTATTGG	300
AANCNGGGAG GACAACAGNA GTTACAAGNG CCCAGGT	337

(2) INFORMATION FOR SEQ ID NO:738:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GGAANAGAAT GGTCTGCACC ANTAAAACCA GGNGCACCCA CACCCTGGAA CCTCTCCANG	60
AAGACTCTCG	70

(2) INFORMATION FOR SEQ ID NO:739:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

CAGCAAGACG TCCCAANTAA GTTTAAGTAT AAGGAAGGCA CTCTNAAGGT CGGCCAGAC	60
TGGGCAAGAC CTCAAANAGG AGCATCCTGG GTCGGCTACA CTGCCCCCTT CCTTGAATNC	120
ACTCTGCCTG TTTANNAACC TGGGAGTGCT GGNACCCCTG CAGCAGTNCA GCGAATGGAG	180
CTTCATGCAG GCTCTATNCT GTAACCTGT GAAGCCCTTT GCCTGGCCA GGTNGACAGC	240
TTTANGTATT TGAAGGNTCA GGGGTGGAGT NAGGCTG	277

(2) INFORMATION FOR SEQ ID NO:740:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

TGAGCCTAGG NGCTAGGTTG CAGTGAGCCA GATGGCCCAT TGCACCTCTAG CCGGGCAGCA	60
GGCNGACC	68

(2) INFORMATION FOR SEQ ID NO:741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

AGGAGCTGTC GGGAAAGATCA GAAGCCAGTN AGGATGACCA GCGCGACCTT ATCTCCANCA	60
ATNAGCAACT GCCATGCTGG CCGGCGCCTG GGGCCCGGAA GAGCAAGTCC AGCGCGGANC	120
CTTGTACACA GCTTTCCAN CTGGTGACTT NCTCTCGN	158

(2) INFORMATION FOR SEQ ID NO:742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GGCAGAGNCT TGCTCTNCCC AAATTAAATT TGCAGTTTT AACTCTTNAT GACTACCTGC	60
TAAGTGACTT TAACCTCTTC CGCTTAGAAT CAACTTATGA AATTCGTCAG GACATTGAAG	120
ATAGTGTCAG CAGAATGAAG CCATGGCAAT CTGAAATATG GCGGTGTAGT GTTTGGTGGT	180
TGGGCGCGAA TGGCCCAGCC CATTGTGGCT TTNACTGTCG TAGNAAGTGG CCAAACCCAA	240
CATAGGTGAA AACTGGCCAA CCCGAGTTCG TGCCAGATGT TACCATAAT CTCCAATGTC	300
CAGAGATCCA CATCAAAGNT GANTGGGAAG GNCTTCGTNA GCATGATGTA TGCTTTTAA	360
ATTACCGTAC GNTCCCACAA AACCTT	386

(2) INFORMATION FOR SEQ ID NO:743:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GGCANAGGCT TGCTGCTGGG GAAGATCTGG AGGTCCAAGT GCTGCANGGC ATCTCTGGGA	60
AGAGCCAGAT CCTGTTGCT CTCGTCTTCA CCACCAGGTA CCTGGACCTG TTCACCAACT	120
TCATCTCCAT CTACAACACA GTAATGAAGG TGGTTTTCT CCTCTGTGNC CTATGTTACA	180
GTGTACATGA ATATATGGGN AAATTCCGTA AAACTTTGT ACAGTGNAGA ATGAACACAT	240
TCCGCCTGGG AGTTTCTTCT GGTCCCAGTT CATTGCCCTT TTCCTTCCTT GAAAACATACA	300
GTTTCACTC TGCTGGGAGA TTCCCTCTGGA CTTTTCTAN GCTATNNGGG AATTCACTGGG	360
NNATCCTGTC CCCAG	375

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

TCGGACGAGT CATGGGCTCC CGNAACAAAC GTGAGGNCTG NCAGNGTCAA ATTTACCCTN	60
GTCCAAGATC CGCAAGTCCG CCCGATGAAC TGAUTGACGC TTGATGAGGA AGGNCCCACG	120
GCGTCTNGTC GAANGCAACG GCCTGTCTAN CGGAGGG	157

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

GGCANAGCTA CAACCAGCTG AGCCGTGCCG TCGCGTAAC TGCGCGCNCT TGCCCAACCT	60
GCCCCAACGC AACCAAGTTCC GCGTGCCNCT TCGGCCGGCT GCTGGACAAG CTGTATGCTC	120
TCGGCTTGGT GCCCACGCGC GGTTCGCTGG AGCTCTGCAC TTTNCGTNAC GGCCTCGTCC	180
TTCTGCCGCC GNCGGCTCCC CACCGTGCTC CTNAAGCTGC GCATGGGGAA CNCTTTCAGG	240

GCTGCCGTGG CCTTTTGGG AGCAAGGGCA CGTAACGTT TGCGGCCCTG AACGTGGT	300
TACCGAACCN CGGNNTTTC CTTGTTNAAG GGGGNAAT	339

(2) INFORMATION FOR SEQ ID NO:746:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

AGGCCTGTAC TACCACCGGT ACCTCCAGGA GGTCATCGAT GTACTGGAAG ACGGATGGC	60
ATTTCCAAGA GAAGCTGCAG GCTGCGCAAT GCGGAGGAAC ATCANGAAGC GGGAAAGCTG	120
AGCCGAGAGC TGGNACTTTN TNAGCCACCA CGTCCGCACC AAGCTGGNAT GAGCTTCAAG	180
CGANCAGGTA GGTGTTCACG GACTGCGGAT GTTGCTTCA AGGCCAAGNA TGGACGCCGA	240
GCAGGGATCC CAATGTGACA GGTGGNATTG ATCTGGAATC TGCCTGGAAA CAGTTTGGA	300
ACACCTGGNA CCCTTCAGGA ACCAGCATAAC ATTTCGAGNG CCCGNGAACCC TGGNAGTT	358

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

GGCAGAGCTC AGACATGCAA GANGTCATTG GCTCANCCAT TGCTATCAAT CTCCGTCTG	60
NAGGAAGAAT TCCTCTGTGG GGTGGCGTTC TCATCACCAT TGCAGATACT TTTGTATTTC	120
TCTNCTTGGGA CAAATATGGC TTGCGGGAAG TAAGNNAGCA TTTTTGGCT TTCTCATCAC	180
TATTATGGCC CTCACATTTG GNATATGAAG TATGTTACAG TGAAACCCAG CCAGAGCCAG	240
GTACTTCAA GGGNCATGTT CCGTNACCAG GCTGTTTCAG GCTGTTCGNA ATTCCACAGA	300
TTGNAN	306

(2) INFORMATION FOR SEQ ID NO:748:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

GGCANAGCCA CTGTCTCCTT TACCACAGGG AATATGTCAG TGGATTTGGA AAAGCTATGA	60
GGATGCCCAT GTGGAGTTCA TACACAGTCAG CCCAGTTGGG AGACACATCG CCTCTGCCTC	120
CCACTGTCCC AGACTGTCTG CGGGCTGATG TCAGGGTTCC TCCTTCTGAG AGCCAAAAT	180
GTTCTTCTA TTTAGCAGAC AAGAATATCA CCCACGGCTT CCTCTATCCT CCTGCCAGCA	240
ATAGAACATC AGATAGCAA TATGGTGCTT TAATTACTAG CAATTGGTA CCTATGTATG	300
AAGAATTCA GAAAAATGTG GGACTACTTC CACAGTGGTN CNTNTTGANA AAACATGGCC	360
ACAGAAAGGA AATGGNGTTA AATGTGGGTT TAGTGGGACC ATNATTGGG TTNTAATTAT	420
GATGGGNCTT TTGGTGTCC AGTGAATTAA CCAA	454

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

GGCACGAGCC GCCTGCAGGG AGGAGAATGT ACCCCACTGG NACCTGNAGC TCCTGGTCCC	60
TCAGCCAAGA CCTGAANGNG TCCCCAGCCA GCCTGCTGCT GGGGACCCCTG TGGCTTGCTG	120
TCAGTGTATG GGGCCTCTTG GCCTTCCCTT GGGGAAGTTC ACCCNTGTTA CCCCAGCTTG	180
CCTTGCCCTT GGGNCCTTTT NCTGGGCCCC AGTGNCTTCC TGCCCTTGAC ATNAGAACTT	240
G	241

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

CCACCTGGTN CTGCAAGGAC CAAGNGGTCT GTCCATTCAA GGAATGCCCG GAATGCCAGN	60
AGAAAAAGGA GAGAAAGGAG NTACTGGNCT TCCAGGTCCA CAGGGTATCC CAGGAGGCGT	120
TGGTTCACCA GGNACGTGAT NGGCTCACCA	150

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GGCAGAGGTA CACGTGCCCTC GAGCTGCCAC CTCCGGAGTG GGGCTGGAGA ACGGCATCCC	60
ACGGGGACCT GATCCGGGGC ACGGTGCTCA CCTACCAGTG CGAGCNTGGC TACNAGCTGC	120
TAGGCTCCGA CATTCTCACT TGCCAGTGGG ACCTGTNTTG GAAGGCCGG CCGCCCGCNT	180
GCCAAAAGAT CATGAACTTG TGCTGACCT GGCGAGATTN CCAACGGGCA CCCCACNGCC	240
TTCGGAACGC CGGCTTCCCC GTTGGNTCCC ACGTTNCAGT ACCGCTGCCT GCCAAGGTTA	300
CAGCCTTCGA GGGGCAGCC ATGTTCACCT GNTTACAGCC GGGGACAAGA GCACANCAA	360
TGGNAGNATT AGGGTTCCCC AATGGGGCTT TGAATAAGGA GCCTNGCCTT AAACCGGGGG	420
TTNCGAGAAT GGTTACCAAA GTTTTANAGA ACATTACCAAG GGGGGGATTT TTGGGTTTTT	480
NTGNTATTAG GGTTTTAG	498

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

GGCAGAGGNN NNCACCCACA TTACCTGCTT TCTTCTTGGG TAGCTTGTC ATCAGCTCCA	60
CCCCTTGTGA ACACCTTCT GAAAGCTGGA GGGCTGGGAG AAGGGGGTTG TATTCAACAA	120
TGGCCAGAAC CTTGGACGTT ACTGGAACAT TGGACCCAG AAGACGCTTT ACCTCCCAGG	180
TCNNCTGGTT GAGCAGCGGG AATCAACCAAG GTGCATCGTT TTTGAAGGAG ACGATGGCGG	240
GGCCCTGCAT TACAGTTCAC GGGAAACCCC CCACCTGGG CAGGAACCAAG TACATTAAG	300
TGNAGCGGTG GCACCCCTC CTGCTGGTGC CCATGGGAGA CTGCCGGCTN CTNTGACCT	360
GAAAGNCTGG TTGGTTGTTG CCCCAACCTT CATTGAAAAA GCATTTNCTT AANTAGNAAC	420
TTCAGGGATT GGGGGTTAAA ATTTGCCCTG TTTTAGTTNA AAACCTAAGC TTN	473

(2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

GCACCCCCAAC ATCGACACGG CCAGTTNTT CCGCTGGCGG CATCAGGCC	GGGTGGAACG	60
CATGGNGCAG TTCCAGAAGG AGAAGGAGGA ACTGGACAGG GGCTGCCGCG	AGTNCAAGCG	120
CAAGGTGGCC GAGTGCCAGA GGAAACTNAA GGAGCTGGAG GTNGCCGAGG	GCGGCAAGGC	180
AGAGCTGGAG CGCCTGCAGG CCGAGGTACA GCAGCTNCGC	AAGGTGGAGC	240
GCAGAAAGCT GNNAGGAGAT TGGCGCAAGAT AGGNNGNAAGT AGCATGCCCT	GGTAACGTGG	300
GACANGCTTC NGCAAAGACG GCTTCAGCA AAGAGCCATG GTTAAATTAC	CAAGCCCCNG	360
TAAGTACGGT GGTAGGNATT CAAAGGTGGT NTAGGGTAGC CAGAAACACA	AGGACTTTCT	420
TGGNAAANAT TACG		434

(2) INFORMATION FOR SEQ ID NO:754:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GGCANAGGNA CTGTAAAAAT GAAAGTCCTA ATGGGAAACC CTCTTCTCCC	CACACCCAG	60
TTGTTGGGCT CAAGTCTGCT CTGNAGTCCT GATCTCCCTT	GAATTGAGTC TCAGCATCTT	120
CNNGTTGCCT CCACCTGCTC GTCTGTNAAT CCCATTCCCT	GCAGACAGTG GAACAAAGTC	180
ACTGGTAATC TTCCTCATTG CCCTGGGACT GCTCCCAGAC ACAGCTATT	GGGACCCAGA	240
TCTTCCCCAC CAAGCCATGG GCGANATCTT GTTGAGTAAG AGTTTCAGTC	CTGGGGTCTT	300
ATTTCACCA AACGTGGTAG GGGATCTTGG ACCCNATGT CTCTGNTTTT	TTCCTAAGGN	360
CACAGAGGNT GTGGG		375

(2) INFORMATION FOR SEQ ID NO:755:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GGCAGAGCAG AGTTTGACAG GGAGATAGAC CGGGGATCCN GGANCCCTTN TNAACAGCTG	60
TTTGAGAAAG ATGGTCAGTG GCATGTACTT GGGAAAGAGCT GGTCGACTG ATCCTAGTCA	120
AGATGGCCAA GGAAGGGCCT CTTATTTGAA AGGGCGGATN ACCCCGGAGC TGCTCACCCG	180
AGGGNNAGTT TAACACCAGT GAATGTGTCA GCCATCGAAA AGAATNAAGG NAGGCCTCCA	240
CAATGCCAAA GAAATCCTGG ACCCNNTGG GAAGTTGGAG CCNTTCCGAT TGATGGACTG	300
T	301

(2) INFORMATION FOR SEQ ID NO:756:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

ACCCTCCTTT CCTGCAGCTC CAGCTTTNTG CTCTGCCTCT NAAGGAGACC ATGGCCCAGC	60
ATCTAANTAC CCTGNCTGCT CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGNAGCCC	120
CAAGGAGGAA GATAGGATAA TCCTGGGTGG NCATCTATAA ACGGCGAACC TNCAATGAAT	180
GAGTGGGTAC AGCGTGCCCT TGNACTTCGC CATCAGCNAG TNATGAACAA GGNCCACCAA	240
AGATGGACTT ACTNACAGAC GTCCGNNTGC GGGTTACTTA AGAGCCAGGC AACAGACCGT	300
TGGGGGGGGT GAATTAATTN TTGACGTGG AGGTNGGCCG AACCTATGTT ACCAATTCCC	360
ANNCCAATTG GGACAANGTG	380

(2) INFORMATION FOR SEQ ID NO:757:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

TTTTGCCCGG TTGGGATTGT NATGGGTTGC CCATTGAAAT AAAAGTATTA TCAGAACTTG	60
GTAGAGAACG TCAGAATCTT TCAGCTATGG AAATTAGANN GAAAGCTAGA TCATTTGCTA	120
AAGCAGCCAT TGAGAACAG AAATCAGCAT TTATTCGTTG GGGATAATG GCAGATTGGG	180

AATAATTGGC TACTATGACA TTTGAATGGG NAAGTNTGAA GCCAAACAGT TGAGAAACTT	240
TTTACCAAAT GTATGATAAG GGCTTGGTTT ATCGTTCTTA CAAACCTGTN TTTTGGNCTC	300
CGTNCATCTA GGACGNACATN GGCTGAAGCA GAACT	335

(2) INFORMATION FOR SEQ ID NO:758:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

AGTAGAAAAA TCAACAGAAC AAAGGAAGAG TATGGCTCCT GAACCTACAC AGAGCTCTAC	60
AGTAGTCGCA TCTGCCAGC AAGTGAAGAC AACGCAAAC TCAAATGCTC CTGAATGTAA	120
ATGAATGCAA TTNTGAAACT GATTCCAATG AATTTGAAT GTTAAGGGAA ACCTCCCATC	180
CATTTAGTGG ATTTCTNCAT CTAGATCTAC ACATATGTGA ATGACATTGC ATGGCTAAA	240
GAAAAAGAGT CCAAACAGAC GTATTACTGG AGGGGCCAAT GCCAACTTNT CTTTNACAC	300
AGCTAACTAT AGGNTTATTT NTNCCTTATC C	331

(2) INFORMATION FOR SEQ ID NO:759:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

ACTGTGGACA TGATGTATGG TGGCATGAGA GGCATGAAGG GATTGGTCTA TGAAACATCA	60
GTTCTTGATC CTGAATGAGG GCATNCGTTT CCGAGGCTTT AGTATCCCTG AATGCCAGAA	120
ACTGCTACCC AAGGCTAAGG GTGGGGAAGA ACCCCTGCCT GAGGGCTTAT TTTGGGCTGC	180
TGGTTAACTG GGACATATCC CAACAGAGGA TNAGGTATCT TGGGCTCTTC AAAAGAGTGG	240
GCAAAGAGGG CAGCTCTGCC TTNNCCATGTG GTNNACCATG NTGGGACAAC TTTCCCACCC	300
AATCTACACC CCATGTTTC AGCTCAGTGT CAGTGTTCAC ANCCCTTCA ACATGGAAAG	360
TTAACTTNN CCCGNGCATT ATGGCACCAG GGN	393

(2) INFORMATION FOR SEQ ID NO:760:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GGCANAGGAT TTTGTGCCCG GCTGGGATTG TCATGGGTTG CCCATTGAAA TAAAAGTATT	60
ATCAGAACTT GGTAGAGAAG CTCAGAACATCT TTCAGCTATG GAAATTAGAA AGAAAGCTAG	120
ATCATTTGCT AAAGCAGCCA TTGAGGAAAC AGAAATCAGC ATTTATTCTGT TGGGAATAA	180
TGGCAGATTG GGAATNAATT GCTACTATAC ATTTGATGGG GAAGTATGAA GCCAACAGT	240
TGAGNAACTT TTTACCAAAT GTATGATAAG GGCTTGGTTT ATCGNTCTTN ACAAACCTGT	300
GTTTTGGTC TCCGTGCATC TNAGGGACTG CCATTGGCT GGAAGCAGAA CTTGNATTN	360
ATCC	364

(2) INFORMATION FOR SEQ ID NO:761:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

AAAGCTATGA GGATGCCCAT GTGGAGTTCN TACACAGTCC CCCAGTTGGG AAGACACATC	60
GCCTCTGCCT CCCACTGTCC CAGACTGTNT GCGGGCTGAT GTCAGGGTTC CTCTCTCTGA	120
GAGCCAAAAA TGTTCCCTCT ATTTCAGACA CAAGAATATC ACCCACGGCT TCCTCTATCC	180
TCCTGCCAGC AATAGAACAT CAGATAGCCA ATATGAATGC TTTAATTACT AGCAATTG	240
TACCTATGTA TGAGGAATTC AGAAAAATGT GGGACTACTT CCACAGTGTT CTTCTTATAA	300
AACATGCCAC AGAAAGAATG GNNTAAATGT GGTTAGTGG CAATATTGN TTATAATTAT	360
GGTGGGCCAT TTGNNGCTCC CGATGGAATT ACCAACCTT TGGGCAACA NGGTGTT	417

(2) INFORMATION FOR SEQ ID NO:762:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

TTAAGAGTTC CCAGAAATAC ATTTGCCACC AACAGAGTAG CCAAATTAT AAGGAAAAAT	60
GATTCCAAT GGATATTGA TGTTTGAGGA TGAAAATTT ATTGNGTCTT CTGTTGCCAA	120
ATTAATGCC CTGAGGAAAA GTGGCCAGTT CTGTGAATGT TCGACTTCAG GTCTGTGGCC	180
ATGAANGTTA GCACACAGAG CAGTGCTAGC TTGCTGCAGT CCCTATTAT TTGGAAATCT	240
TTAATAGTGA TAGTGGTCCT CATGGAATT CTCACGTTGA AATTTGATG ATCTCAATCC	300
CAGANGCTNG TTGGAAGTCT TGGTTGGNAT TNTGGCCTAC ACTGNTCCAG TT	352

(2) INFORMATION FOR SEQ ID NO:763:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GGCANAGCTC GGCATGTGNC GGGAACCTGA GGGACTTGTG GGGCCTCAAT NATCTGCTCA	60
ACGTGCTGCA GAGCCTGCTG CTCCCGTTCG CCGTGCTGCC CATCCTCACG TTCACCCAGCA	120
TGCCCACCCCT CATGCAGGAG TTTGCCAATG GCCTGCTGAA CAAGGTCGTC ACCTCTTCCA	180
TCATGGTGCT AGTCTGCGCC ATCAACCTCT TACTTCGTGG TCAGCTATCT GCCCAGCCTG	240
CCCCACCCCTG GNCTACTTCG GCCTTGCAGC CTTGCTGGCC GCAGNNNTACC TGGGCCTTAG	300
NACCTNACCT GGT	313

(2) INFORMATION FOR SEQ ID NO:764:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GGCACGAGAG AGAAAATCAT CAAAGAAGAT TCTTTGGGA TCCTCTTCCC TTTTAGAGAC	60
CGGGGTAAAT TTAAAAACAC TGCTTGTAAC ATTTGTGGCA AAACATTTGC TTGTNAGAGT	120
GCCTTGGNAC ATTCACTATA GAAGTCATAC CAAAGAGAGA CCATTTATTT GGCACAGTTT	180
GCAATCGTGG CTTTTCCACA AAGGGTAATT TGAAGCAGCA CATGTTGACA CATCAGATGC	240
GAGGTNCTGC CATCCCAGCT CTTTGAGCCC AGTTCCAACC TTGGCCCAN TCAGAACTTC	300
AGCGGTGATT TCCCGNCAAN TCGTTGTTCA TCTCTTCATT CAAGACAGAG GGTCCAACGG	360

GNTTCGTGG CCAGTTTTT TCCNCCAGGG CCCGTTAAAG GGCCANCCCC CA

412

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

TTGTGCCCGG CTGGGATTGT NATGGGTTGC CCATTGAAAT AAAAGTATTA TCAGAACTTG	60
GTAGAGAACG TCAGAACATTT TCAGCTATGG AAATTAGAAA GAAAGCTAGG ATCATTGCT	120
AAAGCAGCCA TTGAGAAACA GAAATCAGCA TTTATTCGTT GGGGAATAAT GGCAGATTGG	180
GAATGAATTG CTACTATACA TTTGAATGGG AAGTATGAAG CCAAACAGTT GAGAACTTTT	240
TACCAAATGT GATGATAAGG GCTTGGTTTT ATCGATCTTG ACAAACCTGT GTTTGGNTC	300
TCCGTTCATC TGAGGACTGN CATTGGCTG GAAGCCAGGA ACTNGNAATN	350

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

GGCACGAGCC AAAGGCCATG TACTCTGCGG GCAGGATGTG GAGAGGGGCA CATTCA GTNA	60
CCGGCACCAT GTTCTCCATG ACCAGGAGGT TGACCCAGA CGTGTGTNCC TATAANTCAT	120
CTCTGGCCTG ACCAGGCCCG GTACACCGTG TGCAANAGCT CCCTCTCGGA GTACGGAGTC	180
CTGGGCTTTA AGCTGGGCTA TGCCATGGCC AGCCCCAATG CCCTGGTCCT CTGGNAGGCC	240
CAGTTTGGGG ACTTCCACAA CACGGCCCAG TGCATCATCG ACCATTCA TC AGCACCGGCC	300
AGGCCAATGG GTGCGGCATA ATGGCATTGT GCTGCTGTTG CCCCTGGGA TGGAAGGCAT	360
GGGCCAGNG CATTNTTNA GAAGGCCNNNA AGTTTCTGCA GT	402

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GGCAGAGCCT	CTCCGCACCA	CCTCAGCGGG	CAGGAGGTCC	CACCATGTGN	ACAGACATAG	60
CCCAAGGAGG	CACCACAGGT	CTATGTGTGC	TGGGGATGT	NAGGTGCCAC	CCAACGCTGT	120
CCTGGTGGTA	TTTACAATGA	ACATCCTCCT	CCTCCATCAC	TCCAGGGGTG	GTGTCTCGGC	180
CGCCCCCTACC	AGCTGGCTGA	GCCCCCCTGGC	CTCCTGCGNT	TCCCTCACTT	CCCTCAGTTC	240
CCAAAGCTGC	CCAGTCCATG	GGGGACAGAA	CCGTNACTCA	GANTCCACAT	TCAAGTGTGG	300
CCCACCCCTGC	AGTCTTCATC	CTTCATTCAAG	CTGCTGCCTT	NTGGAGGTGN	CTTTTGGGCC	360
ACATGTGCTG	TGGTGTGTG	TTTCCTNGGA	CAGGAGNCTT	TTCCANCAGN	AGGTTGGGTT	420
CCANGGGTGC	GTGGAAATT	CTTCCTTTGG	GANCTGGTT	TTCCGGNGAA	CTTTCTTTGG	480
GGCCTGTTA	AGAAGGTGGT	GCNG				504

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GGCANAGCAA	AGAGAGAAGG	TCGGGTACTT	CAAGAAGAAA	TGAAAGAAGG	GACAGACATG	60
TTCATCATCA	AGGCTGTNCT	GCCTGTTGCT	GAANCTTG	TTTCCTGAT	GAAATCAGNA	120
AGAGGACAAG	TGGCCTGGCC	AGCCCACAAAC	TAGTATTCAAG	CCATTGGGAG	ATCATTCCCA	180
GTGAACCCCT	TCTGGGTGCC	AANNACTGAG	GAGGAATACT	TGCACTTTGG	GGAGAAGGCT	240
GACTCTGAGA	ACCAAGCCCG	GAAGTACATG	AACGCATACG	GAAAGCGGAA	GGGGNTTTA	300
TGTTGGAAGA	AAAGNTTTG	GGGCATNCCA	AAAAAGCCA	GGGNCCCTT	NGGCAAAATT	360
						360

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

GGCAGAGGCT CCAACGGCTT CTCAGACCCC TACGTCAAGA TCTACCTGCT GCCTGACCGC	60
AAGAAAAAGT TTCAGACCAA GGTGCACAGG AAGACCCTGA ACCCCGTNTT CAATGAGACG	120
TTTCAATTCT CGGTGCCCT GGCGAGCTG GCCCAACGCA AACTGCAC TT CAGCGTCTAT	180
GAACTTGAA CCGCTTCTCG CGNCAGGACC TCATCGNCA GGTGGTGCTG GACAACCTCC	240
TGGAGCTGGT CCGAGCAGCC CCCTGACCGN CCGNTCTGGA GGGGACATCG TGGAGGGCGG	300
CTTCGGGAAA AAGCAGATCT TGGGGAGCTT CNNCTNTGC ACTNTGGTTA CCTNCCAAG	360
GGCCGGGGGG CTTCACCTGG A	381

(2) INFORMATION FOR SEQ ID NO:770:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GGCAGAGNAG CAGGCACTGG NGGAGGGGGC TTNAAGGAGG GAGTGCCCCC TCAAACCTCCC	60
TGCTTCCCTG GANCTTCAGG NAAGCTCAGC CTCAGCCTTC AGGCCTGAGC AAGTGCAGGG	120
CGGANTAACC AGCCCAGGTT CAGATGTTGG GGTGTGAAAG CCTCAAGTGA ACTCAGCCTG	180
GTTGGAGAAC TGCCCCACCC AGTATCTTCT GTGCCATGGT TCCCACATTC GCACTCCATG	240
GCCTCCTGTC CTGGNACCCC ACGTTTGNA ANGTAACCC TAGGNACCAT GGGATTACCT	300
CTGTGAATTG ACGNTTGAGC CCAAGTTCCC CACAATGGAA AACTGGGAA ATGGCCAGTT	360
GTGTGTTCCC AGGAATTNCT TCCCTTANTG TTNCCTTGAA GTGCCCGAGC ATGTAGGGCA	420
AGAAGGAAGG TTGAAGCGTT TTCCCTAGGNG GAATTTTCC TTCAGGGGG CTCNATTNTT	480
GNCCAT	486

(2) INFORMATION FOR SEQ ID NO:771:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

GGCAGAGNCA ACGNGNGNCT TCCTGGAGAG CAGCAACAGC ACGGACTACA TTGCCATGCA	60
CGACGTTGAC CTGCTCCCTC TNANGAGGA GNTGGACTAT GGCTTCCTG AGGCTGGGNC	120

CTTCACGTG GCCTTCCGG AGCTCNACCC TCTCTACCAC TACAAGACCT ATGTCGGCGG	180
CATCCTGCTG CTCTCCAAGC AGACTNACCG GCTGTGCAAT GGGATGTCCA ACCGCTTCTG	240
GGGCTGGGC CGCGAAGGAC GGACGAGTTC TACCGGGGGC ATTAAAGGGA GCTGGGNTTC	300
AGCTTTTTT CCGCCCTCG GGAATTACAC AACTGGTNA CAAGACATT TCGCCAATG	360
NCACGANCCA GNCTGNTGGA AGAGGGACCA GAAGCGCATT GNAGTTAAA AACAGGNGCA	420
GTTCAAGGT GGACAGGTNG GGÄAGGCTGA ACATNTTAAG TTACCATGTT GGTTTCCGG	480
ATTGCCTGTT	490

(2) INFORMATION FOR SEQ ID NO:772:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GTGTGGGTG CCGNGGTGAC CGNAGNAAA NAGGNNGTTG TGGCTCAGTG CATCCACTCT	60
GGGAGAGCGT GGACCTGGTT CCTGGGGGCG ATCGACAGTC ACNNNTNAAC ATTGGTGGA	120
GGGACAGTGT TTATGATCCC GGCTTAAAC CACTGACCAT CTCTTATGAC CCNGCACGT	180
GCCTCCACGT CTGGAATAAT GGGTACTCTT TCCTCGTGGA ATTTGAAGAT TCTACAGATA	240
AATCAGCTGC ACTTAGTGNA TTGGAACGCA NCAAATTGA AAACTTGAG GATGCAGCAC	300
TGGAAGAAAA TGGTTGGCT GTGATAGGAG TATTTTAAA GATTCGGGA AACTTCTGGC	360
AGCCCAGTGT CTACTGGAAG GCCCAAGCCG NTTGCCAGAA AGTGGGGCCC GCCCAAAAG	420
ACTGGGTTT GCAGTCCAGG CCTTNCTNAG TTNCCAGTNC CAGGGAA	467

(2) INFORMATION FOR SEQ ID NO:773:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

AGGCACGCAG CCTACTAGGT GTGGCGCGA CCCTGGCCCC GGGTTCCCGT GGCTACCNGG	60
NGCGGCNGCN CCCN	74

(2) INFORMATION FOR SEQ ID NO:774:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

ANACCACCTG TGGTCTCACT AACCCCAAAA CTGCGCTCNA CCCGGCTGCN TCCAGGGTCT	60
CTAGTCCCCC CACTAGAGAC TGANAAGTTG CCTCGCAAAC NAGCAGGGGC CCCATTTGGT	120
GGGAGTCCTG GGCTGGCAA GCGGGGCCGC CTACAGCCCC CAANTCCCCCT GGGGCCTGAG	180
GGTTCANTAG AGGAGTNTNA GGCTGAAGCC TTAGGTGAGT TAGGAGGAAG GGGATGGGAC	240
CCCACGGCCG ACNTCCTGGC CCCCGNCGGC TTGTTGGAC CACCAACCAA GGGGACCAGC	300
GNATCCTTGG CAGAAGGNCC CTTCCCTCCT TGGTTGGNCC TGTTTTTAAN TCAAAAGGGG	360
CCNAAGGCAA	370

(2) INFORMATION FOR SEQ ID NO:775:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GGCAGAGCGA ATTTGTATGA NATTAGCCGG CCGTGGATTG ANAATCGCTC TTTGTGTGAT	60
GGGTCCCAGG GGTTCCCTTT NACCACAGAG CCAGCCTGAA ACTACCCACG GGTGCTGTGG	120
ACCCCTTGAA TCATGGCGGG ATGGAAATGG GCTGTGCCTN CAGCCGGNA CTCAGGACTG	180
NAGCATGTNT GGGCAGCAGC CTGGTAAGCT GGCCAGCCTC GGCGCCCTTG GGGACAGCCC	240
TTGAANACTC TGGCTTCGGT GCCCTGAGTG AGGGGGCGCC ACCCTGGGCT TCCCTGGGAT	300
GCGAGCAAGA CCCAAGNCAG GNTGNTGGAA CCGGGACAAT TCGNGTCATG TTGCTGTTGT	360
NCCCTTCCTG	370

(2) INFORMATION FOR SEQ ID NO:776:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

ATCCCCGGG NCTGCAGGAA TTGGNACGA GAGTTAAACA CTTNATTCC TCCCAACAAC	60
ACTAGAGCGT TGGCNATNAT AACCCCCATT TAATGGATTA GGAAACCAAG GAACCATGAA	120
ATTAACAAAC TTGCCCGAGG ACATACAGCT AGGTTTCCC AGGTCTGCT GCAAGGAGGC	180
GGCCAGGTCC TGCTCGTTG GACACTCCAT TACTTCCGT TTTTCCTGAT GGGCCGGTC	240
CTCTACTTCC ACCACTACTT CCCAGCCATG CTCTTTCAA AGCATGTTGA CAGNCTTCT	300
TTGGGNACAC CCTCCTGAGG GCTCTTGCC CTGGGNCTT GGNCTCCATG GGCCCTGGG	360
CGAAGGGGGC ATTNACANTG GGCAGGGGAN TCCTGANGCC NGNTTCCCTGG GGGAACTGNC	420
CTNACAGTTT TTTAACNTTT TNCCAACCTT TGGGTTTAN GGGGATGGTT TGGTNCCCTG	480
GGGCCAGGA CCCCCCAAAT TCCCATGGGN AGGACTAAGG T	521

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

TATCCATAGA TTCAGTGCAA TTCCAATAAA ATCCCAGCAG GCATTGTTGA AGAAAATGAA	60
CAAGCTTATT TNCAAATTCA CGTGGAAATG CAAAGAAGCC AAATTAGTCA AAACGGATTT	120
GAAAAAAAC AAACTAGTGA CTTAACGTTT ACCTGACTTT AAGNATATAT TATNAAACCT	180
ACCTTACTCA AAACAGTATA GTAGTCATAT AAAAGATAAT GGGAACAGNN TTAGAGAACCC	240
TAGAGGTAGG ACCCGGCACA ATTATGGACA ACTGCTTTTC CAACAAGGGT GCCAAAGGCA	300
TTCCGTGGGA AAAAGGAAAG TTTTTTCCAA CAATGGGTNT TCCTNTGTAA AATGGACNTT	360
AAATTCTTC CCCTGTNTTT TNGGCCAAAT TGNCCCCACT GGGGTTTCG GTCTAATGTA	420
AACCNCAATT TTAACTTCCT TGGGGAAAGG AACGTNGGGG AACCTTGTIN CCCGGGNTTG	480
GGGNACGTTT TAGGTTGGG TCCA	504

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

AGGGGCTTGT TTTTTTATAT AGTGTGTTG GGGGAGGGGG GACGCCGGAG GNTGCATGTT	60
TTGGGAAAG GGGGTGACAG ACAACTTTA AAAGGGCAGC ANACTCCCTC AGCCATGAGA	120
AACCAGCTT GGGGAGGAAG GCCGGAAAT CAAAGCGAAG TCCAGTTAAT CTCCCCTGAA	180
CANTTTGGGA AGTCATTTT NCCCTCANTG CCAGCCAAAT CCGGGCANGA CCCTCGAAAG	240
AAGNACCGAG GGTCCCAAAG GACCAATGCT ACAACCAGCA AATGCTGCCA CATCTTNNN	300
CTGATTGGGG GGTNGGGGAT GGGTTGGGGG GGATTGGGAC TNGGGGCAA AGGGTTCTGG	360
GGTGGGGCCA TTTTTAAC TTTGGGNGGN CTTTCCATT TNTTTGGTTN AGGCCAT	418

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GGGCACACGT GGAGCTNAAC TTAANGCCAG CGGGGAGNCG GGGAGGCACT GCCCTCATNN	60
TTGCANTNCC TTNATTCTTT TGAGGGCACT GCCAGCCCGG GAACCACTCA ATCTNCTTNT	120
GGTTGAAAGG TTTGGTTCAG GAAGGNTGGT CTCCTGGTTC CCNTTGGGT GCTTAATGAT	180
GCACTTNAGG GGCTTGCNAG GGGTGAAAGT CCTTGNAGGC CCTGATNGGT CCAGCTTNTC	240
CACAGGGTGA TNNTTGTGTT AGTCNAGCCG GGTCAGCAAN GTTNAGAGGC AGCAGGCCCT	300
GTTCCTTNCAG GTTGGTTCT CGTGGATCCT GGCAAAGNTT TTTGGGTGAT TGATGGCCCC	360
GGCCCCCAAG TTGGCGAGNT TCCAAAGCTG TATGTTCCCG GTTTNGAAAC CTTGNCCTAA	420
TTTGGTTTC CAATNACCAN CCACTGATGC CAGTTTTTT TAATAACGGG G	471

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

TTCCCGNTGT GGAGCGAGTG GACTCCTGCC CCTCCATGTA CAGCCGCTCC ATCCAGGGCC	60
ACCATGTCTG CCTCCTGGTG AAAAAGGGTG AGAACTCTGT CTNAGTCGAC GGGAAAGTGCC	120

AGTGAACCTCC ACGCTNACTG AAGCAACTTG TTAGNAAGAG AATGAAGGCG AACGCTGGCC	180
AAGTGTGAA AGCTGCCCTGC AAGCCCCGCA CCACCCCGAG GAGCACGTNA CCCAGGGAAC	240
CGCAGCCCTG ACGTGTCTCG CCTCTCCTGN AGTCGTGTGT ACTGTTACCC ANGCCTGNNG	300
TGTTTAATTT NAACTCTAAT GTTTGTNCCG NCCTTGTNTG GACATCCGAG GGTCCATTNG	360
TTNGGGGTTT GAAATTATTC TGGAACCNTC CTTTTTAAC GTGGAATTNT TANCCCTTC	420
TTTTTNGGGG CAAGAAGTTC CCTTTTTGG NGCCCCAAAA CCAG	464

(2) INFORMATION FOR SEQ ID NO:781:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

AAAACGGGNA GTAAGGCAGT GGTGGAGATG GAGAGCCCTG AGCNTCCACT NTCCTGGCCC	60
CCAGTNTTCC TACATAAGGC CACGGCCCGG NTAATGGCGG GGGCNAGCCC CA	112

(2) INFORMATION FOR SEQ ID NO:782:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

CGNATGGCCC TGTCCCTNAAA ACGGGGAGTA AGGCAGTGGT GGAGATGGAG AGCCCTGAGC	60
NTCCACTNTC CTGGCCCCCA GTNTTCCTAC ATAAGGCCAC GGCCCGGNTA ATGGCGGGGG	120
CNAGCCCCA	129

(2) INFORMATION FOR SEQ ID NO:783:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GGCACGAGCA GGCACGGAGC CTNAGCCAT CGCNATGCTG GTCCTAAGGG GCTCGTCCTN	60
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GAGGGGTCTT GATGCTGGGT GCCTGAAANA AGAGCTCGGG GAGCCCGCTG CAACCNAAG	120
GCCTGCCAG CGGGGAAGCT GCCAACCCCC TGGTGGTGGG AAGCCGTGGC CCTCCTGGGA	180
CCTCAGCCTG GAATTCCCTGT TCTCCCAGCT CCTNACCTGA GGCTANTTCC TGGCCTGGTT	240
CTGGCTTTGG TTGCNTGCCT CTTNACCCCT TTGAACCTGC CTTTTTTTTC TTCTCCTNTT	300
CCTGGGTGTN TTTTTTCCCA	320

(2) INFORMATION FOR SEQ ID NO:784:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GGCACCGAGTG GCAGCAAGCC TCTCCTGCC CTTCAAATTA GCCCATCGAA TGGTAAGGTT	60
CCTNAACTTT GGGCAGGTNA AGANCTGTGA AGGTGGAGCA GGTAAAGGGG GTCACCTACT	120
CCCTGGAAGT CGTTCCCTGGG CCCGCTTATG TGCCACAGAG GACCTGCCCT TCCCACCAGC	180
CGNGTCGTGT GAACTCCTTC AAGAACCGAGC TGGTCACCCG GGAAAGGGGA ATGAAGCCTC	240
TATTNACTGT NTTCATCTTA CCTGGGCCCC TGGGGACTA CCAGTGGTTT NCACTNCCCC	300
ACCGGACTGG NACTGTNTCC CACCGGGGGG NCAATTTCAGGAGTCCTG ATGTTCANTG	360
AAAANCCTGG GNATGGGTTG GTTGGTTCA AAGAGGTTT TTTGNCCATA AAGGAGGNGG	420
GTTGGGTTCT T	431

(2) INFORMATION FOR SEQ ID NO:785:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GGNANAGNCG TNAAAATAC CCCTAAAAGC CAAAATGGGA AAGGAAAAAG ACTCATATCA	60
ACATTGTCGT CATTGGNCAC GTTGTNTTCG GGCAANTCCA CCANTACTGG NCCATCTAAT	120
CT	122

(2) INFORMATION FOR SEQ ID NO:786:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GGCACGAGAG AAGATAAAAA AGTGAGGTGG ATTAAAGGGC CCATAGAGGA AGCCACCTGA	60
ACCCCCGGCC TGGCCTCCTT NTCGGCTCTT CCTCTCCGGG GGCCCAATAG GGCTGTGCGT	120
TTAANAGGCA GTTGGGAGAC CCTGGTGGCC GGTGGTGGTC GGTCACTGGG CACGCCGCTG	180
GAGCCAATCA GAATCTCCCG GCAGTTGGTT CCCGGGAGGC AGAATCTGTT NAAACTGACA	240
AAGCCCACGT TTCCGGGTCC CTGTTTCGGG GAGTCGGGGA CTNATTGGGT CACCCCGGGT	300
TAGTCGAGA CTTTAGACTN GAGCTGTTT NGGTNCACTC AGGGAGGCNA GTT	353

(2) INFORMATION FOR SEQ ID NO:787:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

CACGCATNCA ACAAGGGCCC CTCGTACGGN CTGTCGGCCG AGGTCAAGAA CCGGCTCCTG	60
TCCAAATATG ACCCCCAGAN GGAGGCAGAG CTCCGCACCT NGTATCGNGG GANCTCACCG	120
	120

(2) INFORMATION FOR SEQ ID NO:788:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

GGCANAGAAA AGCCAAAATN GGAAAGGAAA AGACTCANAT CAACATTGGT CGTCATTGGA	60
CACGTAGATN CGGGCAAGTC CACCACTAAC TGGCCATCTN ATCTATAAAT N	111

(2) INFORMATION FOR SEQ ID NO:789:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

ACGATTCACA CCGTAGCCCT GGGGNAGACA NTGATTGAT TACAAAACCA CCCAGACCTT	60
CCGGCTTGCC ATCATGNNTG TG	82

(2) INFORMATION FOR SEQ ID NO:790:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

CATTCGTACG CGGGTGTGGT GTCAGTACAG CCACAGCCAG ATNCAGGAGC ACGTGANGCC	60
TGCNCANCCC AGCATCCGNG AACGTGCAGG AGCTCAAGGA AGCCATCAAG AGCCTGCATT	120
GGAT	124

(2) INFORMATION FOR SEQ ID NO:791:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GGCANAGTGA GTGACCGGCC TTTNAAGTGC GGCTACTGTG GTCGTGCCTT TGCCGGGGCC	60
ACCACCCCTCA ACAACCACAT CCGAACCCAC ACTGGAGAAA AGCCCTTCAA GTGCGAGAGG	120
TGTGAGAGGA GCTTCACGCN GGCCACCCAG CTGAGCCGAC ACCAGCGGAT GCCCAATGAG	180
TGCAAGCCAN TAACTGAGAA GCCCAGAATC AATCGAAGTG GGATTAACGG GNTTGACTGG	240
TTGGNATTAA AACTGCAGGA GAAGTCCATG NTTNAA	276

(2) INFORMATION FOR SEQ ID NO:792:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

AAGACCGGNC TTCNTAATAA NCTTAATTAA TTCCCCGGN AATGTGGATT TTTCCTNGGA	60
AGGACGAGCA GGAGCTTGC ATCACCATCA AGTAAACTGC AATCTCCTT TTTTANGAAN	120
NTCTGGAGG AATGAATTG AACTTAATNA AGCAGNACAC G	161

(2) INFORMATION FOR SEQ ID NO:793:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GGAGAACAC GTGGNACAGC ACCATGAACA TNTTGGCGG GGNAGGCAGT NCTGGCCGGT	60
AAGCCCCTCA AGTCGGGTAT GAAGGAGCTG GCCGTNTTCC GGGAAAGAAGG TCACTGAGCC	120
AGCACCGGCA GATGGGCCAA GGNTGGCAAG CATCACCTTG GCCTGGAGNT AGCCAANAA	180
GCTNCGAACC ACCCCCTGCN AGGACTCCCT GGCCAACAGG GAACTGG	227

(2) INFORMATION FOR SEQ ID NO:794:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GGCANAGCTG AAACGGCAG AAGACAAAGC AAAGCTAAA GAGCTGGAGA AACACAAAAT	60
CCAGCTGGAG CAGGTGCAGG ANTGGAAAGAG CAAAATGCAG GAGCAGCAGG CCGACCTGCA	120
GCGNCGCCTC AAGGAGGCAG GAAAGGTAAG CCAAGGNAGG CGCTGGAGGC AAAGGAAACG	180
CTATATGGAG GAGATGGCTG GATACTNGCT GATGCCATTG AGAATGGCCC ACTTTGGGAC	240
AAGGGAGATT GGCTTGAAGA GCGGGGTNGA GTTCCCTNGC ANGCAAGGGA GGTGGGAGGG	300
CACTTNN	307

(2) INFORMATION FOR SEQ ID NO:795:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GGCAGANNCT TTGGATGACA ACGTCTGCAT GGCCTTCCA GGTCTNCACC GCCGATGCAA	60
GGNTAGTNAT CAACAGGGCC CGGGTGGAGT NCCAGACCCA CCGGCTGACT GTGGAGGACC	120
CGGTCACTGT GGAGTACATC ACCCGNTACA TCGCCAGTTT GAAGCAGCGT TATACCGAGA	180
GCAATGGGCG CAGGCCGTTT GGNATCTNTG CCCCTCATCG TGGGTTTCGA ACTTTGAATG	240
GCGCTCCTAG GCTTNTATNA GACTGACCCC TTCGGGGCAC ATAACCATGC NTGGTAAGCC	300
ANATGCCATA GGCCGGGGGG TGCCAAGTTC AGTGCCTGAG TTNCCTGGNN GAAGGAATTAA	360
TAT	363

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GGCANAGNCT CAAACAGTGC AAGATGTCTC TAAACGGCA GCGTGGNGGA GTNCTGGTGT	60
GTAAACCCCCA ACACCGGGGA AGCTGATCCA GGGAGCCCCC ACCATCCGGG GGGACCCAAG	120
ATNTNAATCT CTTCTACAAT GAAGGCAGCA GGTGGCTCGC GGGGTGCACA CCCAGCGGNA	180
TGCAGTAGAA CCGCAGCCAN CCGGTGCCCTG GNGCCCTNA NCCCC	225

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

AGGCACACAG GACCATAAAG GTNCTTCTCC TNAAAGGGCT GGGGGCCCTT TNCTTNCGCC	60
TATAATTGGN ATGANAACCTT CAACCCGNGT AAGCACCTGG AGTTGAAGGG AGGNAGAAC	120
CGGGCCAGCT GTCCTGTCCT CCGCCCANAG TGACCACCCC GGNTATGCC AGCNAGCCTC	180
CNGGGAGCGA GAGTCCTGCT GAAAGGGGCC ANGNTGGTTT TGGTGAGNAG CTGGCCTATC	240
ATTAGGGNGT TTGGGCTTCC ANCTGGTNGT NAATGCCAA CTTAGGGTT TCCTT	295

(2) INFORMATION FOR SEQ ID NO:798:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

GGNANAGTGG ACAAAATTGN GGAGACCGCA TCAATTAAAA TCCAGATCAT TAACCGTCCG	60
GNTCCACCCC AAATTNTGAA AGATTAAGGA TGTCTGGGA GAAAATNTCG CTCTCANATG	120
GGNCTCCACC AAAGGAATG A TGGNAATGC CTGCTTATCA NAGGCTTTN CCATTNAAAA	180
GGCTGACAAA AGAGGCTGGA ATGGTTTAC TGTNNATTGA AGCTTTNTTC AT	232

(2) INFORMATION FOR SEQ ID NO:799:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GGCAGAGNAT CAAATATTAT TTTATTATT ATTAAATTAT TAATCAAATG TTTGTGTTAGG	60
TCTATTCTG GGATCTCTGT TCTATTCAT TAATCTGTG TCTGCTCCTC TACCAATACC	120
ACACTGTCTT TATTACCGTC GCTATATGGT AAGCCCTGAC ATCATGGAAT TTNCCTCTNT	180
TTCATACGTT TTGGCTATTC TAGTGTCTTT CCCTTCCAT ATAAATTTA AAATAAGCTT	240
GTCTATGTCT ACAAAAAAAT CTTGCTGNG NATTGGGG NAAGGAATTG GCATTTAAAG	300
CATCNCGGGT CATGGTGGGC TTCACGGCTG TAAATCACAG CACTTNGGA GGGCTGAGGG	360
CAGGNAGGGT TGTTGTGGG GCCAGGTGGG TNNTGGAAC T CCCGGNT	407

(2) INFORMATION FOR SEQ ID NO:800:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

GGCAGAGCAA AAAGCAGGTC AGACAGGGCC AGGTCAAGA GGTATACATC TTTAATGCTC	60
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CTCANTTCT TGCAGACCAC AAGGACCAGG ATGACCAGGC TGTTTCCNG AAGATTGANT	120
ACAAACAGGA GGCAATAAAA GACAGCAAGG NGCAACTTGC CATTNTTTG ATTAAGTNCC	180
GCATCACAGG GGCTTGAGAA AGATATCAGG GTAGTAGTAG TCGGTCACTG TTGTCACACT	240
GAGGTCAAGT GTATAATCCA TCAAGGCAGC GGGACCTGGT CACNGAGGAC ACATAAAAAGA	300
CATTCCACTC CTTAAAAACA TTTTTTTTT TTAAAAATTA GGGGGATGTT ATGGGACTGA	360
ACTGTGTNCC TCCCCAATTC CAGTTTGAG GTGCTAACCC TCCGGTGTGG GTGTGACCAT	420
TGGGGTGGGN NNGACTATTT NGGGNCCTTA AAGTTGTAAT TAAGGTTAAA T	471

(2) INFORMATION FOR SEQ ID NO:801:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

CTGGTGGGGN TGCTGGAGAT GCCTTGAAAT GGCTTGAAAT TTTGGGNGTT GATCCTNGTG	60
ACCAGTTTTT CCCATCCCAT NNTGGCATGC GGTCAGTTC CTGGGACCAT GACCNTGGTA	120
AGTTTGAGGG C	131

(2) INFORMATION FOR SEQ ID NO:802:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

CTGGAATTT AGGCCANTNA GCCCAGGGTC TGGNAACGCA AGGCCTAACCA ACCCAAATTG	60
GGGCACATTT TAAGGAGGTN TNAGGAATTT TAAGTCCCGG GGACAAGGGG GGGTTACCNC	120
ACGGAAAAT TGGTCNNTT	139

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

CAATTCTCCT ACCGCCAGTG GTNTGACCAA AACCGGATTC CCAAAANTTG CGCCATGATT	60
NTCGCCGCCG ATGNANTTCA TTCCTGGCAA CGGTATTCCG GTCGATAGCN TGGTTATTGA	120
CCGCAAAATC AATCCGCTAC AGATCAAACA AGACGGTGGC AAAGNCTTNA AAACTNCTGG	180
TGCTGTGGCG TAGTGATGAA GATGCGAAA CGTNTGGTTA TGGTGAAAGA NTTCAACGAA	240
CTGTGCCACT CACACGGTCT GGTAAGCATC ATTGAGCCAT NCGTCCGTCC ACCGNGTCGT	300
GGCGATNAAT TTCGATCGGN ACAAAGCGAT CATTGATGN CCGCCAAAAA GTT	353

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

GGCACGAGCA GCCCCCATT TTTCCCTCCG GCCTGGCGG CCCCTGGTCC NGGNNGCNAA	60
TGGAAGANCA AGGGACCTGC CGGGGGNC	88

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

TGTTGTTTG TNGTTTCATT TTTAAGACT CCCAGNTGGA CATNTTAATT GCTTTGCAA	60
TNACCTGCTT CAAGGATGTG GGAATTCCT AATTNTTNCT GTGAACCCTT TTNAATTCCC	120
CCACCATGCG TNTNGTGAAC ACCTTCACCA ATAACATAGT CATGTATTTC CCTGCTGCCA	180
TATTTGGTTT TTTTCCCACC TCGGGGGATC CTTTTTNTN ACTATNAAAA TNNGNTTCCT	240
CCATTCTGAA GGGT	254

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

TGGTGCCAT CNTAGACCCC CACATCAAGG TGGACTNCGG CTACCGANTT CACGAGGAGC	60
TGNGGAACCT GGGGCTGTAT GTAAAAACCC GGGAAATGGCT CTAACTATAA GGGCTGGTGC	120
TGGCCAGGCT CAGCTGGTTA CCCTGAACCT CACTAATCCN ACGATGAGGG CCTNGTTGGN	180
TAACATGTTN CAGNTAATG	199

(2) INFORMATION FOR SEQ ID NO:807:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

CCCANGGTGT NANCGACATT GAGGAGGGTT TATTAAGTGN CCGTGGTCAT CGACCCCTTG	60
AACAAGAAGA GAGANGTGGC TCACGGCCTG AGGCCTAACCC NACCGACCNT CAGTGGAGGT	120
GGCTATCGGG NTCGTCC	137

(2) INFORMATION FOR SEQ ID NO:808:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

CTCTTCAGCN TCGAGGTCAC CTCCACCTTC TTTGCAGTGC GGGNACTACT NGCGGGGGCT	60
TCTTNGGTTG CCCCTTCAG TGGCCTTNCA TCTTCCGGGT TTTTGGGCGT CTNGGG	116

(2) INFORMATION FOR SEQ ID NO:809:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

TTACCAAACNT GANGCTGATT GAGTATTGNG GGAGCTTTGG TTCGGAGACA GGCAAAGGAG	60
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NCATGTTGG TGAGNTTGGT TTTTCAGTAC TTCCAGAAC C GNGANTGATT ATGGAAAGGA	120
CCTNATGGAG AAGGT	135

(2) INFORMATION FOR SEQ ID NO:810:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GGNAGAGGGC AAAGGTGCTA TTAACCACTA CGTAANACCT GTAAAGCCTG GCCGCCTTGT	60
TGTAGAGATG GGTGGNCGTT GTAAATTAA AGAAGTNCAA GGTTTCCTTA ACCAGGTTGC	120
CCACAANTTG CCCTTCGCGAG CAAAGGCTGT NAAGCCGCGG GAANTCTAGA GAAGATGCGA	180
AAAGATCAAG AGGAAAGAGA AACGTTAACCA NCCAGAACCC CTGGNACATT TNAGCCGATT	240
TAGCCACTGC CCAACATNCT GGGGCTTACG GGAAAGTTAC TTGGGCCCAT ATGAATTGAA	300
CCCACAAGGG GGAANTACTG GGGGCAAGTT NCTTACATGC CCCAAANGTG TGTAGTGNGT	360
TTTAGGGGGT TAANTGT	377

(2) INFORMATION FOR SEQ ID NO:811:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

AGGTGAAATG GATGANAATT CANTNTCCCC AAAGGCTTGT AACGANTTTA AGATCANTGG	60
CTACCCAAA CGGGGNCAGN AAACGGAGAA GCACAAACNA AACTNAATGC NTCCAATATC	120
GAGGATCANT NTGAGANCAG AAGCCAATGT NAGTTTGCA AGTTGGGATG TTGAGAAAGA	180
CAGCCATCTT TGNCTTCAA TATTCCCAC GTCAGAACCA AGGTTCGATT CCTAGGAAC	240
CCTTCCAGCT CTTACAACTN TGAACGGTTT CACAAACAGAT ACTTGATCGN TTCTGGAAAT	300
GAAAGNTGGC TTCTTTAAAA TCCAACCAAA GGNGGGGTC CGCTACCTCC ACTTTCACAA	360
GGAGGAGCCC GTGGGTGGNA NCCC	384

(2) INFORMATION FOR SEQ ID NO:812:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

CTGGGAAAAG ATTGTCAGGN CATTGCCATT AGGGAGCTAA ACAGAGCGGG CTTTACTTTN	60
TTNAACCCTC TGNGAGATTN ACCGGCATTC TTAGTCTACT GTGAAATTCC NTGGGTCTGG	120
G	121

(2) INFORMATION FOR SEQ ID NO:813:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GGGGGCCTGA TGTGCTCAC A GCNACAGTTA GTGGGAAGCT GCCTACACAG AGCATNACTT	60
TCCAAACGGA GTCCAGTGTG GCAGAGCAGG AGGCAGGAGTT CCAGAGCCCC AAGTATATCT	120
TCCACAAC TT CATGGAGAGG CTCTGGNCA TACCTGAAC ATCCAGCAGC TGCTGGAGNC	180
AAACTGTTTC CGCATCCAAT GCTGATCCAG CAGGCCCTCC GGNAACCAAG CGCTGNAATT	240
TNTCCACTTG CCTACAGCTT TGTNACGGCT CTTNACATCT TTGGTTAGTT CACCAAACCC	300
GGTTGACCCA AGAGGCAGTT TTCAAGTTG NTTGNNGAAG GCCC	344

(2) INFORMATION FOR SEQ ID NO:814:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

ACCTGACTTA ATTCTGTCGN ATACCACCTG TTTCTGTNCT TCATTAAACA CAGGAGGTG	60
ACCAAAACGT TTCCCTGCGC CGCGGGCTCT NACTATCCCG GAATGAGTGC GTTCAAGTAA	120
AAGGTCTCGT TCAAATTCAAG CGACTGCTGA AAATTACTTG CATCATCATT TTTCCGTNG	180
GGNCTTGGTC AGGTCAATGC CCACCCCAAT GGTAAAGGCA AATGCACTGN NGATNACC	238

(2) INFORMATION FOR SEQ ID NO:815:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GGCANAGGGA AATNAGTTT TGGCTAAACT TGGAACGTGC GTNATACCGC ATCCAGGAGA	60
AACGGGAGAG CCCGGAAGTT CTCCTGACTC TGGATATCTT GNAAACATGG CAAGCGCCTT	120
CCATGCCACC GTNAGTTTG AACACTGAAC ACAGGTCTAA AACAGGCTTT GGGAAACTGT	180
GAAATGAACT ACAATCCTCT GAATGAAAGN TTTCCCTCTG AAATGGATTG GCTGTCTGCC	240
ACGGGGCTGN NACAAANTAA GACAGGCGCT TGTTGCCATT TTCACACATT TNAGG	295

(2) INFORMATION FOR SEQ ID NO:816:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GGCAGANAAG GTTCTGTGGG CTGCNTTGCT GGTACACATTC CTGGNAGGAT GCACTCNAAG	60
GTGGAGCAAG CGGTGGAGAC AGAGCCGGAG CCCGAGCCTG CGCCANAACN CGNAGTGGCA	120
GAGCGGCCAG GCTGGGNAAC TGGCACTGGG TCGCTTTGG GAATTACCTG CGNTGGGTGC	180
AGACACTGTN TNAGCCAGGT GCAGGAGGAG CTGCTTCAGC TCCCCAGGTT CACCCAGGTA	240
ACTGAGGGGC GCTGATGGGA CGNGAACCAT GTAAGGAGTT TNGAGAACCA AGTCTNNAAC	300
CAACATGGTG GAAATTCCCC GTTTTTTAT NA	332

(2) INFORMATION FOR SEQ ID NO:817:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GGCACAGCTT GGCCTCCAA AGTNCTGGGA TTGCGGGCTG GCTGCACGGG GGCAGGAGCC	60
TGNCCTTGAT TCAAAGGTTC CTGAGAGACT CGGTCTCTGG GGCAGAGGCC TNGCAAGGG	120

GACCTCGCTG GGGTGTCTCT NTTTAGCCA CGCTNCGGTG TTTCTGGTC CTGTAACCCA	180
CGTTTAAGCA GCCTGTGGTG CTGGTGGCAC AGGNGAAGGA AACCGAGGTC AGGGNAGCCT	240
TTGGGGCTG CTTTGNAGGG NACAGGCAGN TCCT	274

(2) INFORMATION FOR SEQ ID NO:818:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GGCACGAGGC GGCAAGAGCT TCANCCACAG CTCGCACCTN ACCGCGCACC AGGCATNCCA	60
CCGTGGCGTG CGGCCCTACC ACTGCCTCGA CTGCGGCAAG AGCTTCAGCC GGCTGAGCCA	120
GTTCGAACCC CGGNATGCAG CTCCGCNAGA CCCCAGTTCC CACGGAGCCC CAGGNAGTTA	180
CCGTNTCCCG GAGAAAGCCC AACGAAGGAG GAGAAGGGCG CCCCCGGAAGA GTNGCGAGGA	240
GGGCCTGGNC CCTNAANAGT NAAGGTGGGG CAGGAAGAGC TTACCGGT	288

(2) INFORMATION FOR SEQ ID NO:819:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GGGGCTGGAC GCANGTGCAC TAANCATGGG TGAACCCCAG GGATCCATGC GGGNTCTAGT	60
GACAGGGGGT CTNGGCTTGT AGGCAAAGNC ATCCCAAAGG T	101

(2) INFORMATION FOR SEQ ID NO:820:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

CATTGNATGT GGTTACCACC TTTNGTNNAAT CCACTCATCC ATCGATGGNC ACGTGGGTTG	60
NTTCCACCTT NAANCTGCTG TGAAATAGTG CAGTGTACCC TNTAACATG GGTGTACTGA	120

AGAGCTCTTA TCAAGTGCCT TGANAACATC ACTGGAAAAT GTCCATGGGA CTCTGAAAGG	180
TTGCCANAAG AATGGCNNGA GGCTCTATNA CGA	213

(2) INFORMATION FOR SEQ ID NO:821:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GGCAGAGNCA CCCTTCACC CTTCCCCCTA TCCAGGACAG TTTCACCGAA ACCCCGGNGC	60
CCCGGNGGTA TCCTTGAGCG GAGAGGGCGG GGCGGGAGCA GGAAGGCCGC GCTGTCGGGA	120
AGGGGCGGGG ACCTGCCGN TTGGCCAGG TTTTGGACAC CTGGGCGCCC CTGGCCCTTC	180
GGCAGAACAC GGTGCCGGAC AGTAAGAGGT CCAGCGTTA GTGGGCGCGG NCGGCGGCAC	240
GTAAGGCTGG AGCCGCCTGC ATTTTCCAGC AATGAACGGC GCCCTTTCC CCTTGCCCGC	300
AAAGGGTCTT TNCAGGNCAA CTTTCGAGGC CCTNAATGGT GGGTTTTCCC TGGTTGNTTG	360
GGGTTTNCTT GGG	373

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

GGCANAGACG CGGAGAAATNA GGAGGGAGGAT GACGTTCTG AAATNAACAG CAGCTTTACA	60
GCCGTTACTG GTGAACAAAGA GGAGCACACT CTCCAAGAAA CAGCATTACC ACCTGTGAAA	120
TAGTAGCATC ATCGCTGCTC CCATCACGGA CCCTTCTCAG AAGTTCCCTC AATACTACC	180
TCTTTCTGCA GAGGATAATT TAGGTCTCT ACCTGAAAAC TGGGAGATGG CCTATACTGA	240
AAATGGAGAA GTCTATTTA TAGAGTAAAA GTATNACCAT TATTTNTACC TNAAATCTCT	300
NCTACTCTTT GTTTANCCT TGC	323

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GGCANAGNCA GACGATCATC CACTCTGGAT GTCATCCAAA TGGCTTCCA TGANTGTTT	60
AATGCTAGAT GAAAAACGTG TTATGGTGGA TGCCAATGAA AGTTCCAATT CAAAANATGT	120
TTGAAAANGT GGGTATCACT ACCATTAAG TTAACATTG TGATGCCAAT TCCCTGGAG	180
GAGGCTTCCA TTGCTGGACC TCGGAATGTC CGGCGNNNGNG GCACCTTACA GTCTACTTG	240
GACTAACAG GCCTGATGGA GCTNTGGCT GGCCTCAGAT ACACCTNAGN AAGCTTAGGG	300
GCAAGGTTCA TTCTNTGCTT TNAAAAGTG GCATGGAAC GTAGTGGCTT T	351

(2) INFORMATION FOR SEQ ID NO:824:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GGCAGAGNCA AGAGCGAGTA CTCAGTCTCA AAATAAAAAA AAAAGGGTGA ATTTGCCTG	60
ACTCTTATGG CTGTGGTTA AAAGAACATAG AGTTTAGNTC GGGCATGGTG GTCANCCCT	120
GGATAATCCC AGCACTTGG GAAGGCCGAG GTGGGAAGAG CAAACTCCG TCAAAAAAAA	180
AAAAAGGGAA AAAAAAACC CNNGNNCCNG GAAAAN	216

(2) INFORMATION FOR SEQ ID NO:825:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

AGGNNAACC TTCGAGCAGA CCAAGTACCT GGNGGGCCCG GAGCGCGCCT TNNTGCCTA	60
CTCGCTGGC ATGACCGAAA GCCAGGTGAA GGTCTGGTTC CAGAACCGCC GGACCAAGTG	120
GCGCAAGNGN CATNTTNGGN AGAATGGCGT CGGCCAAGAA GAAGCAGGTA NTCGGAACGC	180
CGAGAAAGCT GAAGGTGGGN GGCTCNGNAC GCGGNAGGAA CGACGGACGN AATTACAACC	240
GGCCCCTGGN ACCCCAACCTT CGGNACGGAC GAGAAAGATT CACGCGGGCT GCTNCAGGAA	300

AGCACAAAAC CCTTCGAAAC TTGGCGCTG GTTCANCCG TTCGGNCGGC GGTGCGGGGG	360
GNACGCCTT NTTTAGGTAC CC	382

(2) INFORMATION FOR SEQ ID NO:826:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAAGGAAGCN GGGGACAGGN TGAAAGCAAC AACACCTTN CAGACAGTNG ACCGGCCAA	60
GGACTGGTAC AAGANGATGT TTAAGCAAAT TCACATGGTG CACAAGCNGG ATGATGACAC	120
AGACATGTAT AATANTCCTT ATACATACAA TGCAGGTTTG TNCAACCCAC CCTACAGTGC	180
TTCAGTCACA CCCTGCTTGC AAAAGACCCA AAACCTNCAG GCCTTTTTT CCAAAAAGGC	240
CANTTCCGGN CAACAGNCCC CAATTGNTTT TTTAAGGGTT	280

(2) INFORMATION FOR SEQ ID NO:827:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GGCANAGGGA AAGAAGGCAA TGATGTAGAT GAGGCTTCCG ATCAGAGCTG CAATGTTGGT	60
GTTGTTGAAG AAGACACTGA TAAGATAGCT CATGGCAATA ACCGAGAACG TGTAGTCCGA	120
AAAATACAGG AACAAAATGA ACCCATTNT TTTAGGGAAG AATATTGCCA AACTTGAGTA	180
TAATGATGAG GATCACGATG GTAACCAGTN AAAAATCCAA CACTCTCTAT AAGCCAGGCA	240
AAGAAATGGC TGCAGGAGTT CACACCCATC ATCTTCATG TACTGTAGGA AGGAAAATG	300
TGAGGCACTT GTTATGCTGA TATTCTTCCC AATTAAAATT ATTTCCCGTG TTGTGTTCAA	360
AATGTNCNGT TAGCCTCCG TATATGGANN AGGGCTTTT NATTATTTG	410

(2) INFORMATION FOR SEQ ID NO:828:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GGCANAGCGG CACGAGCGTN AAGGTGACCC TCCGACTGGA CACCCACCCT GCCATGGTCA	60
CCGTGCTGGA GATGGGGGCT GCCCGCCACT TCCTGCGCAT GCACAGCTGG CCAAGACCCG	120
GAAGGAGCGC GCACAGCTGC CTGCAGCCCCA CGCTGGNAGA TCAACCCCCAG GGCACCGCGCT	180
TCATCCAAGA AAGCTGAATG CAGCTGCGCG CAANAAGGCC TGGGCCTGGT TCCAGCTGCT	240
GGTGGTTCCA NATATAACGAG AAACGCCATG GATTGCTGCT GGGACTTGTT GGACGGACCC	300
TNGGGGCCAT GGTGGGGCCC TTTGNANTGA GCTGCTTGTT TCAAGGGCCN TGGGAGNGGA	360
CAATG	365

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GGCACGAGCT CGTCNANGGA ATCGGCGTTT ACTGGGGGCC AGGCCGTNGT TTAAATGTAG	60
GCATTAGACT TCTTGGCGG CNGACAGACC AAAGAGCGGA ATTTCATCCT GCAAAGCCAT	120
TGNAACAAGC AAAGACTCAA AACATCAATA AACTGGTTCT GTATACAGAC AGTATGTTA	180
CGAATAATG GTATTAAC TG AACTGGGTT AAGGTTGGAA GAAAAATGGG TGGTANGACA	240
AGTGCCAGGG AAAGAGGTGA TCCAACAAAG AGGACTTTGT GGGCACTGGN GGAGGCTTTA	300
CCNNGGGTT GGACATTNG TGGATGCCNG TTCCTGGTCC TTTCGGG	347

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

ATGAAGTCCA GCGGCTTCCT CCGAAAAATT CTGTACANAA GGGTGGCTGT TTGGGGCANC	60
AAGTAATGCG TTNAAGGGNA GGCAGGTGGG NGTGAAGGAG	100

(2) INFORMATION FOR SEQ ID NO:831:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

AGGTATGGTC AANCTGACGG CGGANTGGAT AGAGCAGGAG GCGCAGTGCA CCAACCGGGT	60
GCGCAACCGG GAAGCTGGAC CTCCGGGGGT ATAAAATTCC CGTNATTGAA AATCTCAGGT	120
GCTACGTTAG ACCANTTGTA ATGCTATTGA ATTTTNCTGN ACAATGAAGA TCANGGAAAC	180
TNGGATGGTT TTCCTTGTT GAGAAAGACT GTAAAAACAT TGTT	224

(2) INFORMATION FOR SEQ ID NO:832:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GGCACAGCTC AGTACAACAC TGAAATTAAA CTGCCTTGTN CATGCTTTCA TGTCTCAAAT	60
CAAGGCCTAA ATGAGTAAAA AGATGATTAC AGATTACCTA AAACCCTTAA CCAGTTTGG	120
TTTTGAATT ATGCATATGC TGTTGGCTTG CAATTGAGGT TTTTAAGTTT CTGTTTATGT	180
GAACTTGTTT GAAAACATTG GATTCGTCTT CTCTCCCACA GTTTCTACTT GNANCCTTAG	240
TTAGCTTTTT NNNGGGGG	258

(2) INFORMATION FOR SEQ ID NO:833:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

TTTCAATAT CAGACCTGAC CTATAAGAGA TGCTAAGGGG AGCTCNTAA TCTGAAAGGA	60
AAGGACATGA GTNAGCAATA NGAAATCATC CAAAGGTACA AAACTCACTG GTATCAGTGA	120
AGTNCACAAG ANCAGATTGG CTTGACACAC TAATTGCCGT GTGTAAGCCA TATTTGAGT	180
AGGAAGACTA CAAAGCCTAT CAAAANTTAT NATTNCAATT TTTTAAGCGN TNAATATAAA	240

ANGNTNAAAT AGGAAACATT GGCCGGGCCA CGGTGGCTCA CACCTGTTAA TCCCAGCANT	300
TGGGAGGCTG AGGCAGGTGG TTTCANGAGG TCCAGTNCGA GAACCANCCT GGGTTAACAC	360
GGTGAACNTC CGTTCTCCA	379

(2) INFORMATION FOR SEQ ID NO:834:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

TGAAATCACA GGCGCNTTGC TGGCAAATT CATAAAACC ACCATGCCTA AAACAGTGTC	60
ACACTGTNTT TCAACTTGAN TCCTTGTAAA ATAGTGATTT TTTTTTTTNN TTTTTTTTTT	120
TTTTTCCCCCT TAGAAAGCAG CCTGGCGCG GNNGGCTCAGG CCTGTNAANC CTAGCGTNTT	180
GGGAGGCCNA GGTGGGCAGT TTGTTTGAGC TCAGGGGTTC GAGACCNGCC TGGGTAACNT	240
GGGCAAAACC CCANTTTAC TAAAAATACA AAAATTGGCC GGGCGTGGTG GCGCTGTCCG	300
TNANACCC	308

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GGCACGAGCT CGTCCNTNCÀ ACGACTGCAA TATGGCGCGT CAGTGCAGGG CAGCATCCTC	60
AGCCTCTCGC TCTTGCGGGC GCCTAAAGCC CCGGACGCTA CTGCTGACAC GGGGCGCCAC	120
GAGTTCACCT ATGCACTGAT GCCGCACAAG GGCTCTTCC AGGATGCTGG CGTTATCCAA	180
GCTGCCTACA GCCTTAAACT TCCCCCTGTT GGCTCTGCCA GCCCCCAGCC CAGCGCCCGC	240
CACCTCCTGG GAGTGCCTT TCCGTGTCTT CACCCCGGGT CGTATTGGAG ACCGTCAAGC	300
AGGCAGGAGAG CAGCCCCAG CGGCCGTTCG TTGGTCCTGA GGNTGTTATG AGGNCCAAGG	360
GCAACCAAGT TGGGATTNGT TGGGNTGNAA	390

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GGCACGAGCC TACACAGAGT GCTGCTGCCT GTATNGAGAG GCCTNGGGCA TGGNCTGCGC	60
CCTCTGCCCT CGCGAGGACT CAGATGACTT CGAGGCCCTG TGCAATGTGC TACGCCCCCC	120
CGCATATAGC CCCCCGCGAC CAGGTGGCTT TGGACTCCCC TACGAGTACG GCCCAGACTT	180
AGGTCCACCT TACCAGGGCC TCCCATAATGG GGCTNAGTTG TACCCACCAC CTGCGCTACC	240
CTACGACCCC TACCNACCGC CACCTGGGNC CTTCGNCCGC CGGGAGGNTC CTTATGGGGC	300
AACCGNTTC GACATTGCCA GACTTGAGG ACGATGGT	338

(2) INFORMATION FOR SEQ ID NO:837:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GGCACGAGAA AAAAAGATAAC CCAGATTCCA AGGACCTCAC GATGGTGCTG AAAACCTATG	60
ACACCAGCTT CCTGGACTTT CTCAGAAGGT GTTTGGTATG GGAACCTTCT CTTCGCATGA	120
CCCCGGACCA GGCCCTCAAG CATGCTTGGA TTCATCAGTC TCGGAACCTC AAGCCACAGC	180
CCAGGCCCCA GACCCTGAGG AAATCCAATT CCTTTTCCC CTCTGAGACA AGGAAGGACA	240
AGGTTCAAGG CTGTCATCAC TCGAGCAGAA AAGCAGATGA GATCACCAAA GAGACTACAG	300
AGAAAACAAA AGATTAGCCC CACGAAGCAT GTTCAGCATT CAGGTGATCA GCAGGACTGT	360
TTCCAGCACG GAGCTTGACA CTGTTNAGCT GCCTCAACTT GGTAGACGGT CCCAAGGAAG	420
TCAGAGGCAG TTGTCGGGGG CGGGAGGTGT NCATGACCTT CCCAGGGCAG NGCAAAAATT	480
TTTCCTTCAA GGACACA	497

(2) INFORMATION FOR SEQ ID NO:838:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GGCACGAGGC AGGGTGCCTG TNATTCACTG TGTTATTGGA TTTAAATCAA AGTGATTCTG	60
GGGGAAGCTA TGCTCTTCA GTGGATAATA AAATTGGTAA CTCTATTGTA AACATGTCA	120
ATGGTGTGTG AAGAAAATC AACCAATCTG TAGGTGTTGA TAACTAGACA GTACTGTGTA	180
TGTCACGTGC CTGTNTGGGA TGTNCACCTC CAGCATGGTA TGTGTTAGCG ATGTGGNTCA	240
TGCCAGAGN TCGTAGATCC TGTTTGCCCC TTTGCACATG GATCGTATGT TAAGCTNTTT	300
NCTTTTNCAT TAAATGAATT TT	322

(2) INFORMATION FOR SEQ ID NO:839:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

AGTACATTCA AATGTGGGCA NCTCANCGCC AGAAATTCCCT GTTCNCCCTG AGCCAGCATA	60
TCAACTGGGT NCGCTGTGCC AAGTTCTNCC CCGACGGCGG CTCATCGGGT CTGCCATTAA	120
TGACAGGNCT GTTAANGCTG TGGGGACAAG AGCCAGCCGG GAAATTTTC CACTGGNNNTT	180
NTAGGCATGG GGG	193

(2) INFORMATION FOR SEQ ID NO:840:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GGCAGAGAAG ACTTCAACTC TNTCGGATGC TCAACCTCAC TGACCGGCAA GTNAAAATCT	60
GGTTCCAGAA TCGCAGGATG AAAGAAAAGA AACTGAACAG AGACCGTCTG CAGTATTCA	120
CTGGGAAACC CCTTATTTG AAGAGCTCCA GGTAAGCGCC CTCACCCAG CCCCACTCAC	180
CCACCCCTCCT TCCCACCAAGC CTGCTCTCCG CAGCCCCACT GTCCCTTGGG TTTAATGAAC	240
GTCTCTTCTT CTGTGGGAAT TTCACGATTC CTTCCACGG TCAACTCGGG GACCTTCCCA	300
GCGNACCATT GCAGCCTGCG GGANGAGGCC GGGGANTTGG CCGAGNNNGGG TTCNTANTAA	360
GGGGGGAAAA TTGGGGGCCT GGGAGATTCC ACAAGGAGGG GCGGGGTTNA AGNTTNCCAA	420

AAGNCCGGGT TTTTNANCCA ANAGGNCCGG GTTACCTTT TTTTNCCAA AATGGGTTTT	480
TNATTAGGGG G	491

(2) INFORMATION FOR SEQ ID NO:841:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

CGGAAANTNT GGGTNCCCCG GGNCTGCAGG AATTGGCAN AGGGTACTG AACGCGGTTTC	60
TGGGAGCAGC AAGCCCACGG GTAGCAGCCG AGGCCAGA ATGGCCAAGT TTCTTCCCA	120
AGACCAAATT AATGAGTACA AGGAATGCTT CTCCCTGTAT GACAAGCAGC AGAGGGGAA	180
GATAAAAGCC ACCGNCTCA TGGTGGCCAT GAGGTGCCCTG GGGGCCAGCC CGACGCCAAG	240
GGAGGTGCAG CGGCACCTGGC AGACCCACGG GNATTAGACG GAAATGGAGA GCTGGGATT	300
NTCCACTTT CTGTACCATT ATGCACATGG CAAATANAAC AAGAAGACCC AAAGGAAAGA	360
AATTNTTTCT AGGCCATGT TTTGGATGGG TGGGGACCAA GGGAGGAAGG ANAAGGGTTT	420
AACGGTCAT GGGNGTTCC GAACCCTGGC GGNTTCCAAA AAANACTTNA ACGGGGGTTTC	480
TTTGGGGGG	489

(2) INFORMATION FOR SEQ ID NO:842:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GGCAGAGNAA GGAGCCCACC TGGAACCTCT GGAAGTACCT AGTAGCCCCA GATGGAAAGG	60
TGGTAGGGGC TTGGGACCCA ACTGTGTCAG TGGAGGAGGT CAGACCCAG ATCACAGCGC	120
TCGTGAAGGT AAGCTCATCC TACTGAAGCG AAGAAGACTT ATNAACCACC GCGTCTCCTC	180
CTCCACCACC TTCATCCCGC CCACCTGTGT GGGGCTGGAC CAATGGCAA CTTCAAATGG	240
GTGCTTCAA AGGGGAGGAG ACCCACTGGA CTCTCCTTTC CTTTGACTTC TTNATGGCCA	300
TTGGGTTCCC CATNATTCT TTGTGGGGGG GAAAAATTTC TTAGTNATT TTGGATTNAA	360
TTTTTGAAA TTCTTTAAC CAGGCAAACC AAAATTAGGG GGAAACTTNC CCTNGGGGN	420

CCCAAT

426

(2) INFORMATION FOR SEQ ID NO:843:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GGCAGAGGNN ACATCTCCGC CAGCAAGATG GAGAAGGCGG CACANCGNAG GGCCAGGGCC	60
ACGGCATCCA AAGCCACACG CTGCATCAGC CTGGGCTCTG GGACCTGAGG GGGCATGAAA	120
CCCGTGGGA TGTCGCCAGC CACGCTCGAG CCAAAGNGCT TGTGGAGCTG NCCGAAGTGC	180
GACACGAGTN TGGCCACCAC GATNTACCAG CAGCTCCGTG GGNAGCGGCA CCCTCAGGCG	240
GTGTCGGTAG CGGTCTGAGA GCTTCTTCGC GGCTNGCAGC ACCGCCAGCA CACCGTGNTG	300
GTGGACCACG TCGCACAAAGT TGGCCTGCCCG GGTGCCNGCA AAAGTTTCAG CCATGTNAAG	360
GACCACCATG NCGGGNCCTT GTTGCC	386

(2) INFORMATION FOR SEQ ID NO:844:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

TGGCACGNA NTGGAGAGCC GGCAGCCAGG CAAGGCCACT GAATTGCCNG GGAGCCGGGG	60
NCCAATTCCA CNAACACCAAG CCCAAACTGA AAGTCCCTCT TCCTTCCCCT GNCTGGNGCT	120
GCTCCGCCCT	130

(2) INFORMATION FOR SEQ ID NO:845:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GGCACANTGA ATGATCCTGG GGGAGCNTTT GNCCACCCAG GGCCCTTATA ATTTTGGNTC	60
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GGGGAAACG GCCCGCGCA TACAGGACCT CATCCGGTC CTGCTGCGGC ACNGTCTGTT	120
TCCCCCACCC AAGGAGACCT ATGCCCTGCA CCGNAAGCNG GCAGGGGCTT TCNTGGCCTN	180
T	181

(2) INFORMATION FOR SEQ ID NO:846:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GGCTGNNTAG GGAACAGAGG AGGCCGAAAT CCCTCCCCCA TGATTCCCTCA ACCNTTGTG	60
GNCAANGCA TCTTTNATGG GTACAAGGGA GAGGCTCTG GAAGAAGCTC CCTGNACACA	120
NTACAGGTGC CCTTTCCAA GGGCAAGAGN ANTTTGGGCT TCCATGG	167

(2) INFORMATION FOR SEQ ID NO:847:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GGCANAGCTC GAGGCTGTGA ATGCTCACAC AGCGCCTGGG AAAGGGGATN AACTCAGAGN	60
TGCCTTTTG GGTTACTTTT GTNCTGAGGT AAGAGAGGGC AGCAAGTGGA CCCCAGATGGG	120
CTGCAGAACG CGGTTCGCAN CAGGGACTGN TTACATAAGT TTTGGCAGTG AACCCCGGTG	180
AAGTNTGGTG TTCCTTATGA AACCTGCTT TCCACAGTTG AGCAGAAGAC ACCACAAATN	240
AAGNAGGGNA GCCCCTCCCT TCACTGNAGT GGGAGTNTTC AATGGGGACG TTTGTGAACT	300
CTGCCCTTGG GGACAATTG TGACTGCTTT T	331

(2) INFORMATION FOR SEQ ID NO:848:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

TTAGAGTACA GATGTAGCTT GANATTGAGA GAGGCTGAGG TGGAAGGATT NCTTGAGCTC	60
AGGANTTAA ACCAGCCTG GGCAACATAG TGAGATGTTG TCTNNANTAA AAAAAAAA	120
AAAAAAA AAAA	134

(2) INFORMATION FOR SEQ ID NO:849:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GAGCCCTTNA ATCTAACCTTC GAAGCCCTCG GACTACGCTC TGGACCTNAG CACTTTCCTC	60
CAGCAACACC CGGNCGCCTT CTAAACTGTG AACTCCCCGC ACTCCCCAAA AAGANTCCGA	120
AAAAACCACA AAGNAAACAC CAGGGCGTAC CTGNTGCCG AAGAGCTAAT GCCCCAACTG	180
GGAACTTCCG AGGTCAACTT GNAACTN	207

(2) INFORMATION FOR SEQ ID NO:850:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GGCANAGGAG AAAGCAGCAT CAGGTAGACT ACATTCTTAA AACCTGGACC CCTCCTNAGG	60
TCCTTAAGGA TTACTACGCG GNAGGCTGGC ATCATCACGA CAAAGAATGG GCGGGCCCTC	120
TACGTGCTCA GGCTGGGCA GATGGACACC AAAGGCTTGG TGAGAAGCGC CTCGGGGAGG	180
TAAGCCCTGC TGAGAATTAC GTTCTCTCCA TAAATGAAAG AAGGGGCTAA GGCGAATGCG	240
AAAGAGGAAT TACAAAANTT TTTGGTCGGC CTATTCAAGCT TCATGGGACC TGCCTGGTGG	300
GAECTTGGGAA GGGCTGAACA TGCGCCCACT TTTGGGAGGA CCTGGTTNA AAAGNCCTNT	360
TGGGGATTCA TCNNNGTT	378

(2) INFORMATION FOR SEQ ID NO:851:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

TCTAGTGCTG ACTGGTCCCC AANGTCCCC TGGNTCTACT GGTGCTCCTG GCAAAGAATG	60
GNCTCAACGG TCTCCCTGGT CNCCATTGGG CCNCCTGGTC CTCGCGGTAG CACTGGATGA	120
TGCNGGTCT GTTGGTCCCC CNGGGACCTA NTGGACCTGC TNGTCCCCTG GTCCTCCCGG	180
AGATGGTTTC GACTTNAG	198

(2) INFORMATION FOR SEQ ID NO:852:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

TTCATTGCCT TTGCCAGAA CTGGTGCATC AAGCGGCGGT CGCAGTCCAT CTACCTGCAG	60
GTGCTGACTG ANAACGATGC CCCTGAGCAC TACAGGGTGC TGGGCAGTGT GTGCCAGTT	120
AAGGAGTTTG GCCGGGCTTT CCACTGTCCC AAGGACTTCA CCCATGNAAC CCTGCCACAA	180
AGTGTTCGGT GTGGTGAGCC TGGCTGCCCG CCTGCACGCC CCCACTGCC CCGCACGAAT	240
NACCTCCTGG TGGCTACCGG GGCAAGGCATG CAACCGGTGC CAGNCCCCTT TTNGGGNACC	300
ACCTGNTTTT CCAGCCCTTN CAGANCCGGT NCCNCTGNTG GCCCTTGAAT TTAAGAGGGG	360
CTNCGAAGCA GGTTAAGGTT GGGATTTGG GGGGGTTTTN AGGGGAATT AATGGGGTTC	420
CNAATTTTG TTTTAAGGGG GCCAGANCTT TTGCAAAGTT GGNTTTAAG GGGCCCAN	478

(2) INFORMATION FOR SEQ ID NO:853:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GGNAGAGGTA TCCGCAGTGT NCTGGAACGG CCCTGTCTG AGCAACATTA ACCGGATTGG	60
AGCAGACCAT GTCCAGAGCC TCCTCCTGAA ACACGTGCC TCCTGTNCTG GCAAAGCTGC	120
GCCCCACGCC TGAAAATNA GGAACGCCTA TCGGGCAGAA TTCGGGTCCC TTGGGCCCCCT	180
GCCTCTGCCT CCCNAGGTGG TCAAGGCTCG GGCCCCAGGC TGCTCTGCAG NCTNCAGCAG	240

GTNAACAGGA CCACTCTGAA CCATN 265

(2) INFORMATION FOR SEQ ID NO:854:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

AAGTCGGACA GGGGCCATGA CAAGTCGGAC CGCAGCCATG AGAAAATAGA CAGGGGCCAC	60
GACAAGTNAG ACCGGGGCCA CGACAAGTTT GACAGGGATC GAGAAGCGTG GCTATGAACA	120
AGGTAGACAG AGAGAGAGAT NTAGACAGGG AACGGGAATC GGGAACCGCG GGTATGAACA	180
AGGCAGACCG GGNAAGAGGG CAAAGTAACG GCGCCACCAT CGCCGGGNAG GAGCTGGCTC	240
CCTTATTCCC AAGAGCCAAG ATGGCAGTTA GNCGANAAGN TTGAAAGAGT TTAGACCCCCA	300
TGGACCCCTAG CTTCATACTT CAGACGGCCC CCCGGGCAC GTNGTTCAA CAGGANTCCC	360
CAAGCGGNAT TTAGGCCAG NTTTGGGGT TGACACCACA GCAGTTGGNC CCTTTT	416

(2) INFORMATION FOR SEQ ID NO:855:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

GGCACCATAA AGGTTGTCCA ACTAATCTTN AAAGCTGAAT TTCCATTGGG AAGGAAATTC	60
TTTCCCGAGT TCATAAGTNG CCTTTCCATC TTCCCATCGA GTATTTGGNA ACTCTCTNAA	120
GGTTCTCTCC ACTTTCCCAG GCTTTCCAA TCTGGTCGGC GTATACCTTC TCCTTTGGAT	180
TTCCAAAAAT TGCTTCATAT ACAGCCTCTA GTGTGTATGT NGGAAAGATT TAATTGTGCC	240
TTGTNAATTA CATGGATACA AGTGGAAATG TATTCTTGCC CNTGAACCTTC TGACAGCCGT	300
TNATATCGCC TNTTCC	316

(2) INFORMATION FOR SEQ ID NO:856:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GAAGGGCTTCG GNCACGCAAC GAAANTACAA GGTAGTGGNT CCTTCCTTGC CCACCCCCAA	60
NTCCAACAGG CGGCCCTTT ACCGCTTGAA AANTTTTCG CCCTAATCCA TGTGGTCNCC	120
AAGTCCCGNT TCTGAGTACT TTNTATCTAA TTTNAAGAA GATGAAGAAG TTTTCAGGGG	180
NGATTNTTT ACTGTGGGC ANGTNTTTG AGAAAGTCCC CCTGGGGGTG AAAGAACTTC	240
GGGATCTGGG NTGGCTATGA TTNCGGGAG GGGGNACCCA CACTTGTNC CGGGNATTAC	300
GGGGACCTT	309

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

AAAACTAGTG GATCCCCCGG GCTGCAGGAA TTCNGCAGAA GTTTTACTCN CCAACTTNAT	60
CATCAAATG CAAGTGANCA AANAGGCCCC CAGCTCTGGC CATCACGTAT AGCATCACCT	120
TCCTCCTCTT CCTCCTNATC CTTTTGTCT GCTTCTAAAA GGACCTGAAT GAGGTGTGTC	180
CTGAAGGCC CANGAATGCT GCACTGGCTG CCTGCACTGT NTGGCCTGGT GGCCACACGA	240
ACCAGGACTG AGAATAGCCT TGGGCACCGN CACCATCCTC CTTGTNTTG GCCATGGCC	300
ATTAACCAGN CTGTNCTTTT TTNCC	325

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GACCTATTGC TTTAANAACA AGGCCCTCTA TNANATCTCC TTCCCCACTC TAAAGCTAAC	60
CACACCAACC TACGGGAAAT CTGAANCCAC CTTTTTNAG CNACCATGAA NTGGTGTNAA	120
CCNCTGNCTT CCTTTCCCTT GGCCAGCTCC AATGCTGACC TCCGCAAGTN GGNCAGTNAA	180
CATGGTCCCC TTCCNACGTT TCCATTTTT TATGCCTGGT TTTGCCCTT TAAACCAGCC	240

GTGGNAGCCA GCAGTTATCG AGGNTCTCAN AGTGGCCGGN AACTTNACCC AGCCAGGTTT	300
TTCGAATGGC CCAGGAACAT GATGGGCTGN TCTGTGAACC CCGGG	345

(2) INFORMATION FOR SEQ ID NO:859:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

ATCCCTCTTT GTCTACAGAG TTGTNGAATG CTCCACCGGG ANGGGGTGGG CAGTTNTCCC	60
CTTTGGGGAT GTTGNGNTTG TGGGAAACC ACTTCCCCGT TTGCTGGACT TAGGGGCTGG	120
TTTGGGNGAA ATTTTTGT	139

(2) INFORMATION FOR SEQ ID NO:860:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

ANAGCAAAGA GCAGGTGGCC AACTNACCTT TTTGGAGCA ATT CGGNAAA CGGGGCTTCA	60
AGGTGGTATA TATGAACCGN GCCCCATTGN ACGATTACTG TTTGCAGCAG CTNCAAGGGA	120
ATTTNANTGG GGAAGAGCCT GGGNCTGCAN TTAACCAAGG AAGGGTCTGG GAGCTGGCCT	180
GAAGGATGAG G	191

(2) INFORMATION FOR SEQ ID NO:861:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

TTTAAAAACA AGAAGAGGGT CCTNCTGGGA AGAAACTGGC AAGGNAGAAG CTCNCGCGGT	60
ACTACAAGAN CATCGGTNTG GGCCTTCAAG ACACCCAAGG GGGCTATTAA GGGCACCTAC	120
ATTGAACAAG AAATGCCCT TCANTGGTAA TGTTCCATT CGAGGGCCGG ATCCTTTG	180

GCGTGGTGAC CAAGAATGAA GATGCCAGAG GACCATTGTG AATCCGCCGA GACTNATCTG	240
CACTTACATC CGCAAGTGAC AACCGCTTCG AGAAAGGGCN CACAAGAACC NGTTTGTAC	300
ACCTGTNCCC CCTGNTTTC	319

(2) INFORMATION FOR SEQ ID NO:862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GGCACGAGCA GAAAGTGGTG CGGGANAGNG CCCANAGCAC CCACTTCCCC GGNTCAAGTA	60
CACACATNAC CAGCTCTTNT TCATTGCNTT TCCCCAGAAC TGGTGCATCA AGCGGCGGTC	120
GCAGTCCTNC TACCTGCAGG TGCTGACTGA NAAGCATGCC CCTAAGCACT ACAGGGTGCT	180
GGGCAGTNNTN TCCCAGTTA AGGAGTTGG CGGGGTTTC CACTGTCCA AGGACTCACC	240
CATGAACCCCT GCCCACAAGT TTTCCGTGTG GTGAGCCTGG NTGCCCCNT GCACGCCCCC	300
ACTGCCCCCG NACGANTNAC CTCCCTGCTGG NTTACCGGGG NAGGNATGCA CCCGGTGCCA	360
GNCCCGTTTT GGGNACNACC TGTGTTCCAG CCCTTCCAGG ACCGGTCCCC TTGTTNGCCCT	420
AATTTNAGGA GGGGCTGGAG NAGGNTNAGG TGGATTGGG GGGTTTAAGG GAATATAATG	480
GGGT	484

(2) INFORMATION FOR SEQ ID NO:863:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GGCAGACCTT GANCCCAGGA GTTTAAGGCT GCAGTNAGCT ATANTNATGC CACTCCACTC	60
CAGCATGGGT GAACAGANCA ANACCCCATC TTTAAAACAC ACACACAGAT CATTATCAGA	120
ATGTACANTA ACACTGAATG TNTTGAAAAA CTCTGTTCCCT TGTTTTATAT TGGCTGCTTC	180
TGGCATATTC ACTATTTCC CATGAGNATC CAGTATTGAT GAAACTNTAT TTTTGGTAAG	240
TGAGATGAAC GATGTNAAGA TTGTGCCATA GAGGCGGGGC ATGGCGGCTC TGGCACTTTG	300
GGAAGGCTGA GGCGGGTGAN CTGCCTGNNGC NCTGANTTCG	340

(2) INFORMATION FOR SEQ ID NO:864:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

AATNACCGCG GACGATCAAC AGCAGGTCGT NATGCAGAAG TCCGGTGAGT GTAANAAGTT	60
GCTCATTGAT CGCCGCATTC GGTCCGTTTT TTGGTAACAA CNGCAATAGC GTTTNTGGAC	120
TGGCAAACAG ACTCATAGCC TGGNATAACG AAAAGATCGC ATTCCAGTNA GTNTTGGGAT	180
NAATGGAAA AGTGTGGTGT TCTTCGAATC CTTGTGCCCG CAGTTACCTG NACGGAACAG	240
CGTCCTGNTT NNNTCCCTGGC AATAACAGAG GNTCGTTTAC CAAGTAAAAA G	291

(2) INFORMATION FOR SEQ ID NO:865:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GCTGATGGAA GTAAATGGGA ATACAGCCAN TTNTTGTACG GNCGCACCTA CGATGTAATG	60
GTGTTCGGTG CGGCAGGGAT TATTTNCCTG GTCGTTAACG GCCTGCTGAC GCTAANGATN	120
CGTNTGAANC GACCGCAAAG NTGGACATTC GAACGGCGAA ATTAATGTGG CTGCGTACAT	180
TCGCCGGGGG GTTTTGT	197

(2) INFORMATION FOR SEQ ID NO:866:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GGCAGAGNCT GAAAATAAAG ACAAGAAAGC CAGGTCTACT TTAAAATAGT CTTAAGCCAC	60
TATTATTATA TTTTNAAAAT TTAGCCAATA ACTTCTAACT AGAAGCAAAA ATAATAACAC	120
ACGATCTAAT AAAAATACTT GGGAAAACAA AAAGATGAAA TACTTGAAAA CGGACAAACA	180

GAATTGTGCT TCATATGCAA AAAAATCTAA GTCACTTCCC CATACTGGAA AATCTTAATA	240
GGAACAAAGG AACAGCACCA NGCATTACT AAGGCCATAC CACGTGGCA TTAACAATGG	300
AGGCCGTTA TTGNTTGACC GTTGNTTGA CTGAGNTGGN GTCTCGNTCT GTTCACACGG	360
TTGGGGT	367

(2) INFORMATION FOR SEQ ID NO:867:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

TGGNAGGCCA AGGCAGGCCGG ATCTCCTGGG GTTGGNAGTT CACGACCAGC CTNACCAACA	60
TGGNAGAAAT CCCGTCTCTA CTAAAAAAAAA AAAAAAAA AAANCNCGGG GGGGGCCCCC	120
T	121

(2) INFORMATION FOR SEQ ID NO:868:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

TGGAAAAACT GTATCAGGCG CAGNGCTNTA GCCAACAAAGA AAGNCACCAN CTGTTTNAG	60
GNTGNTGCGT GGCGAGCTGA AGCCGGAACA ACTGGCGGCG GCGCTGGTGA AGCATGAAAA	120
TTCGCGGTGA GCACCCGANC GAAATCGCCG GGGCAGCAAC CGCGCTACTG GGAAAACGCA	180
ACGCCGTTCC CGCGCCCGGT TTATCTGTTT GCTGATATCG TCGGTACTGG CGGTGNAGGC	240
AGCAANCAGT ATCAATATTT TTNACCGCCA TGCCTTTTC GCCGCGGCCT GTGGGCTTGA	300
ANTGGCGAA ACACGGCAAC CGTAGCGTTT TCCATAAATT TGGTTCNNTTC CGTTCTGCTG	360
GCGGCAGTCG GTATTAATCT TTGATNTTGA ACGNCNNNTA ATCGGGCCAG G	411

(2) INFORMATION FOR SEQ ID NO:869:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

CACTACCGGT ATCCAGCACC TTAAGCNTGA CGTGTTCCTG ATCCACTTCG GCGCTTAGGT	60
GNATGCAACC GCTCTGGGG GTAAAATCGA TGGCGTTATC CAGTAAATTG CCCAGCGCCT	120
GCTCCAGTGA ACGCCGGTTC AGCAGCAACG TTAACCTCGG TGGGCGTAAC ATGCAGAGTG	180
ATTTTTTTT CTGCCAACTG CACGGTGCAG GCTTCGCTGA CGCGGGGGGA ATNAATGCCG	240
CCACATNCAA CAGCAGTNCA GAACGACTTC CTGGACGATT CTCCAGTNTT GCCTGGNGTA	300
GTAACGTTTC TACCAATGCC TGCAAACGNG CATTGNGT CAAAAGTTGT TCATGAAANG	360
GGCCACCATT TTCGGTGGNG GACCTTCGGG TAAAATTNC GNCGTTCCAG AATTGCCGC	420
CATGGGGTTT TTTAGCTCCT GAGTTAACATT C	461

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

TTGGCACCGGA CTTTACCGTT AACCTGCACC ACGACCAGCG TGNAGTCTTN CACCATCGCT	60
TTTCGTCAG CAACCGGCCA CGGCGCGTTG TCGATATCGC CTTCGCCTTT NAGTTCCCTGC	120
CACAGCGTGA AGCAGATGTN CGGGGTGAAC GGGTTAACAGCA TACGGACAAC GGCCAGCAGT	180
GCTTCCTNGC ATCAAAGCGC GATCCTGCTC GCCATCGGTT GGTGCTTTCG CCAGTTTGTT	240
CATCAGCTNN NNNNNCGNCG CAATTGCGGT GGTTGAAAG GTCTGACGAC GGCGATATC	300
ATCGGTCACT TTAGCGGNTC GTTTTATGCA CATCGGAGGG GGGGGCCCGG TNACCCANTN	360
CGNCCTTAT	369

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

TTTTTTNTGC CATTAACCTTC GGTATGCCTG CNGGACTGGC TTGCGCTGGTG TTACAGGCAC	60
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AGGCCTTTT AACTATCATG CTTGGCGCGT TTACTTCGG GGAGCGACTG CATGGCAAAC	120
AATTGGCGGG GATCGCTTAG CGATTTTGG CGTACTGGTG TTAATCGAAG ATAGTNTGAA	180
CGGTCAAGCAT GTGGCGATGC TCGGCTTAT GTTGACCCCTG GCGGCACATT TAGTTGGCG	240
TGTGGCAACA TCTTCAATAA AAAGAACAT GTCGCACTCA ACGCGTCCGG CGGTGATGTC	300
GCTGGTAAAT CTGGAGCGCT TTTAATCCC AATCATTCCCT TCTTTGGTNG CCTCGCTGNN	360
TCNTCGGATG GGTTCCGCAA CCAGGNTTCA CA	392

(2) INFORMATION FOR SEQ ID NO:872:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

TTCCGGTCTN ATCCAACAAG CCTGCATTCC GCTGCGAATT GCCCCACCCA CGTNAGTGNA	60
GAATCGTCCC CAACATGTA GATCTCGCCG ATCGGCACGT TGAGTTTTC CGCAGCCAAA	120
AAGTACATAT CGCTGAACGG TTTAAGCGC CCGTGCAGGC CAGCGCGCAN ACAAAACTCA	180
AAATAATCCC CCAAACCAAA CAGCTCCGGC TGGGNCGTTA CCGTTGGTGG ATCGCCACCA	240
GCAGCCATT CTTGCCAGC TGTAAAGG TGTCGTGAGT TTGCTGCAGG ACGTTCGAAT	300
TCGGCTGCGN CATTGGCAA AAGTTGGATT CATTGGCTGC GTGTGGCNCC TTGNATGGGG	360
CTTCTTTCG GGGCANTCAG CCCGGNNNNN GGNGCAATNG TTTGGTTCA ATTGGAAACG	420
TAAAACGGCC AACGCGGTTA AAGGTGTTGA TNAAATTTG GGGGTTCCG GTTTCCNNT	480
AACCGGCTGG NGGCAG	496

(2) INFORMATION FOR SEQ ID NO:873:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

ATGGTCTCGC CGATAGTCAG GTTAAAGTAC TCTTGAAACA GCCAGAAGCC CGGTTCGTTC	60
ACATGAGAGA AAATCACACT ACCGGAACCA ACCGCAATAA CCATCAGCTC CGGGNTAACAA	120
CCCGTGGTTG CCAATCAGCG GTGCCGCGAT ACCACCCGCA GTGAATTNCC GCAACGNTTG	180

CGGGAACCA GCGCGATACG CATA CGGNCA GCAATCGACC AGGCCATCAG CAGCGGGGA	240
AATGTTGGTT TTCGTGGCAT CCATGGANGC AATGTTATTT TTTTCCACGC CGTTNTTNTN	300
CCCAGCAACC TGTTTGAAA CGGNACCCG	329

(2) INFORMATION FOR SEQ ID NO:874:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

CTTNATGCAC AACGGCTTT TCCTGTNCCG GCTTAACTCC TACAGTNAGA TCTTTCCAG	60
TNAAGTCTCC GGC GTGGCGT TAAAACGCTT CTTTAAC TTT TNNATCCCGG CGAATGCTGG	120
TGGTCTACTT TCTGNGCCA GGGACAGCAA AGNTNGGCTG TTATTCCTC GTNAGCACGG	180
TCGCCTTG GCTTGCGTAC TTANATGAAT TGTGNGCGN GCACTNCGNC CCAATATCAT	240
CATCGCATTG GCTAATCTTC CTGTTTATTG GGCATTATTC GCGGGCTGGG ATTCGTTGT	300
GGGATGCNNG GNCNGCGGGC GGGCGTGCNT GGGGGATT TTGGGCA	347

(2) INFORMATION FOR SEQ ID NO:875:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

CGTTNTCGCG CAGGTTTTNA ACGGCCCTAA NTAAAATNAT GACCAGCTAT GTGGTTGGGC	60
AGGCGCTTAA GGCGATAAG ATTAAACTCA CCGATATGGT GACGGTCGGT AAAGATGCCT	120
GGCGACGGG AAATCCGGCA CTGCNTGNTT TCATCGGTAA TGTTCCCTCAA ACCGGGCGAT	180
CAGGTTTCGG TGGCAGACTT GAACAAAGGT GTGATTATCC AGTCCGGTNA ATGAACGCCT	240
GTATTGCGCC TGGCTGATTA CNTTGCCGG NAGCCAGGAG TNCA TTTAT TGGTCTGATG	300
AATGGTTATG CCCAAAAACT GGGTCTGNAC CAACATTACC TTCCAAACGG TGGCACGGC	360
CTGGTTTGCG CCCGGGGCAT TTCAGNACCC GGCGGGATT TTGGCATTNC TGGGTAAAAG	420
CNTTTTCCCC CGGTTTNCCC GNAGAGTACG CCTTTT	457

(2) INFORMATION FOR SEQ ID NO:876:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

ACTGGNTCTC GGCTGCCCTN TTGAAGANTT TAACGCATT TGNNATGCCC ATCCCGATCG	60
GACTGTCGTC GTCTACGCCA ACACCTCTGC TGCGGTAAAA GCGCGCGCAT ATTGGNTGGN	120
AACTTCAAGC ATTGCCGTCG AACTTATTGA TCATCTTGAT AGTTTGGGNN GAAAAAAANC	180
NCTGGGCACC CGACAAACAN CTGGGGCGTT ACGGGCAAAA ACAGACGGGT GGGAGACANT	240
CTATGCTNGT CAGGGTGCCT GTTTTNGTGN CATGGATGAA TTTAAAGTCT TCAGGGCGTTG	300
AACCCNCTT	309

(2) INFORMATION FOR SEQ ID NO:877:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

TATTTTGCC GCATGCAAAG GTTTCATTAC ACTATTAAC AACGGTGTGC TATCCGTTTC	60
TGGGAAAGTA AGAAATATTG TCAACATGAA GCCGGCGCAC CCATGGNAAG CTGAAGAATA	120
TTTGTGAACG GCCTGTACAT CAGTGAAAG CCTGTTGAAG AAAAAACTTA AGCAAGAGCA	180
AACGAACATT CTCACAGATT CTTTTAGATG CAAGAATGCA GCACGCAAAA AATTGGTTA	240
CGCGTGGAAAG GTTCCAGTNC AATAAAATTG CCGAACAAATG TGGTTATGCC ATACATCTTA	300
TTTTATTTAT GCGTTCCGCA AACATTCGG NAACATTCCG AGGGGGNTTC TNAGGGGTTA	360
CCNTTGTCA AGGTCCCCCG GGTTTGNTTA CGGGGCAAC	399

(2) INFORMATION FOR SEQ ID NO:878:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

CATTGGCAAA GAAGAAGCCA ATCGGTGCCG CCAGCTGCCG AAAGGAGCCA TACAGTGCAC	60
GTTTGCCCCG TGGGGCGTTT TCAGTCGCCA GCAGCGCCCG GCCGCCCAT TCACCGCCTA	120
AGCCCAGACC CTGACCAAAT CGAGCCAGCG CCACAGCAGC GGGCGAAAA TACCAATCGT	180
GGCATAGCCC GGNCAGCAGA CCAATCACCA CGGTCGAAAT CCCCATCGTT AGCAACGAGG	240
CGACCAGCGT CCCCATTACG AACGGNTGTT CCCTCGTGNG GACGTTTTC AANGACCGTT	300
GGNCNTGAAA TTGTGGGTT AGCAAAAACG GCAGTTG	338

(2) INFORMATION FOR SEQ ID NO:879:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

TCCTGGCAGA TGTCCCGGGA TATCCGCNAG CCCAACANT TCGAAGAAC TTTNCTAATG	60
CAGGCTCATT TNTTNGCNC TGAGATAAGC CGGANTGCTT TCTCCGGCAT AGGTTCGCAG	120
CGTTCCAGGT TCCAGCCCGT AGTCAATNCG CATCGAGAAT CAACANATGG CTGGNGCTTT	180
CAANATAACC CAGCAAGTTC AGTCCCTNAN TACCGCCATC GACAATNTCC ACATACTCGG	240
GCCAGTGGTA ATGGGCATAC AGCCGTTCCG NCACCCGNAC GNCGAAGCCT TCATCGGCC	300
ACAGCAGGTT GCCCAGCCCC ATGACCACCA CGGTTTTNNNT CGNTTCATGA AACGGTTCCCT	360
TGTTAAATTT ATTTTNCCA AATTTTG	390

(2) INFORMATION FOR SEQ ID NO:880:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

CGTNAGCAGC CTGTNGCTTT ATACCGGGGC GATTCTGGAA GCCAACCTGC TGCCACCGCC	60
GGAGCCGAAA GANAGCTGGC GTGCATTAT GGATGAAC TG TCAGTNATNN NCTGCNATGT	120
CTACCGCGGC TACGTACGTN AAAACAAAGA TTTTNTGCCT TACTTCCGCT CCGCTACGCC	180
GGAACAAGAA CTGGGCAAC TTGCCGTTGG GTTCACGTCC GGCGGAAACG TCGCCCAACC	240
GGCGCGTCTG NAGTCACTTA CGGCGGCATT TCCGTGGNTT CTTTCGGCTG GGACGGCAAA	300

AACCGTCTTG AANTGNTCCC CGNCTGGGNT TGGGGTGGCA GGTTACGGGC GGNTTGCAAA	360
AAGTGGGTTC GAAGACGGGG CAAAACAGAG CGAG	394

(2) INFORMATION FOR SEQ ID NO:881:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

TCGAGTTTTT TTTTTTTTTT TTTAATTTGA TGGGATGTTC CTAAACTTCA TCTGCTAATA	60
AATATTTGCC AAATTAAAAT GAGCCTAACT AAATTGAAGA CTAAAATTAT TCAGTGGAGG	120
ACCAGACCAT TTGCTTTATT TTCAGGGTGA AGAAGACCTG GNTTGCTCTA TTCAGGTCTC	180
TTAGAAAAAC AGGCATACAC ATGAGTTCT AGTATCCTCA GCAACACACT ACATCATACC	240
TTACCCCTGGG TAATCCTTCA GAGCACTGTC AGCAATCACC TCAAAATCCC TTCCCTAAAG	300
NCACATACAC TTGGGGTTT ACTCTTATTAC ACCTACTCCT CCCTACTCTT TAACATGGAA	360
TGNNCTCAAG GCTTTGGGG GGGGNAAAAT TAAAGNATCT ATCCTTTTTT TTTTAAGGTT	420
CCNTTTCAA AATTGCTTTG GGGGCCCGT GGNCAGNAGG GGAAACAGGC ACTGTTNAAT	480
AGGTTCCCC	489

(2) INFORMATION FOR SEQ ID NO:882:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GTAAATTTAG CCGCGCCGGT GAACAGACCC AGAAATNAAC GTNCGCNTTA ATCCTCATGT	60
NATTCTGGC ATGGTACAAG CTGAATCTAT AAGCTTTTT ACCGGACTCA CCATGCGNTG	120
GTTCCGCAAT GCTTCTGTG CCGAAGAAA ACTGATTGCG GAACGTTAG GCATCGANAC	180
CTATACGCTG CTGGAAGAGA TGGCCATGGG GTGCCGCCTG GGTCGTGGGG GCGTAAATNC	240
NGATCTTTT NCGACAAAAT CGGGTTTAA AACNGGTAT CACGTTGGNG	290

(2) INFORMATION FOR SEQ ID NO:883:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

CACCAATGCG GCAGGCTCGC TGCCTCCGGA AGTGGGGCA GGCAGCCTGG TCGCATTGAA	60
AGANCATATC AACACCATGC CCGGTACGCC GATGGTGGGT CTTAACGATG ATCGTTTNG	120
AGAGCNCTTC TNCTCACTGG CAAATNCCTA CNATGCGGAA TACCGCGCAC TGTTACAAA	180
AGTGGCGAAA GAAGAGGGTT TCCCTCTGAC GGAGGGCGTG TNCGTNTCGT ATCCGGGCC	240
GAATTTCGAG ACTNCGGCGG AAATTTCGCAT GGATGCAAAT TAATTGGTGG GGATGTTGTT	300
GGTATGTNTG TGGTGCCCTGA NGTTATTTCA GNTGCCATT GGGACCTTA AAGTCGTTN	360
GCGNTCTCT	369

(2) INFORMATION FOR SEQ ID NO:884:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

ACGCATTANA CCANTAAAAG CTCGAGCNT TTACCGACCG GAANTGGCAA TATCAGCAAT	60
CTGCTGAGAA CCAACCCTGC GGTACGTTGG TTTCAACGCA AAGTACCTCG TTAAACCAGG	120
GAGATATTGCG CCCTGAGAAA NTNTCTTTTC ACGGTGCCTC GCCCTACCAN ATTGCCTATT	180
TAATTGAGGG GTATTAGTGC AACTAAATAA CCCTGAACCC CAGCGAATNA NTTNNCCNATG	240
CCCAT	245

(2) INFORMATION FOR SEQ ID NO:885:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

GGCACAGCTA GGCTGGACGN TACTCCGGAC GNAAAGNNGT CATCGTGTAA GAACAT	56
---	----

(2) INFORMATION FOR SEQ ID NO:886:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GGCACGAGGA GGACAGCATT GCTGCTCCTT GCACCCCTGG NTGTGGCTAC AGGGCCAGCC	60
CTTACCCCTGC GCCTGCCACG TGTGCACCAG CTCCAGCAAC TGCAAGCATT CTNTGGTCTG	120
CCCGGCCAGC TCTCGCTTCT GCAAGACCAC GAACACAGTG NNAGCCTCTG AGGGGGAATN	180
TGGTGAAGAA GGACTGTNCG GAGTCGTGCA CACCCAGCTA CACCCCTGCAA GGCCCAGGTT	240
AGCAGNGGCA CCAGTTCAA CCAGTGTGCA CAGGNGGACT NTGCAATTGG GAAGTTGNAC	300
AACGTTGNAA C	311

(2) INFORMATION FOR SEQ ID NO:887:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GGCANAGAAA CAGCGCTCTG ACCTCTTTAA ACACCACAGA ATCCACACTG GGGAGAAGCC	60
CTATGGATGT TCCGTCTGTG GGAAACGCTT CANTCAGAGT GCAACCCCTCA TTAAACACCT	120
NAGAATTCAC ACTGGGGNAA AAGCCTTACA AATGTNTTGN AATGTGGGG AAGATTTAGA	180
CAAAGTACAC ACCTTATCCG ACACCAANNA ATTCACTAAA ATAAAGTGCT GTCGGCTGGG	240
CGTGGTGGCT CACGNCTNAT AATCCCAGCA CTTTGGAGG NCA	283

(2) INFORMATION FOR SEQ ID NO:888:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GGCAGAGCAG GTGCGCCTNT TCCGCCCTG GNTAACATG GACCGGATGC TGCGCTCAGC	60
CATGCGCCTG TGCCCTGCCG AGTTTCGACA AGCTGGAGTT GCTGGAGTGC ATCCGCCGGC	120



S.N. 08/401, 881

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of:

**William A. HASELTINE, Craig A. ROSEN, Steven M. RUBIN, Patrick J. DILLON,
Haodong LI, and Julie EARLE-HUGHES**

Serial No.: Unassigned

Filed: Unassigned

For: HUMAN GENES, SEQUENCES AND EXPRESSION PRODUCTS-17

SEQUENCE LISTING

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TNCATCGNAN	TGGGACAAGG	ACTGGGTCCC	CGATGCCGCC	GGCACCCAGCC	TCTATGTGCG	180
GCCTGTGCTT	CATTGGGAAC	GAAGCCCTCG	NTGGGTGTNA	GCCAGCCCAG	GNGCGCGCTC	240
CTGTTCGTNA	TTCTCTGCC	AGTGGGTGCC	TACTTCCCT	GGAGGCTCCG	TGNACCCCCGG	300
TTTG						304

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

AGAGAGAGAG	AGAGAGAGAG	AGAGAGAGAG	AGAGAGAGAG	AGAGAGAGAG	50
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(2) INFORMATION FOR SEQ ID NO:890:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GGCACGAGCG	GCACGAGGAG	AAACCCCATA	TATGTGAAGN	AGTGTGGTAA	GGCCTTCAGT	60
CTCCCCTCAA	ATNTTCGAGT	CCACCTGGGT	GTTCACACAG	GGNNAAAACT	CTTGAAATG	120
TGATAGACTG	TGGTAAAGGC	TTCAGTNCA	GAGTGCACGT	TTTGGNAGCC	CATCAAAGGG	180
TCCACACTNG	GGGAAAAGCC	NTACAAN				207

(2) INFORMATION FOR SEQ ID NO:891:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAAATCCCTC	AGCTTTGTT	TGTNTGGAAG	TCTTTATTTC	TCTTTCATGT	TTGAAGGTAT	60
TTTTGCAGAA	TATACTATTC	TAGCATGAAA	GGATTTNCC	CTCAGCACTT	GCAGTATGTC	120
GTACCATTCT	CTCCTGGCCT	GTAAGGTTT	CACTGAAAAG	TCTTCTCCCA	GACATATTGG	180

AGCTTAATTG TGTGTNGTTT CTTTCTCTT GCTGCTTTA GGGATCCTTT CTTTNTTACA	240
GNCCAGTTTT TATCCTTGAC CTTTGGGAGT TTATTAAAAT GCTTGAGGG TACTTTGGT	300
TTGGGGTTCC AATCTGCTTT GCTGGCTNCT ATAAACCCTC TNGTNACTNG GGNATTGG	358

(2) INFORMATION FOR SEQ ID NO:892:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

NTATNTNAAT AATGCTTTG GCACTGATCA CAGAGCCCAA ANATACCATG GTAGGAGTCA	60
ATNTGCCACA GAAGGTTGGT GGGTTTTAA TGACGAAGGC GCTGAACTAN CTTTNNAAA	120
GGCCTTGGAG CGCCCANCAG NGACCCTTCC TGGCCATACC TGGGACGGA	169

(2) INFORMATION FOR SEQ ID NO:893:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

TTTTTTTTTT TTTTTTTGGG NAACCCTTTT TTTTTTTTTT TTTTTNAANN ANGGCCT	57
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(2) INFORMATION FOR SEQ ID NO:894:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GGCAGAGCCA CCATGATGCT GTNATCTTCC TGGCCGAGCA GCTCCCCGGA GCCCAGCGTT	60
GCCAGCACTA TAAGTCCGT TACCACCAGC AGGGAGAGGG CCAGGAGGGAG CCGCCCTGA	120
AATCCCCATG GGGNCTGCTC GGGCAGAGGT CTATCTCCGG AAGTGNCAACC TTTGAACATG	180
TTCAACTTCC TGGCCTCCCA GCCACCAGGT GCTTCCCTGA GGGGGCCACC TGTNAATGAG	240
GAAGAGGATG AGGTGCAGCT TCAGGTTCAA CCAGACGTGN CCACCAGCCT GGGAGCTGCC	300

CCATGGCCAT GCNTTTTCG TTCACCTTA AGGAAGNACG TTCCAAAGAA AGTTGTTGGG	360
GTGTTTACA AGNTTCAGCC CATTNCAAGG GGGGGAGGNC TGGTTCTTG TTAAGCGGCN	420
AAACATTCGA AGGCGGGGG NAGATTGGTT CATTGAGGT TAATTCTGGG GCAATTGTTN	480
ATNCCGTTCC GGTT	494

(2) INFORMATION FOR SEQ ID NO:895:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GGCANAGGGA ATGACGTGCT CCACAGGTGT TTGCCACTGA AGGGGGTAG CCAGTGGCNC	60
CAATGAAACC AGCTTACCTG GCCCAATTCC CACTTGAAAT GATGTCAGCC CCAGAAAGGA	120
TGAGCTCTTC TACCATCTCT CCTGTTACCA CATTCCCTGC CTGAGAACAG AGCAATTGAA	180
ATACAGCATH CTTAGGGCCA GAAACAGGAG GTCATGTATT GTTACGGTAT GCATGGACCA	240
GGACTTTCCA ACATTATTAC AANGAAAGGA TAACTAGGTC CCCTCTTACT GGGGCCCTCT	300
GNAGGGGTTT TNACANTAGC CACTTTAGA GGAACCTGN TTCCCTNACC CATTCCAACC	360
CAACAACCAA G	371

(2) INFORMATION FOR SEQ ID NO:896:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

TGCAAAAAGG GAGCCAGNAA GAAAGTGGTT GNATCCATT TCTAAGGAAG ATTGGNATNA	60
TGTGAAAGCA CCTGCTATGG TTCAATATAN GAAATATTGG GAAAG	105

(2) INFORMATION FOR SEQ ID NO:897:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

TACAGGGCTC CAAGTGTCTT ATGAGAGCAG GACTTGGGCT GACCATGTCT CTCTGCCCTC	60
ACCCATGCTC TGCTCTGAAT TTCAGATCCT AAGTGTGAAA CGAGAAAGTC CCCAGCCCTG	120
CTGCTGAGCC AGTTGCTGCC CTACATGGAG AACAGGAGGG GTGCTGTCAT CCTGGTCTCT	180
TCCATTGCAG CTTATAATCC AGTAGTGGCG CTGGGTGTCT ACAATGTNCA GCAAGACAGC	240
GCTGCTGGGG TCTCACTAGA ACACCTGGCAT TGGAGCTGGC CCCCAAGGAC ATCCGGGTGA	300
AACTGCGTGG TTCCAGGAAT TATTCAAAAT GGACTTTCAC AAAGTGTTTT CNGGGAATG	360
AAGTCTCNCT GGGAGAAACT TTCAGGGACC NTCNTCAGTT GTCAN	405

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

NAGTNTGCGA NCCTCTACTG GNNGGGTGAA GGAAACCTCA TTCGTTACAG GCCTGGTACT	60
GTGGCGCTCC GTGAANATTA GACGTTATCA GAGGTCCACT GAANTTCTG ATTGCAACT	120
TCCCTTCCAG NGTCTNGTNC GAGAT	145

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

GGCAGAGGTT GGATGAAGAT GTGGAGGAGA TGCTGCTGCA GATTGCTGNT GNNTTTATCG	60
AGAGTNTGGT GACAGCAGCC TGTCAGCTTG CNCGGCATCN AAGTTCTAGC ACCCTGGAGG	120
TGAAANATGT CCAGCTGCAT TTAGAGCGCC ATGNNAACAT GTGGTTCCA GGNATTGGC	180
TCTGNAAGAA ATCCGACCCT ACAAAAAAGC TTGCACCACA GAAGCTTCAC AAACAGAGAA	240
TGGGCATTGA TCCGGAAAAC AACCAAGAAA TAACACACGG AAAGGTCCAG GGAATGGGAC	300
AGCAATGTAT TTGGGNGATA CTTGAGCTGA GGAACCTTCAG CCCATCTCAT CCTTGGNTTT	360
TTTTTTTAA ANGGTTTTA CAGGGAGCNA TATTTTTAA TTTAACATGC AGCAATTTTC	420

TTAATGNCTG GAGGTTCTNN CCAAAGGNTA AAGCCTCTTA CCCAATTTCG GNCCCTTTTC	480
CNGNCCTTN AAGGG	495

(2) INFORMATION FOR SEQ ID NO:900:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GGCAGAGGTG TCTCACAAATG CAGTCGAAAC TGGATACTTG ATTTCAGTTT GCCAGAGTTT	60
GTTAGACAAT CTGGATTTCG TTCTGGCAA CACTAGAACAAAATTGGCT TCATAACATT	120
TGACAGTACA ATCCATTTCT ACAGTCTTCA GGAAAGTCTC TCTAACCTC AGATGCTAAT	180
AGTTTCAGAT ATTGAAGATG TTTTATACC TATGCCAGAG AACTTATTAG TAAACTTNAA	240
ATGAGAAGTN AAAGAGCTCG TGCAAGGTTT ACTGAAAANT TTNGNCACAA ATGTTTG	297

(2) INFORMATION FOR SEQ ID NO:901:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GAATTCCACC CATGGNAAAT TCCATGGNAC CGTCAAGGNT GAGAAACGGG AAAGNTTGTT	60
AATCANTGGA AATCCCATCA CCATCTTCCA GGAGCAAAAT CCCTCCAAAT TNAAGTGGGG	120
CGATGCTGGC GCCTGNAGTG ACGTGCCTGG NAGTCCACTG GNGTTTCAC CACCATGGAA	180
GGAAGGCTGG GGGCTNCATT TNCCAGGGGG GNGCCAAAAG GNTNCATCAT CTNTGCNCCC	240
CTNCTGGTGG ATGCCCCAN GTTCCGTTAA TGGGNTGTTA AACCATGTGA AAGTTATGGA	300
CAACAGGTCT NCAAGGTGCA TTCAGCAATG GTCTNCCTGG AACCNCC	347

(2) INFORMATION FOR SEQ ID NO:902:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

AGNAGAGCTG AGATCACGCC ATTNCACTCT GGCCTGGGTG ACAGANTGGA GACCCTGTNT	60
CAAACAAAAA AAAGTTCTT TCCTTNCTA GCTCAAAAGC CAAAANTTC TGAAAAACGA	120
ACTTTGAAAG ATCTNTNGTN CCAATCAAGG CTTCTNCCTC CAGGTNTGAC AAGAAAGGGC	180
CAAANACCAT TGCAGAGATG AGGAAGCAGG ACCTGGCTAA AGACACGGGA CCCACTCAAG	240
NTGAAGNTCC TGGNCTGGAT TGAGGGCAAG GANGCGGAAC ATCCGGGGCC TTGCTGTTCC	300
ACGTTGNACA AANTGTGTG GGGACGGGGA GAGGCCCTTG GACGNCTGG GGNATGG	357

(2) INFORMATION FOR SEQ ID NO:903:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GGNACAGGGGA GATCTGGTGG CCTGGNTTGT NCCAAGAAGG CCGCTCAGCT GGGAAAGGAA	60
GGTNTCCGTG GTGGACTATG TGGAACCTTC TCCCCAAGGN ACCCGGTGGG GCCTTNGCGG	120
CACCTGCTTC AACGTGGGCT GCATCCCCAA AAAGCTGATG CACCAGAGCG GCACTGCTGG	180
GAAGGTCTGA TCCAAGATGC CCCCAACTNA TGGCTGGAA GGTGGCCCAG CCCGTGNCCG	240
NCATGANNTG GGAGGTAAG	259

(2) INFORMATION FOR SEQ ID NO:904:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GGCACGAGGN AGAAGCCGGT GTACAAGAAC TTACAGCTCT TTATGGAGAA CAAGGACCCC	60
CGGGACGACC TCTTCGACAG GCTGACCACG ACCAGCCTGA ACAAGCACCT CCAGGAGCTG	120
ATGGACGGGC TGACGCCAA GGTGTTCCGG ACCTACAACG CCTCCATCAC TCTGCAGGAG	180
CAGCTGCGGG CCCTGACGCG CGCCGAGGAC AGCATAGCAG CTTAAGNATC TTATCCTACA	240
ACCGAGCCAA CCGAGTTCGT GGCCATTCTT TGCAACCATT CAGCGGAGCA ACCCCCAGTA	300
CGTTTCGGAG GAAGTCGATT GCAGAATTTC CCAGANGGAG GNTTCCAGGT CAAAGAAGGN	360

NGCAGGTTGG TTGAGGCCAG GGCAGAGTTG AGGNGGNNNG AGGGTTTAG CACAAGGCC	420
AAGGGGTTGG CAANTCCAGG AGTTTCTGG TGAAGANGAG TTGGTTCTTG G	471

(2) INFORMATION FOR SEQ ID NO:905:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GGCACAGGTT TGCGTGTNA GCAACCACAG TNACCTTGCA GTNAGGCTGG AATCTTGGC	60
CACCCCAAAG TCCTTNCTG AAGGATTAN ACGGGGATGA AGTGCCTCAG GCCTCAAAG	120
CTAGCCACAA AGCCCCCAGA GCTGAATTCA TTGAGTATTT GTGCCTAAGG GCTTGGCTT	180
GTTTGTTTT AATACCCGGN CCCCCGNCAG AAAATAGNTT TNGCTTGACA ACCCAGNCTA	240
ATTTCCCCGA TTCCTGGGC TCCCTCTTGN ATTAATTTT TGAAAATTN CCAGTTGTC	300
AGGNATCAAT GGGGGTTAAT TCCGGNA	327

(2) INFORMATION FOR SEQ ID NO:906:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

GGCACGAGCC CAGCTGTACC CCGTGTAGG TGGGTGGCAG GTGGCAATTN GCCCTGACAT	60
GGCACAGCAG GGCTCTGCA TGGCCCGCTG ATTGCTCCTC ACAGGCACCT ACGGGCTGAG	120
CAACGCGCTG CTGGAGACTC CCTGGAGGAA GCTGTGCTTT GGGAAAGCAGC TCTTCCTGGA	180
GGCTGTGGAA CGGAGCCAGG CGCTGCCAA GGATGTNCTC ATGCCAGCC TCNTGGATGT	240
NCTCAACAAT GNAAGAGGCG TGAGTGNGC GGGTCCTGCT TGGGTGAGCC CCAGTNTCCC	300
GCNACCAGGG NCAGAGGGAA AGGCAGGCC TGTTGCCACG GGGANGGCC ATGAAATTG	360
GCCAAGGTTT GGAGACCATG NCTTTGGGA AGCCCCATTN TNAGCAAGGC CNTNGTTTT	420
TT	422

(2) INFORMATION FOR SEQ ID NO:907:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GGCATCTGGG TACTTGGTGA GGTCGAAGGT CAGGACTTTG CTGATCACAC AGTCNNNTTG	60
CTCAGGATAG ACTCCAATNA GGCTCTCGGC CTTNGTGTAG AACTCCTNCT TGAGTGAGAT	120
GACGATGGCC TGGTAAGTTG CAAGTCGACT GNCTCCTTGG NTGTAA	166

(2) INFORMATION FOR SEQ ID NO:908:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

TAATCCCGTT GATCATCCAC ATCGCCGNTA CANCCCGCTC ACCGGGCAAT GGATTCTGGT	60
TTCACCGNAC CGGCTTAAGC CCNCCTGGCA GGGGGNNCGN GGAAACGGCA GCCAACAGG	120
TGTTACCTGC GNCACGATCC AAATTGCTTC CTCTGCGCAG TTAATGTGCG GGTGAACAGG	180
CGATAAAAAC CCCGATTACA CCGGGGACTT ACGTTTCAC TGAATGAAC TTGCGGCTTT	240
GAATGTCTGG ACACGTCCAG ATGCGCCAGN AAAGTNCACG ATNCNGCTGN ATG	293

(2) INFORMATION FOR SEQ ID NO:909:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

NGCCNCATGG GCCANATAGG TGGCCCAGGG GCCCTGGNAG CCCCAAGTCC CAAAGGTANA	60
TCGGAAGACT ACAAGGCCAC CCAGAAAAAT CGCCTTCTAC TGCCACANGA ACCATTCAAC	120
GTCCCCCTGC GACCAGGAAC CAGACCATCC GCTTCGNACC ACGTGAATGC ACCAGCATGA	180
AACAACAATT AATGAAGCCC CGCAGTGGTC AAGTTACACC TGTNAAGTCT CNCGGGTCTT	240
CTGACTAACT TNNACCTNAC CACGC	265

(2) INFORMATION FOR SEQ ID NO:910:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

AAAAGAATTT CTACGANTTG AATATTGGGG AATATTCTGG AACACTGGAG ATTCCCTTCC	60
GGGGGAATTT NGATCCTGAA GGTGCAGTGG TGGGCTAGTC ACCAAAGAAT GAAATTCA	120
CACGTGGGAC AAAAATCATG AACAACTATG AAAGGGNAAC TGCGCCNNAN GNAAGGATCC	180
AGTCTGGTCT GGTGGTTAA CAGGTGTGCA CTCTGGCAA CCTGTAATGG TGTATACTTA	240
CAGNGGGCCC CTTACACGGN TNAAAACAGN CANTGGGG	278

(2) INFORMATION FOR SEQ ID NO:911:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

TGGAGAGCCT GGTNTCTCAG TACTTCCAGA CCGTGAAC TG ACTATNGCAA GGACCTGNAT	60
GGGAGNAAGG TCAAGNAGCC CAGAGCTTAC AGGCCGAGGT CAAGTTCTTA CTTTGNA	119

(2) INFORMATION FOR SEQ ID NO:912:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

CTGTNTCAGG TTCAAGGTGA AGAACCCAG AGGNACTTC CCTCTGTCAC GGTTCCGCTG	60
TGCCCAAAGG NTTCCAAGGN CTGATGGCTC CCAC TGCTAA TGCCTTGTTT TTGTCACCAA	120
AATCCTGGGA CAGATGCAGA TCTGGNGTC CAAAAGCGGG CCTGCTGGGA AACCTGGGTG	180
TGCTGGTGCT NCANTGGGG TGNAGGGTT CCNTGCGTG	219

(2) INFORMATION FOR SEQ ID NO:913:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

GGCAGAGGTT TACTTCAAGG GCCTGTGGAA GTNAAAGTTC AGCCCTGAGA AACACAAGGN	60
AAGGAACCTTG TCCTACAAGG CTGATGGAGA GTCGTGTTCA GCATCTATGA ATGTACCAGG	120
NAAGGCAAGT TCCCCTTAAT CGGCNCGTG GCTGAAGGCA CCCAGGTGCT TGAATTGCC	180
CTTCAAAGGT GATGACATCA CATGGTCCTC ATNTTGCCCA AGCCTGAGAA AGAGCCTGGC	240
CAAGGTGGGA GGAAGGAAC TCAACCCAGA GGTGCTTGCA GGAGTGGTTG GATGGAATTG	300
GGAGGAGATG GTGCTTGGTG GTNCCACATG NNCCGGTTT CCGCANTN	348

(2) INFORMATION FOR SEQ ID NO:914:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GGCAGAGGTT TTATAGTGCA AGGNATTGGG GTACAACHTT ATNATTTCCTT TTGTGGATAT	60
CCATTGTCTG AGAACATTT GTGAAAAGA GTGTTNTTTT TCCATTGAAT TGTCTTGGTG	120
TCCCTTCTGA AAATCAACTG ACCATAAATT CAATGGTTA TTCTTGACTC TCACCTTCAT	180
CTCATTGGTG TATATGTCTG TCGTTATGCC AGTACTACAC ATTAAATTAC TATAGCTTTG	240
TAATAAGTTT TATTTATTAA NTTATTTNAT TTTTGAGATG GAGTCTCGGT CTGTCGGCCA	300
GGTTGGAGTG CAATGGTGNC CATTNGGTT CAATGCAGGN	340

(2) INFORMATION FOR SEQ ID NO:915:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

GGCANNGCGA CAGTGAATC CCATCTNTAC TAAAAATACA NAAAATAGTT AGCTGGGTGT	60
GGTGGTACGC ATANTNTAAT CCCAGCTACT CGGCCTCCCA AAGTCCTGGG NATTACAGTC	120

ATGGACCCAC GGNGCCTGGC CCTGAANCAG TTCTTTAAGG GGATGAGAAC TTGGCCCTCA	180
AGATCTGGGT TTCCATTACC CCTGCCATCG TCAAGGGTAA AGTNCACTGA ACCTCTGAGA	240
AAGGGTCTC CCAACCAGGG GGGATCACAG GATCTCCAA CCAGGGNGGN TGCCCCGGGA	300
GAGTGTGGTC AGGGTTTCAT GAATGTTAC ACATTTNAA AGTTCTTTG CAAGCTATTA	360
GTGAATAATT TCCAGNAAA TGAANTGGGA TTATTAAATN TCTGTAAAAA TT	412

(2) INFORMATION FOR SEQ ID NO:916:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

TTTGGCTCTG GGGACAGTTG GCATGCNAGG CCTGANTGCC TACTTTGGCC TACTTAAAT	60
CTGTGGTGTG AAAGGGTGG AAAACAGTGA ATGGTTAATG CAGCAGCTGG AGCTGTGGGA	120
CTCAGTCGTG GGGCAGATTG CAAAGCTCAA GGGCTGCAA GTTGGTGGAG CAGTAGGGTC	180
TGATGAAAAG GTTGCCCTACC TTCAAAAGCT TGGTTTGAA TGTCGTCTT AACTACAAGA	240
CGGTAGAGTC TTTGGTAAGA AACCTTGAAG AAAGCGTCTC CTGATGGTTA TGATTGTTAA	300
TTTGATAAT GTAGGTNGGA GAGTTTTCA AACACTGGTT AATCGGCCA GTTGNANGAA	360
ATTGGNAGG GTTTGNCC	378

(2) INFORMATION FOR SEQ ID NO:917:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

GGCAGAGACG GGTAGGAGCC CTGAGTGAGT NTCCATTCCA AGGGGACGAG TCCATCCACA	60
GTCAGGTAA CACAGAGACT TGTTTGCTGA CATTGGACCA CGGGATCCTG TGGNGTTGG	120
TGACTCCTGT GTTCTGNAT CTCCCTCTCC CTTAAAACCC ATTCCTTGG CTCACCTGTT	180
CCTAGGGTTT CTAACCTGTT ATTCCAAATC TGTCACCTGN ACTCCACAAT CTTNCANTAC	240
ACCCATCCGA GAAAAAAAGT NGNTCTAAGG	270

(2) INFORMATION FOR SEQ ID NO:918:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

CTGTCTAGCT TNNCAAAGTT CACCAATACT TTAATGTAGA GCTTATCCAG CCTNGNAGCA	60
GTCAAGGTTTC TACGCCTATT ACACCCTNGA GGCAAAGCTG TACCCGTTT CTACCATCCG	120
GAAAANGNTA GGATGG	136

(2) INFORMATION FOR SEQ ID NO:919:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

TTCGGCACGA GGTCAGAAC ACCANGGN GTGAGGTCAGN GTGTCACTTT TNTGTTTCT	60
NTTTGAAAGA TCATTCGAGA AACACGTCAC TGATCTCCCC TGCAACCATG TNTCCATTA	120
AGATTGAGTG TGTTTNCCA GAGAACTGCC GGTGTGGTGA GTCTCCAGTA TGGGAGGTAA	180
GTNTCCAAT CTNTGCTCTN NGTAGACATT CCTGTAAAA AAGGTTNCC GGTGGGATTC	240
ATTCACCAAG CAAGTTACAG CGAGTGNACC ATGGGATGCC CCAGTCAGCT CCGTGGGCTC	300
TTCGCCAGTG CGGGGAGGCT CATGTTGCCA CCATTGGAA CAAAGTTCTG TGCTTTNAAC	360
TGGGAAAGAA CAATCAGCCA TTGTTCTGG CCACGGTGGG TTAACGACAA GAAAACANT	420
CGCTTCAAT GATGGGAAG GTGGNTTCCC CCCGGAGGTN ANTTGCTGGC CAACCGCAA	480
AGTGTTTAC AAGNTAGGAA AAGGANGAAC AATTCCCANT TGGGANTTGG TATTGATGC	539

(2) INFORMATION FOR SEQ ID NO:920:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

GGTCANCAGC GGCTGCAATA TGGTTGTACC TGGGTCAATA CCCATTCAT GCTGGTAAGT	60
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GAAATGCCGC ACGGTGGCA GAAACTTCT GGTTACGGCA AGGATATGTC ACTTTATGGG	120
CTGGAGGATT ACACCGTCGT CCGCCACGTC ATGGTTAAC ATTAAAGGATA ATATTGCAGA	180
TCGTAAGAGT ATGAGATGAT CTTTCNTACT GTCAGAGCAC TGATTCTCT GACAGTAGTG	240
CTGCGTGCAA AATCCACTAC ATCAAATAAA CCAGCCAAAT CTGCATAGNG GTNAAGAGTG	300
AAACAAACCA ACAGCAGCAA GAATTNTNC ATANTACATT CTNANGGAA ACNTNCTTT	360
TGCCACCTTT NTNCNTGCC NNTGTGTGTN AGTACGGTT NAGGAAATTC CGCATNATNA	420
NTCNTCNGAG NTGGGTNAGG GCAGTNGCTG TTTGATGTT TTNTTCAAA NGGTGNAAAA	480
ANTGNTGGCA CGT	493

(2) INFORMATION FOR SEQ ID NO:921:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

AACTGGTCTT TCATTCACTG TCCAGCTTGC CAATGCAACG GCCACAGTAA ATGCATCANT	60
CAGAGCATCT NTAAGAAGTG TGAGAACCTG ACCACAGGCA AGCACTGCAA GACCTGCATA	120
TCTGGCTTCT ACGGTGATCC CACCAATGGA GGGAAATGTC AGCCATGCAA GTGCAATGGG	180
CACGCGTCTC TNTGCAACAC CAACACGGGC AAGTGCTTCT GCACCACCAA GGGCGTCAAG	240
GGGGACGAGT GCCAGCTATG TGAGGTAGAA AATCGATACC AAGGGAAACC NTNTCAGAGG	300
GAACATGTTN TTATNANTCT TCCTTATTGG ANTATNCATT CCACNTTTAG TNTNTTCCA	360
GGAAGTTGNT TCGTNATTAA CACAGTTATN CATTGTTGG GTTATTCTTG GAGGAACAAA	420
ACAGGGTTT GGGACNGTTN CNTCATGGCN TCCAGGATTT TCAACCTCAA CNTCACNGGG	480
GTGCCATTT TC	492

(2) INFORMATION FOR SEQ ID NO:922:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GGCACGAGCT TGAACAAACC TGGACTGAAA TATAAACCAG TGACTAACCA GGTTGAGTGT	60
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CACCCATACC TCACGCAGGA GAAACTGATC CAGTACTGCC ACTCCAAGGG CATCACCGTT	120
ACGGCCTACA GCCCCCTGGG CTCTCCGGAT AGACCTTGGG CCAAGCCAGA AGACCCTTCC	180
CTGCTGGAGG ATCCCAAGAT TAAGGAGATT GCTGCAAANA CAAAAAAACC GCAGCCCAGG	240
TTCTGATCCG TTTCCATATC CAGAGGAATG TGATTGTCAT CCCCAAGTTC TGTGNACACC	300
AGCACGGCAT TGTTGAGGAA CNTNCAGGTG TTTGGACTTT GAATTGAGTG NTGAGGAGAT	360
GGCAACCTNA TTCAGNTTTC AACAGAAATG GAGGGNCNGT GAACGTGTTG CATNCNNNTNC	420
NTTGGGAGGA TTTTCCTTCG GTGCAGATNT TGAGGTTGAT CTCNGGTGNG TTNTACAGAG	480
TTCTNTNTT CGTTGAGTGT GATTACTN	508

(2) INFORMATION FOR SEQ ID NO:923:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GGCACGAGAA GAAAACTAAG CAAGNGGCAC CAGTACCACA TCCGTGCCTA TGAATCCAA	60
GGGAGGCCTG GGACAATGCC CGACGTCTAA CTGGNNNTCC ATGAAACCTN CAACATNAAC	120
GAACCTTTCT NCTGGTGTAG CCAATACGTA GCGCCANATC ACGCCATTCC CCGGACTGTT	180
GGCCAGGAGA NGAAGGGTTA CTTTGAAAGA TCGTNGCCCC TCTGCCAACT GNGAACCCCT	240
TTTCGGTGNN CAGANGCCCT NCATNCGCAC GTNTTCTTAT TNAATGGNAA CCGGGGGATT	300
GAGGCCTTTA NCAGTGACAA AAATTAAGTG GGACTTAGAA CTTGCCAGCT TGTTTGNGC	360
CNCTAGGCTT NGTTTCTTT GAAAACCNGA TT	392

(2) INFORMATION FOR SEQ ID NO:924:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

GGCACGAGTA GACATTNCCA GAGCTCTATG AGTTAGTGAA CAACTATCAG CCTGAGGTTTC	60
TGTGGTCGGA TGGTGACGGA GGAGCACCCGG AATCAATACT GGAACNTCAC AGGCTTCTTG	120
GCCTGGTTAT ATAATGTAAA GCCCAGTTCG GGGCACAGTA GTCACCAATG NATCGTTGGG	180

GAGCTGTGTA GCATCTGTNA GACATGGTGG NCTTCATAC CTGGCAGTGA ATCGTTATNA	240
ACCCAGGGCA TCTTTNTGC ACATNAAATG GGGAAACTTG GATGNCAATA GACAAACTTT	300
TCCT	304

(2) INFORMATION FOR SEQ ID NO:925:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GGCAGAGCCA GGGTGGCAGC CGGTGCCTTC CAGGGCCTGC GGCAGCTGGG AGATGCTGGA	60
NCTCTCCAAT AACTCACTGG CCAGCGTGCC CGAGGGGCTC TGGGNATCCC TAGGGCAGCC	120
AAACTGGGTA CATGCGGGAT GGCTTCGACA TCTCCGGTAA CCCCTGGATC TGTGAACCAG	180
AACCTGAAGC GAACCTCTAT CGTTGGCTTC AGGCCAAAAA AGACAAGATG TTTTCCCAGA	240
ATGAACACGC GCTGTGCTGG GCCCTGAAGC CGTCAAAGGG CCAAACGGTC CTGGCAGTGG	300
CCAAGTCCA GTGAAGACCA GGGGCTTNGG TTNAGGGTGG GGGGTCTNGT TAGGAACANT	360
GCAACCCNTT TTAACAATGA TTCCTGGCTT TTGNNCNGGT GCGGGGGTTC AGGCTTAAAT	420
NCCAGCATTG TGGGAGGGCC AGTGGGGGGG ATCACGGGTT	460

(2) INFORMATION FOR SEQ ID NO:926:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

CCACCTGCAC ACGTTGTAA GNTCCCAGCC GGCAGCCTGG GACTTCCAGT GCTCAGAGGG	60
CGGGGAGAAT CTCAGCGTGG GNCAAGAGGCA GCTCGTGTGC CTGGCCCGAN CCCTGCTCCG	120
NAAGACCCGC ATCCTGGTT TAGACGAGGC CACAGCTGCC ATCGACCTGG AGACTGACAA	180
CCTCATNCAG GCTACCACATC GNACCCATTG GATAACCTGCA TGTCCCTGACC ATCGNACAAAC	240
GGGTTAACAT ATCAGGGTAC AACAGGGNNNG GTCCTGGACA AGGGTAGTNG TGANTTGATC	300
TCCA	304

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

TATATTATCT	CCCCGATTA	CCGTCATCGG	AGGAGATATA	ACTNTNAGGC	AAATATCGTC	60
ATCAAATAGG	CGGCAAACAG	TGCCAGATGC	GCTGCCCAT	TGAGCACGTT	ATACGTNCGG	120
TGGAGAAGGA	GATATGGCAC	AGCACTAAAG	AGGCCACCAT	CACCACCATT	TCTGGCGCAC	180
CAAGTGAAA	CTNCAATTG	TTACCCGTCA	TAAAGGCAAT	TAGCGTNACG	ACAGTACGGT	240
AAGCGNAATG	GTTGCTAAC	NGGACCAAAG	NACAGATTCA	TCGCGCGTNG	TACCTGGTTG	300
TTCAACATGG	TTTTAATGCA	CNTAACCTTN	CGGGGACAGA	TCAACA		346

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

CCACCTGCAC	ACGTTTGAA	GNTCCCAGCC	GGCAGCCTGG	GACTTCCAGT	GCTCAGAGGG	60
CGGGGAGAAT	CTCAGCGTGG	GNCAGAGGCA	GCTCGTGTGC	CTGGCCCGAG	CCCTGCTCCG	120
CAAGAGCCGC	ATCCTGGTTT	TAGACGAGGC	CACAGCTGCC	ATCGACCTGG	AGACTGACAA	180
CCTCATCCAG	GCTACCATCC	GCACCCAGTT	TGATAACCTGC	ACTGTCCTGA	CCATCGCACA	240
CCGGCTTAAC	ACTATCATGG	ANTACAACAG	GGTCCTGGTN	CTGGACAAAG	GANTAGTTGN	300
TGAGTTTGAT	TTTCCAGCCA	ACTCATTGCA	GTAGAGGCNT	TTTTACGGGT	TGCCA	355

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

GGCAGAGTTG	TGGCCCACTT	TCTTTNAGAG	ACCCCTTGTA	AGGAAAGCCT	TTAAGAAGAC	60
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CCTCAAGGAC CTGAAGCTGA GCTATCTGGA CGTCTATCTT ATTCACTGGC CACAGGAATT	120
CAAGTCTGGG GATGACCTTT TCCCCAAAGA TGATAAAGGT AATGNCATCG GTGGAAAAGC	180
AACGTTCTTG GATGCCTNGG AAGGCGATGG AGGAGNGGTG GATGAGGGGC TGGTGAAAGC	240
CTTGGGTCTG CATTTCAGCA TTNCAGNCGA GAAGTCTTGA CAACTGGCTG AATATAACCA	300
TGANTACCAG TGGTGTCAACC TACTNAGNAG GG	332

(2) INFORMATION FOR SEQ ID NO:930:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

GGCAGAGCAA CACTCATTTC GGGAGGAGGA GGCTATAACC TTGCCAACAC GGCTCGATGC	60
TGGACATACT TGACCGGGGT CATCCTAGGG AAAACACTAT CCTCTGAGAT CCCAGATCAT	120
GAGTTTTCA CAGCATATGG TCCTGAATTA TGTGCCTGGG AAATNACGCC AAGCTGCCGG	180
CCAGACCGCA ATGAGCCCNA CCGAATCCAA CAAATCCTCA ACTACATCAA AGGAAATCTG	240
AAAGCATGTG GTCTAGTTGA CAGAAAGAGG TCCAGGTTTC CAGAGCTGAG GAGTGGTGCC	300
TATTAATGGA AGACAGCGTG TTTTATGCAA GCAGTTGTT GGGATTGTTG GACTNCAGGA	360
AAATTTGGAA GGAAATTAN TCCCGNAAAT TTCCAGGGC ATCAGTGGGC ANTGGNTTCC	420
CGGGGTTAAG	430

(2) INFORMATION FOR SEQ ID NO:931:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

ACGGTTNCGC TGTCCCAAAG GTTCCAAGGG CTATGGCTCC CACTGCCTAT GCCTTGTGTTT	60
TGTGNANCAA AATCCTNGGA CAGATGCAGA TNTGGAGTAG CCANAAGCGG GCCCTATGGT	120
AA	122

(2) INFORMATION FOR SEQ ID NO:932:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

GGCANAGAGA AGATAAACGA GGGGCTGGAA CACCTGCCA AAGCAGAGAA ATACCTGAAA,	60
ACTGGTTTT TAAAATGGAA GCCAGATTAT GACAGTCCCG CTTCTGNAAT ATGGAAAAGC	120
AGCTGTTGCT TTTGAAAAAT GCCAAACAGT TTGAGCAAGC AAAAGATGCC TGCCCTGAGGG	180
AAGCTGTTGC CCATGNAAAA TAATTAGGGC TCTTTTCAT GCTGCCAAAG CTTATGGAGC	240
AAGCTGGGAA TGAATGTTGA AGGAGATGCC AGAAACTTAC CAGAGGCCGT TCCAGCTTAA	300
TTGGGGAAGG CCAGCATGAT GTGATCTTAG GAAAACGGGC ACCCCAGACA CAGGCAGCCC	360
TGGGTTTTGG GGCGAGCNTG GGAAAGTTTT TGGGAAAATN TTGATCCCGN GAAGGCTGTT	420
ACATTTTTT CACCGGNCAG TTAATGTGTT TTGAAATNGA NGGACCGTTT ACGCCAGG	479

(2) INFORMATION FOR SEQ ID NO:933:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

GGGCCTGAAG GANTTGGGAA GAGCACATT TAAGGATGAT TGTTTAGNTT TAAAAGTTAA	60
CAAATANTTT ANTGTAGAGC TTATNCAGCT TGGAGCAGTA AAGGT	105

(2) INFORMATION FOR SEQ ID NO:934:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

AGTAAAAGGC TCACTATGGA GGNTTCACTG TNCAGAATGA AGNCAAACAA ATACCAGATC	60
TCAGTGAACA AATACAGAGG NAACAGNCGG TAATGCCCTC	100

(2) INFORMATION FOR SEQ ID NO:935:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

TTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNCCCCCC CNNAAANG 58

(2) INFORMATION FOR SEQ ID NO:936:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

GGCACGAGGT GACAAC TGCC GGNAGGTGCA CCTCGANAAG CGGCGAGGGG AGGGCCTGGG 60
CGTGGCCCTG GTGGAGTCGG GCTGGGGCTC CCTGCTGCC ACAGCCGTNA TCGCCAACCT 120
GCTGCACGGG GGGCCTGCTG AGCGCTCGNG GGCCCTCAGC ATCGGGNACC GCCTGACCGC 180
NATCAACGGG ACCAGCCTGG TGGGGCTGCC CCTGGCTGCN TGCNAGGCCG CTGTACGCAA 240
AACCGGAATC GCCAGACGTN CGGGTGAACA CTTNAGCATT CGTCCACTTG CCCTTCCC GT 300
TAACCACCGN CATCATTCCA CCGGGCCCCC AAGGCCGNA AAGCAAGTTG GGGTTTTG 360
GNTNGGAGGA CGGGATTNAT TTT 383

(2) INFORMATION FOR SEQ ID NO:937:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

CGCGTGGTCG CATGAAAGAT CTGAAAGCCA GCTATGTNCT GAACAGCAGT GAATTGCATG 60
CGCCGCTGCA AAAGANTCAG GTCGTCGGAA CTATCAACTT CCAGCTTGAT GGCAAAACGA 120
TCGAGCAACG CCCGCTGGTT GTNTTGCAAG AAATCCCGGA AGGTAACCTTC TTCGGAAAA 180
TCATTGATTA CATTAAATTAA AATGTTCCAT CACTGGTTG GTTAAAATT AAACACTTGA 240
AAGTGTAAATT TCCGTCCCCA TATACTAAGC ATCAGTAAAA AAACTCCCGC CTTCTGGGG 300
TTGGCCTTNA TTTNAATTAC GTTAACGCCG GAGCTGACAT GGAAAACCAA ACTTAACGGA 360

CTGCTTGATT TNCCNTACTC CTTTACTTA CAAAGTTTG GGGGCAGGCG TTACCGNGGN	420
TGGTTGATCA GNGGGTTGAA GTGGTACAGN GCCTGCCAG GTGGCTACAC CCCACGGTNA	480
A	481

(2) INFORMATION FOR SEQ ID NO:938:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

GGCAGAGTGA ATCATCAGAG AATTCACACA GGGGAGAAC CCTTTNANTG TAATAATGT	60
GGGAAAACCTT TTGGCCAGAA ATCAAACCTC AGANTACATC AAAGGACTCA CAGTGGGGAG	120
AAATCTTATG AATTGCAATG ANTATGGGA AATTATGTAA GAGAGTCTAC CCTAAGCTTT	180
ATACCAGAAA ATTCAGGGN GAGGGGGAA TCCCTATTGA TGTATTAAC NGGAAATNCC	240
TTTTGACCAA AGGGATTNCC CCNTTGAT	269

(2) INFORMATION FOR SEQ ID NO:939:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

CCCAAAATAA CCAGCTAGGG TGGCTGTGGG GCCANANCCG TGCCCTCTAT CCNAGCATCT	60
ACATGCCCGC NGTGTGGAG GGCACAGGGA AGTNACAGAT GTATGTNCAA CACCGTGTGG	120
GCCGAGNGCA TTCCGTGTGN GCTGTGGCT GCTGGTGAAC CCCAATNTTG CCGGTNGTTG	180
CCCTATTGTC CCAGATTTN CTTATGNACA CGGACAAACC ATTTTTTTG CCCCTGGGA	240
TTGAGCTTGG GAGCAAAGNC TTGGGGGGAG AGTNNGGCC CAGGGGGG	288

(2) INFORMATION FOR SEQ ID NO:940:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

TGGGGACCTC AAGGCCGCG GGCTGACCCT NCAGTGGGTG TACTCGGCGC GGGGGGACTA	60
NATCCGGCG CGGGAAAANC TCGGGCAGGA GATCTACAGC TCGGAGGAGA GAGACGAGCG	120
ACTNANACGC ATGTACAACG TGCGCATAAT GCGGGTGGAG TTCTACTTCC TTTCCCAGTA	180
CGTTTCGCCA GCCGACTCCC CGTTCCGCCA CATCTCATG GGCCGTGGAG ACCACANGCT	240
NGGCGCCCTN CTGGACCACC TGCGGGCTGC TTGCGCTTCC CAACAGTTCC GGGNACCCCC	300
GGGGGNCCAA CTTTCTTNCA ATTGGGTTTT CCAAGGAAAA GCNTTTTNCC GGGTTCAAT	359

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

TGCAGGATTN CGGCAGAGGG AAAANTGTT TNNTTAGGTT TGGTTAACGC AGGCAAAACC	60
ACTTTCTTCC ACATGCNCAA AGATGACAGA TTGGGCCAA CATGTNCCAA CANTACATCC	120
GACATCAGAA GAGCCTAACAA TTTGCTGGGA ATGAACCTTT ACAACTTTN NACCTTGGTG	180
GGCACGAGCA AGCACGTCGC GTTTGGTAAA AATNATCTCC CAGCAATTNA ATGGGGATTT	240
TTNTNNNTGG TGGGACTGTG CCAGATCATTT CTCGNCCCTCG TGGGAATCCA AAGTTGTAGC	300
TTGAATGGCT TTANATGGAT TGGATGGAAA ACAATTATCC CAAATGNTGC CCAATCCCCT	360
NATTTTGGA GGAANCAAAN AT	382

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GGCACGAGCC AGGATTGGTG CCTTCTCTNA TGGCTCTGGT TTAGCAGCAA GTTTCTTTTC	60
ATTCGAGTA TCCCAGGATG CTGCTCCAGG CTCTCCCCTG GACAAGTTGG TGTCCAGCAC	120
ATCANACCTG CCAAAACGCC TAGCCTCCCC AAAGTGTGTG TCTCCTGAGG AGTTCACAGA	180
AATAATGAAC CAAAGAGGAG CAATTCTACC ATAAGGTGAA TTTNTCCCCA CCTGGTGACA	240

CAAACAGCCT TTTCCCAGGT ACTTTGGTAC CTGGGAGGCG AAGTGGGACG GAGCCAGCAT	300
NGCCGGAANG TATTGCCCG GGGGTCCCNG TTTTNAAGG TGTTTTTNG AAGTCCATG	360
GGAAAGTTTC CTGGGGAAAC GTTTTTTG GCAGGGTTT TTCCCCGNGA AATCANTNTT	420
TTTNAAGGG TCCCCANTTT TTAGGTTGGG AAAA	454

(2) INFORMATION FOR SEQ ID NO:943:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

GGCACGAGCG GCACGAGCAC CAAGCAGGCA GTGAGCATGT TTCTNGGAGC AGTGGAAGAA	60
GCAAAGAAAG AAGGTGGCAC AGTGGTCTAT GGGGCAAGG TTATGGATCG CCCTGGAAAT	120
TATGTAGAAC CGACAATTGT GACAGGTCTT GGCCACGATG CGTNCATTGC ANANANAGAG	180
ACTTTNCTC CGATTCTCTA TGTCTTAAA TTCAAGAATG AAGAAGAGGT CTTTNCATGG	240
AATAATGAAG TAAAACAGGG ACTTTCAAGT AGCATTTT ACCAAAGATC TTGGGCAGAA	300
TCTTCCGCT GGCTTNGAC CTAAGGATC CGACTGTGGG CNTTGTAAAN GTNCAACATT	360
NCCAACAAGT GGGGCT	376

(2) INFORMATION FOR SEQ ID NO:944:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GGCACGAGCC TGTATCAAAA AAAGGAGACC TGAGGAGGGC CTTGAGCAGA TACATCTCCT	60
CTCTCATCCA CTCAGGTGGC CACTAACACCG GACACCAGCC GAAATGCCGG AAATGCGGTC	120
CTGTTGAGA CAGTACTCAC CATCATGGAT ATCCGCTCTG CAGCTGGCCT ACGGGTTCTA	180
GCTGTCAACA TTCTTGGTCG CTTCCTACTC AACAGTGACA GGAACATTAG GTATGTAGCC	240
CTGACATCAC TGCTTCGAC TGGTGCAGTT TTGATTACCA GTGCTTGTG CAGCGGGNAT	300
TCGGGCCCA CTNTGGGTGG GNAATGTTCT AAGGGGGAAA CTNGANTGCC T	351

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

GGCACGAGGT GTTAACTTCC AGATAAGGGA ATATNATTNA ATAATTNATN ATTTNAAAA	60
TACTGTATTA TGAAGCCATG TTCATAAAGG TAAGAAAGGC AGATTCTACA ACTAGTCAGA	120
CAACTTAACA TTCATACTAA TGACAGCTTC ATTGAAATCA CTTTACTACT CCCCTAGTAA	180
TGGAGTCATT GCATTTATAT TATACATTAT TCTCTTNCA GTTTTGCTAG CCACCCTAAT	240
TATCCATATT CAGATGAATA TTTAACATGG AGGAGCTTG CCTGAGGTCT ACCCAGNAAG	300
CCCTGTGTGT GGGTGGTGAC GNCGAGGACG GTCTCTTTG CCGGTGGACT GGACANATNA	360
CNC	363

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GGCAGAGTTG AGCGGCCAG GGACCGATAC TTGTAATCAG GGATCGCNAC CTCANANAGT	60
GCCAAGCCCC CGACGCACAA ATATGTCCGG GGAGAGAATG GCCCTGGGGG CTTCATCGTG	120
CTCAAGTCGG CCAGTTAACCCCGTNTTG NACCTTTNTN TGGGNTCTTA ATACAGGTCT	180
	180

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GGCAGAGCGG ATCACTGGAG CCAAAACCTG TCCCAGTTT TCCCTGAGGC CATTCTTTTC	60
ATAGATGAAG CCCGGGGCAA GAACTGTGGT GTCTGGTAC ATTGCTTGGC TGGNCATTAG	120

CCGCTGCAGT CACTGTGAAC TGTGGCTTAC CTTATGCNGA AGCTCAATCT GTCGATGNAA	180
CGATGCCTAT GAACATTGTC AAAATGGAAA AAATCCAACA TATCCCCTGA ACTTCAACTT	240
CATGGGTNCA GCTGCTGGAC TTCGAGAGGA CGCTGGGAC TTCAGCAGCC CATGTGAACA	300
ACAGGGGTTT CCAGCACAGC AGCTGTATTT TTACCACCCCT TTCCAACCAG AATGTGTTAC	360
CAGGTGGGAC TTTTGCAAT CTAGGGNAAA GACCCACAC CCTCNTGNTG GGATGTTGTN	420
NGGCCTTCAG CAATTTTTT GGCAGC	446

(2) INFORMATION FOR SEQ ID NO:948:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GGCACGAGCC ATCATCCCC AAGANCTTCA AAGATTTAA AGGCCACCAT TTCCATGCAC	60
ATGTTTCTTG GCGTTGCTGC TGTTTACACT ATGTGGAAAG CTGGACACTC AGCCTGTTTC	120
GGGGGGACCC AGGCTAAAGG TTNTGCCCTA GGTGTGGTAA GTATCTATTG ATGCGTAGTG	180
TGGCTTGCAG GGAAC TACAG GGGCCACACA CCAACCATTA AGCACCAGGC CTAAGGCAGN	240
AAGCAGAGAG AAACCAA CTT CAAGGTCAGA GGAGCCGCTG GGNAGGGAGA AAGGTGTNTN	300
GGTGGAGGNC TAACCAGA	318

(2) INFORMATION FOR SEQ ID NO:949:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

ATGCCAAAGT NTTCGATGAA TTTAACCTC TTGTGGAAGA GCCCTTCAAA ATTAAATTC	60
AAACAAAATT GTGAAGNTTT TTGAAGNCAG NTTGGAGGAG TTACAAATTN CCAGTAATGA	120
GCCTATTAGT TCGTTAACAC CANGTA	146

(2) INFORMATION FOR SEQ ID NO:950:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

AACCCATAAN TCCAAAAGA AGATCAGAGA ATATTATAGA CTGCTGANCG TGGAGGAAGG	60
ATGCCCTGCA GATGAAAGTC AGGGNAATCT TTTCATAAGC TTGCCAAGCA ATATCATCCT	120
GAACAGTGGC TCTNAATACT GCTGATTCTG CCAACATTAA TAAAGGNTTG AAAAGCTTA	180
TAGNAAAGGT GCTCTCCCCT GTGAATAGAN CAAACAAATG CCAGTCAGN GTNAAAGGTG	240
AAGNAGGANG NAGATGTAGG AAAANTCAA ATATNAAAAC ACCCCAACAC CGGCNTTATT	300
TAAGTTTTG AAGGGTTNTT GGTTTGGGG NCTCCAAATT CAAGGGGGGA AGGCTTTTG	360
GGGNANCNTT TGGGGG	376

(2) INFORMATION FOR SEQ ID NO:951:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

TATTTAGGTT TCTTTAATT TATTCAACAA TATTTGTAA TTTTCAGCAT ATAAGTCTAT	60
CACTGCATTG GTTAAATTAA TTCCTAAGTA TTTTACTGTT TTTAATGCTA TTCTAAATGG	120
ATTCTTTTA AAATTCCTT TTCATATAGT TCATTGCTAA CCTATAGAAA TACAACGTAA	180
TTTCATCATG GGCAGTTTC TTTCTACATC TTAAGGAAAT TAGTTATTA GCTCTAAATG	240
GGGTTTATT TGTGGATTCT TTAAAGGTTT TCTTCCATAT TAAGATCCAT GTCCATCTCT	300
AAAATAGGGG ATTAGTTTA ATNTTTCCA TTTNCCCATT TGGGCTGCC TNAAANTTNC	360
NTTTCTGCC CNAATGTTCC CGACCNGAAC TTCCGCAGGT ATTGGATAGA GTGGTGAAGC	420
AGGGANCTT GCCCCGTTTT TAACCTAAGG GNAAAGGTTN CG	462

(2) INFORMATION FOR SEQ ID NO:952:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

GGCACGAGGT TTTCTCATGC TTTTNAAAATC ACTCCATCCG TAGCCAAGAA GATTGCTGCT	60
GTACTTACGG ATTCAATTCC ATTGAAAGTT CGTGGCATCC ATTTGATAAA TGAACCAGTA	120
ATTTCCATG CTGTCTTTG CATGGATCAA ACCATTCCTG GACTGAAAAA NTTAAGGAAC	180
GGACAGGGCC TCACCTTGTG NCAGTGGGCA CGATCTGGG CTCACTGCAA CCTCCACCTC	240
CTGGGGCTTC AAGCAATCCT CCTGCCTTCA GCCCACCAAG TTATCTGGG ACTTACAGTN	300
CCTGCACCAC CANGGCTGTN AAATCCCCGC ACNTTTGGGA GGGCCCNNGC GGGCGGGTTC	360
ACGGGGTTCA GGGGNTCGGG ACCCTTCCGG GTTAAAANGG TGGNAACCCG TTTTTTANTT	420
AAAATTCCAA AAAATTGGC CGGGNGTATT TGCGGGGGC TTTTAGTNCC CATTATTTGG	480
GNGTTTNGGC AGGGATGGGG GTTAN	505

(2) INFORMATION FOR SEQ ID NO:953:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GGCACGNGCG CATCATAAGG GGCGCCTGG CGAAGGCTGG AAGTGGGGCG GCTGCAGCNA	60
GGACGCTGAC TTCGGCGTGT TAGTGTCCAG GGAGTTCGCG GATGCNCGCN AGAACAGGCC	120
NGACGCGCGC TCGGCCATGA ACAAGCACAA CAACGAGGCG GGCCGCACGA CTATCCTGGA	180
CCACATGCAC CTCAAATNCA AGTNCCACGG GNTGTCGGGC AGCTTNAGG TTGAAGACCT	240
GNTGGTNGG GCGCAACTTG ANTTTCCGTT GCCATCGGTG ACTTTCTCAA GGACAAGTTA	300
TGACAGCGNC TTTGGGAGAT TGTTAGTAG AAGAAGNAAC CCTTNNTT	348

(2) INFORMATION FOR SEQ ID NO:954:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

TTTCCTTTAA TCTTCCGCC CTGTAAGTGT TTCCATGCTT TATGAGCAAC AGCCTGACGG	60
ACCGCGACAT AGACATGCGC CGGATGCACG GGTATTTGC CAATATCTGC GCCATCAAGC	120
CCGATATCTC CTGTCAGTGC ACCTAATACA TTACCCGGGC GCATTTGGC TTTTTCCCG	180

NCATCGATAAC ACAACGTTGC CATTCTGCT TCCAGCGTCG CAATGTGAAC TATTAGCTG	240
GCGCGTTT GNCAGTNAAA GTTTTATCT TGCAACATGT NCAGAAATGG ATATTGGGCC	300
CGCTGGTGGT TTNTTCCGG AGNCACAGT	329

(2) INFORMATION FOR SEQ ID NO:955:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GGNAGAGCCA TGGNGGNCT GGTGGATNAG GGNCTGGTGA AAGCCCTTNG GGTCTCCAAT	60
TTCAGGCACT TNCAGATCGA GAAGCTCTTG AACAAACCTN GACTGAATNN TAAACCACCA	120
ACTNNCCAGG TTGCAGTGTC ACCCATACCT CACGCANGAG AAACNTATC CAGTACTGCC	180
ACTCCAAGGG CATCACCGTT ACGGCCTACA GNCCCCTGGG TTCTTCCGGA TAGACCTTGG	240
GCCAAGCCAG AAGANCCTTC CCTGCTGGAG GGTNCNAAGC TTAAGGTAGA TTNTTGCAA	299

(2) INFORMATION FOR SEQ ID NO:956:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

ATCACTTTG ACCTCAGTTT TAACAACTGA GGAGGAGGAG CTCATCATGT ATCTGTTCAT	60
TCATTTACCA TATATTATT AAGCACCCAC TCTATTCTGG GAAATAGTNT ACAGTAGTGA	120
ATACTAAAAT GCCGGGCTAA TATCTCTACC TTCATATAGC TCACATTCTA GTGGCAGGAA	180
GAGATAATAA GTAAGATAAN ATGAAGTACA ATATATAATA TGTTAGATAA ATGCTCCAGT	240
GGGAAAAAAAT AAAGCGGGGA AGGAATACAG GGAATGCCTG CAGAGTTGAA TGGTTAAGGT	300
AGCTTGGGGA AATCCCTCAC TGGGGNNNTCC GNGGAACCTCC AACAAAGGGN CCCCGTGAGG	360
CTTGTCTGGG GGNCCAGAAA GCTCTGTCTG GGGGCCTGGG	400

(2) INFORMATION FOR SEQ ID NO:957:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

AGAAGAGCTA ACANTTGCTG GAATNACCTT TACAACCTTT ANTCTGGTG GGCACGAGCA	60
AGCACGTCGC GTTTGGAAAA ATTATCTCCC AGCAATTAAT GGGATTNTT TTTNTGGTGG	120
ACTGTGCCAG ATCATTCTCG CCTCGTGGNA ATCCAAAGTT GAAGCTTAAT GCTTTAATGA	180
ACTGATGAAA CAATATCCAA TGTGCCAAT CCTTATCTTG GGTAACAAAA TTGAACAGAN	240
CAGATGCAAT CAGTGGAAAGA AAAACTCCGT GAGATAATT TGGGCTTTAT GGGACAGACC	300
ACAGGTAAAG GGGGANTGTG AACCTGAAA GGAGCTGAAT GCTCGGCCCN GGAAGTNTTN	360
CAGTGCCATG TGGTTCAAGA GGCAAGTTAC GGCGAGGTTT NC	402

(2) INFORMATION FOR SEQ ID NO:958:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

CAGNAGGGAA ATNNNTTTT TAANTCCAGC ACGGGGTTAC TGTTTTTTA TCTCAAAGCC	60
AAAAGCCACA GGCATGGCCA CAGTTACTGT NCATCTCAGG GAATGTGAAA AGANTCAAGA	120
TCCAAGCAGC CACAGACTCA AAGGNACATC AGTGAACUGC NTGGCCAAAG CATAACCCACA	180
GTACTACAGA AAGCCGTNCA GTGGTCAAGC GGATGCCGGC CATGCTCACT GGACTCTNTC	240
AAGGTCTGTG GCACTCGGNC AGGTGGTGT TACTAGTGNT CCTCATAAAA NTTAACCTCC	300
CTGGTGCAGAA TTTCCAGTTC ACCTGGTGT TGCGGACTGG GAATTCTTGA GNNTTTGNTT	360
AAGAGCTGTT GCTGTTGGCT GNAGTATGGG TTGTGTTATG TNNAAGGTG	409

(2) INFORMATION FOR SEQ ID NO:959:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

TAAAGCTAAC CAGCAATTTT AAGTCTACTG TAAAATCAAT GGGTCTGGAA ATGGATGGNC	60
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TGTTTTNAA AAGAGAACTT GNATGGCAGT TTAGATTCA AGAAAAACTG GTTCATTAT	120
GAAAGNAAGG NTTGGANCA TCTTTTCCT NACTGGCAC AACAAATTG TGGCTGGAA	180
AATGAGAAAG GTTCATTGA ATAAAGGCNC ACAGTCTGCC ATCCCATATG CTTTNAGAGN	240
TGGGACTGGG AAGGACTGGG ATGGGCAGAN CCCNTACT	278

(2) INFORMATION FOR SEQ ID NO:960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 188 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

CGCGTCGTT TNACCTGTNA CGTTCACGCC CATTGCAGCG GCACAGTCAC GCAGACGTGC	60
AGCGGCGACT TTCCTGTTGA ATACCTGAAC GTGCAGCANA AAACGGCGTT ACATACACCG	120
TGTGGCAGGT TGTAGAAACC GCCCAGCTGG TGCGCCATCG CATGAACATA ACCCAGAGAA	180
GCATTATT	188

(2) INFORMATION FOR SEQ ID NO:961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

TTAACCAAAA TCCTGGACAA ATGCAGATNT GGCCTGCAA ANGCGGCCCT NTGGAACCT	60
GGTGTNTGTC CTCATTGGGG CTTAAGGGNT CCTTCCGTTT CCTCCCTGGT TGAANAGCAT	120
TGGTTAACAN CTACTTCATA ACGTTGGTT TGGGNCTCC	159

(2) INFORMATION FOR SEQ ID NO:962:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

CCGCCTCAAG GACCCTCAGG TNTGGATGGA TGCAGGCACC CANNTCTNNNT TCTCCTTTGC	60
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CATCTGCCAG GGGTGCCTGA AAGCCCTGGG CAGCTACAAC AAGTNTCACA ACAACTGCTA	120
CAAGGANTGC TTGCCCCAT GCTCCTGAA CAGTGCCACC AGCTTTTGG CTGGGTTTT	180
NGTCTAGATT TGGGACATAT CTCTGGAAG GAGCTATTAG CCATGACCCA CAAAGGTAG	240
AGATTAGGGT TGCTGGTATT TTGGTTTTGG CTGNTAAAG AGGCCCTAG GGACCANAAT	300
TTTTCCN	307

(2) INFORMATION FOR SEQ ID NO:963:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

CGTGGTGGNT CATGCCTGTA ATCCCAGCAC TTTGGGAGGC CAAGGCAGGT GGNTCACGAG	60
GTCAGGNGTT CAAGACCAGC CTGGCCAAGA TGGTCAAACC CCATCTCTAC TAAAAATACA	120
AAAATTAGCC AGGCGTGGTG GCAGGTGCCT GTAATTCCAG CTACTCGGGA GGCTGAGGCA	180
GAGAATTGCT TGAACCTGGG AGGCGGAGGT TGCAGTGAGC CGGGATCACG CCACTGCACT	240
TCAGCCTGGG CAACAGAGTG AGACTCCATC TCAAAACCA AAACAAAACA AAAAAAAACTT	300
CTTGCTCATT CTTGCCTAAC NATGCTTCC CTGTTACCGT CANAGTAAAT ATATCTTACT	360
GGGGCTGGNA TTATAATTAA CANAACATTT TTNACATATT TGAGTNTTTC CTCTTGGAAA	420
AAT	423

(2) INFORMATION FOR SEQ ID NO:964:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

CGAAGNCCAT ACCTGATGGA GTCTCTGCCA AAATATTTTT GTCATCATCA GAACTAAAAA	60
GCCACAGCAC CTGAGACAGA AGGAGAAATT CTAGAGTTGA ATGNCACTTC TGAAGCCCTC	120
AAGCAAGAGA CTTTCCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTCCACCATG	180
TAAAAAAATA CCTCTTAAAC CGGNTCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT	240
ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TGCTGTGGAG TGAAAAGCAA	300

CCAAAGGCAA CAGAGTCTTA GCTCATGGCC ACCAGACCAA AAGCATCCAG TTCTGTTGCA	360
CCTCCTGGAA AGCTNGCAGA GGCCCTGGAN TTTCCAGNTC ANCTNAGGGG AAAGGGTTGT	420
TT	422

(2) INFORMATION FOR SEQ ID NO:965:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

CGAAGNCAT ACCTGATGGA GTCTCTGCCA AAATATTTT NTCATCATCA GAACTCAAAA	60
GCCACAGCAC CTGAGACAGA AGGAGAAATT CTAGAGTTGA ATGACAATTG TGAAGCCCTC	120
AAGCAAGAGA CTTTCCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTNCACCATG	180
TAAAAAAATA CCTCTTTAAC CGGNTCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT	240
ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TGCTGTGGAG TGAAAAGCAA	300
CCAAAGGCAA CAGAGTCTTA GCTTCATGGC CACCAGACCA AAAGCATCCA GNTTCTGTGC	360
ACTTNCTGGAA AAGCTGGCAG AGGTCTGGAA TTNCCANTTC TACCTNGGGG	410

(2) INFORMATION FOR SEQ ID NO:966:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GGCACGAGCA AACTATAAAA AATGGTACCC ATGGTAGGA CATAGCTACA CAAGCATTG	60
TAGTTAGAA TATATAATTC ATAAAAATTG GAAGTGAGAG GAATAGTTAA TATGTAATAG	120
AAGAAAAAGT ACTTGCTCAG GTAGTTGAA CTCTTAATAA AACCAATGAC TAGAATACAA	180
GTGGAAGTAA AAAGGTGGAG ATAGATTAAT AGCCTAAATA ACGAGAGAAC CTTATGCCTT	240
TTTTAAAACA AAACAAAACC ATTGAGACAT TTTACTTAGT CCTAAAATCT AGCCTGGGNT	300
TTATGCTATA AATGGATATT CTATTTTCA TGTTAAATTG TACATTACNC AGAAATNATN	360
AATATTNTTA CTTT	374

(2) INFORMATION FOR SEQ ID NO:967:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

CGAAGACCAT ACCTGATGGA GTCTCTGCCA AAATATTTT NTCATCATCA GAACTCAAAA	60
GCCACAGCAC CTGAGACAGA AGGNNGAAATT CTAGAGTTGA ATGACANTTC TGAAGCCCTC	120
AAGCAAGAGA CTTTCCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTNCNCCATG	180
TAAAAAAATA CCTCTTTAAC CGGATCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT	240
ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TAGCTGTGGC AGTNGNAAAG	300
CANCCAAAGG TCAACAGTGT TTTNGNTTCA TGGCCACCAAG TCC	343

(2) INFORMATION FOR SEQ ID NO:968:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GGCANAGCCA TNATGCTTTC ACCAAGGCAA TCCAAGAAGC TCGGCAAATG AAGGAGCAAC	60
TCCGACGGNA ACAACANGTN CTTTANGGGT AAGGTGGCTT TTGTGAATAG TCTGGGTCTC	120
AATAACTGGC CGAACAGAAA AAAAAAAAAA AAAANCTT	158

(2) INFORMATION FOR SEQ ID NO:969:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

TTTTTCTCTG AACTATTTGT TNATATCACT TTGCCATT TAAAAATTGG GTTCCGCC	60
CTCTTAATGA GCAGGAGTAG CCTTCTGTGT ATTGAGTTA ACTTTGTGAT ATAAGTTGCA	120
GATTCTTTT CTCAGGTTT CATTCTATT TTCCCTGTAG TTTGTACCTT TTCCATTTT	180
ATGGATATCT AACTCAACC TTAACGGCA GAACTCACT GATACTTTG TTAGGTAAAC	240

ACACATCTGT CCCCAGGATA ATTTAACACA ACGACAGAGA AGGGAGGTAG NAAAANNAGT	300
TNGTAGAGAG CTCAGNAAGG GGCTGG	326

(2) INFORMATION FOR SEQ ID NO:970:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GGCACGAGCT AATATATAGA ATACACTTT ATAATATATT NTAATATATA GAATACACTT	60
TTATAATATA TTNTAAATATA TAGAATACAC TTTTATAATA TATTCTAATA TACATAATAT	120
ATTCTAATAC ATGTAGACAC ACCCAATTAA ATGCTTGCA TGGGCATAGT TATGCAAAGC	180
CTAGTTCTTA AGTGCAGTGG TCTCAATGTG TCCCCAGAA TTCATATGAT TGANGCTTAA	240
TCCCCAGTGG CAACAGTGGT GAGNAGCTGG GGCCTAATGG GAAGTGTAA GTTTNTGAAG	300
GCCTCTGCC C TGCATGAANN AGGTTNAATG TTGTTGTGG AAAGGGTGTG GA	352

(2) INFORMATION FOR SEQ ID NO:971:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

CTTATCTAAT TCCNCTGGCT AGANCCTCAA GTATAAGGTT AAATACAAGT GGCAAGANTG	60
AATATCCTCG TCCTGTCCT GAGCTTAGAG GAAAAGCCCT ATCTTCACC ATTAAATTTG	120
CATGGTGGTC GTCAGTTAA CATAGCTGTT CTCTATCAGG TTGAAGGTGT TCCATTCTAT	180
TTTNAGTTT ATTGAGTGGT TTTACTATAA AAAAGCATGT TGNAATTTG TNAAAATATA	240
TATGCCTTT TCCTATTGGG NATACTTAGT GGGATTTGG TCCCTTTAAT TCCCGNTNTA	300
TANGGTTTT TAACANTAA TTTGGATTT CAG	333

(2) INFORMATION FOR SEQ ID NO:972:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GGCANAGTCG CATTGGCCC GCGGCAGCCC CACCCCGCT CCCTTCCCCA GGCACCGCGG	60
CGGGANGCCC TGCCCTGCCG CTGAACCCCC TGTGTCCCTGC TCCGGCCCTC TCGCCAGGNA	120
CTCCTGGCCT AGCCTTGCAC CCCGACCCTT TCCCGGGAA GCCGGGGGA CCTTACGCTG	180
GGGGCTTGTT GCCGCCGAA GTNATGACCC CGCGTGGAA GAAGCAGGGT TAGGGGTNG	240
GGAGTCCTTG GTAAGATCCC TGGACGTCAG NACAGTAGAG GCGGGTGGTA GANGGGTNNG	300
	300

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

GGCACGAGCG GGAGCAAGAG TCCGCTGAGC TGCAGTGTCT GGTCGAGAGT ACCCGTGGGA	60
GCGTCGNNCNC GGGGAGGGCAG CCGTCCCAGG TTAGGTGGCG TGGCCGACCG GACCCCCAAC	120
TGGCGCCTCT CCCCGTGAGG GGTCCCNAGC TAGGAGATGG GAGGCACAGC TNCGTGGCC	180
TNGCGGAAA GNAATGCGGG GTCCGTTN	209

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

GGCAGAGCGG GGACATAGTG AACACTTGTG CGGGGACATG NTAGACACTT ACAACTAAGG	60
CATAAGAACCGTTATGGA GTCGCTTATG CCCTGGGAAT GCNAGAAATA CCATGTCATT	120
ACGTACTGAG TTTGTTTNGT TCGCCTCGCA GGNACGGGGC GACATCCGTT CCCTCTGCCG	180
TCGCTTCGGC ATTTNACCTG CCACCGGTTA CAAGTGGCTC CAGCGCTGGG CTCAGGAAGG	240
TGCCGCCGGT CTTCAGGACC CCCCGNGCC ATTCCGCACC ATTCCCCGAA CCGTTCATCT	300
GAACGACATC ACGGCCCTGC TGCGTATGGN CCCATGAACC GTAAGNAACG TTGGGGAGCC	360

CGNAAGTTA AGCGTTGGTT CNAGGGGGGG CCCGTACCAT TGGCCTTAA TNAGTCGATT	420
A	421

(2) INFORMATION FOR SEQ ID NO:975:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GGCACGAA GCGTACTGCA ATTAAGGCCT TCAATNAGAC TATCAAGATC TTTNAAGAGC	60
AGGGCCAGAC TCAAGAGAAA TGCAGCAAGG AATACCTGGA GCNCTTCGG CGTGAGGGCA	120
ACGAGAAAGA GATGCAAAGG ATCCTNCTGA ACTCCGAGCG GCTCAAGTCC CGCNTTGCG	180
AGATCCATGA GAGCCGCACG ANGCTGGAGC AGCAGCTGCG GGCCCAGGCC TCGGACAACA	240
GAGAGATCGA CAAGCGCATG ANCAGCCTCA AGCCGGACCT CATGCAGCTG CGCAAGATCC	300
GAGGACCAGT ACCTCGTGTG GGTTCACCCA GAAAGGCGCC CGGCAGAAGG AAATTCAANG	360
NTGGTTGGGG GTTTAAAATG NGATNNNGTGG TAT	393

(2) INFORMATION FOR SEQ ID NO:976:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GGCAGAGAAA CAGCTGTNTG AATTATGTCT GCACTAAGTC TCTGGCAGAG GAAGCCCAGA	60
GGCCGTGAAC AGCATATCTA AAAGCCCGGA CATGTCTTGA AAAGGTCAGG GANACGTCTG	120
TAAATAAGGA CTGACGTTG GGAAGGAGGC CTGAAGGATT AAGTAGACCT TNCCCCAGTG	180
GGGNCGAAGG AATGGGGAGA GAAGTCCCTG GTAGAGGGGA ACCCCATTAA NCAGAGCTTC	240
CGGAACGTGG GNAAGGAAGC TTGAACCTCTG CCGAAGGNAA CTGGNAGGAA AGACCTGTGT	300
TACTGCCAGG GTCCAAGAGC TTGGGAAGAG GGTAGGTTGG GGGCCAGATG GTGCCCGGGT	360
TTTGGTTGGN CGGTGAGGAG GAGNCTGGGG ATTTGGAACA CCTGCCTTT TGGAGCTGTT	420
NGAAAGGATC CAATGAGTTC ATCCTTCTTN TTACCAATNC TGGNTTCCCA TT	472

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

GGCACGAGTG	GCCACAATAG	AGGCCATTAT	GCAACCTTGA	AAAGTTATTG	TGATAATGAC	60
CACATAGCAA	TGTGAAGAAA	TAGGCATGAC	ATGTATCTAA	GTGAAAAAGA	TGACATAAAA	120
NCTCTGCACC	CAAGTAAAAC	TATGCAAAAG	GTAAATATGC	AAAAAGGAAA	TAATGCAAAA	180
NGAAAAGGGT	TGTTATGGTG	ATAAAATTAT	GGCCATGTTT	TTATTCTTTA	TTTCATAAAC	240
TCTGTAATAT	GTTATTATTT	TCATAATTAA	AAATTATACT	TTTAAGAAAG	GAATGCCAC	300
TNGGAATTGA	GCTCATTAG	GCATTGAGTG	AAATTACTGC	TTTCAAAGNN	ACAGCNTTAT	360
GAAGGATTNA	CAAATGTGTT	TAGAAGCCCN	TTTTTGTGT	TTGTAACATT		410

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GGCACGAGNA	TAAACAGCTC	AATGAAATTA	CTAAAAAGGA	AAACACTGGC	ATAAACGGTC	60
CCCAGATCAA	GATATAGAAT	GTNACTAGCA	CTTGTAAAGGC	CCTCTTGTTC	CCACTTTCT	120
AATTCTGTTTC	CATGGAGAAC	CACTATCCTG	AACTTCTGAA	TACCATAAAT	NAATGCTTAT	180
TTGGGGGTTT	AATTTTGAAA	GGGATTAGGA	AATACATAGT	GTTCTGGGTC	TGGTTTTATC	240
CATGCCATTG	AATTATGCTT	GTGGTTCAT	NCATTCTCAT	TGCTGNATA	TTAATTCCCTT	300
TTGAAATTNT	TNTGAGCACA	ATTTAATT	AANTGTTGAT	GGGACATT	TTCCCTGCA	358

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

AAACATGGTG CTGTTACTG NGGACCCGAN CANCGTCCAG GAAGCATGGG GTCCGGTCGG	60
AGCGAAAGAT GGCGNGTTG GTNAGGAGGC ACTGGCGAGG	100

(2) INFORMATION FOR SEQ ID NO:980:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

GGCACGAGCG GCACGAGGGA ATGGAGTNAA ATGGAATGGA ATAGACTCGA ATGTAATGGA	60
CCAAAATNAA ATGGACTCGA AGGGAATGAN CTCGAATGCA ATGGAAGCGA ACGGAAAGGA	120
ATGGAATAGA CTCGAATGGA ATGGACTGGA ATGGTATGTN AATGGNAATG GNAATGGAAA	180
CGAATGGTAA TGGAATTCAA TGGGAATCGA ATGGGAATCA AATGGNAATG GNAATGG	237

(2) INFORMATION FOR SEQ ID NO:981:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GGCAGAGGNC ATGGCTGGCT AGTTGTCTGG AGTGTGGATC AAGAGAGACA GGATTATATT	60
ACATGCTCTG GTATATTACA TTAAGCTGGG TCCTGATTCA GGGCCAATAT TTAAGTTCAC	120
TGAATGCTTG TTGCCTCGGA ATNTCTCTCT GGCTGAATGG CTGAATTAT CTCCCTGAAA	180
GAAACATGGT GGTTAAGTCT CATGAAGCAG TCCATAGACT TATGAAACAA AATGCTGCAG	240
CACTTTCTG TCTCAGGGAT AGAGACATGT AGGGAAAATG AGCACTGGGC TGAGAGTCAC	300
ATGTACTATA TTCTAGACCT GACACTGCCG TCAAGCAGGT GTTTCACTC AGGGCAATT	360
CTGTTGTATT TCCGGAAAAA CTCCNTTTCT NAATCTATAA ACTNNNGNNGA AAATG	415

(2) INFORMATION FOR SEQ ID NO:982:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GGCACGAGCC CTGCACTCGG GTTGATTCCA ATCCATTCCA TTCCATTCCA TTCGATTCCA	60
TTCCAATACA ATTNTTCCA TTCCATTCTA TTCCGTACCA TGCCATTCCA TTCCACACAA	120
TTCCATTNCA TTCCATTCCA GTCCGTNCCG TTCCGTTCCG TTCCATTCCA TTCCATTCNN	180
ATGCTATTG AGGTTAATTG CATTCCATNC CATTGATTG	220

(2) INFORMATION FOR SEQ ID NO:983:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GGCACGAGCT GGGTCGCCAC CCCTTCCCTC TCCACCTCCT CCAGCCCAAG CCCTAAGGCG	60
TAGNAAGGTG GCCCTGAGGC CCCGCTTGGC GTNGGANNCG GGGGTCTTTT TGCCTTAAGG	120
AACCCGCCGC CGCATTCTA GGGTTTTAA AGATCCTCTC CCCCCGCTCC TCCAGCTCCT	180
CGTTGAGCCG GAGGAAGGCC TC	202

(2) INFORMATION FOR SEQ ID NO:984:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

CTGCTTCCTA GAGGGCAGCA AGGTCTCCCG GGTNACCCTG CACAACGAGA GCTACATAGA	60
GGAGTTGGAC ATCCGCATCG GGGACTGGTT TTTGGTGCAC AAGGCGGGCG GGGTCATCCC	120
CAAGGTCTC CGGGTNCTC AAGGATTNC GCACGGGGA GGAAAGGCC ATTGCTGGC	180
CCGAAACCTG CCCGATTNC GGNCACCGTT TCCTTCAAGG TAGGGGNAAG GTTNCACCGC	240
TGGCCCCCAA CCCCTTTNT CCCCCG	265

(2) INFORMATION FOR SEQ ID NO:985:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

CTTGGCCAGN AATGTGGTTT TAATTTGTAT TCCCCGTATA ACTAATGAAG TAGAACTCTT	60
TTTCATATAT TTACTATTCA TTTGGAGTGN TAAAAAAATT TTATGANCAC TTGCATTTA	120
AANTATTAAA CTTTCCTATG TTÄAGAAGGG CTGTTGAAA TTAGTTATGT NCTAAAACAT	180
TTGGGCATAN TCATTGCAGT CTATCTCTGT GATTTGCNTA AGTTGTGNAT TCTTTGGAAA	240
TATTTTTTTC CNT	253

(2) INFORMATION FOR SEQ ID NO:986:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GGCAGAGNCA CCTGCGGTCT CCTGCATTAT CAGGAAGATC AAGGNAGCTG GTGGAATCAT	60
TCTAACAGCC AGCCACTGCC CTGGAGGACC AGGGGAGAGT TTGGAGTGAA GTTTAATGTT	120
GTCTCAGACA AAATCTACCA AATCAGCAA ACGATTGAGG AATATGCTAT ATGTCCTGAT	180
CTCCAAATCG ACCTATCTNC GACTAGGGAA GACAAGAATT TGAACCTAGA GAACAAATTC	240
AAACCATTCA GAGTAGAGAT AGTGGGACCC ATGGGATTAT CTATCTTNAA CCTCCTTCG	300
GGACCATCTT TTGGACTTTN CATGCCCTTC AAGGAGTTG GCTTGGNACT NGGGGGCCCC	360
AGGCCAAAC TNGGAAAGGA TTTCCGGCGG TTTGGTAN	398

(2) INFORMATION FOR SEQ ID NO:987:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

GGCAGAGGTA ATTCTNCGTT AATTGGCAC CANAGGATTC ACACGGAGA GAGACCCTAT	60
CACTGTAAGG AGTGTGGCG AGCCTTAAT GATAATGCAA ATCTGAATCA GGCATCAAAN	120
AATCCACAGT GGGGNACAGA CCCTATTACT GTACAGAAC ACGTGAATGT GGGAAAAGCA	180
CCAGGACATC CCCACAGTGG AAAAATATCC AAGGAAAGGT TCCAAGGAAT CCCCTGTGCC	240

AAGGGAAACC TTTGCATATG TGAAGGTAGT GTGGGGAAAT CCTTCAGCT TACTTTCC	300
TACTNTTGCT TAGGNCACCA GTGTNTTCC ACACTGGGG NGGAAACCNT ATGGNGTGT	360
ATTGAGTTG GGCAAAGCTT TTGGNAAGGN CTTCCCTTT TAGGCCANCA NCAGCGTTT	420
TCNCACAGGG GGGAAAGGCN TTATTCTTGT AAAGTATTGT GGGCCAGNCT TTCAATT	480
CCTTCCAAAC TTA	493

(2) INFORMATION FOR SEQ ID NO:988:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GGCACGAGGG CTAAGTGAGA GGGGGCAGTG CTTCAGGCTT GCTTCAGGTC ATCCAATAGA	60
CAGCAAATCC TGCCACCTTG TCCATCAGAG AAGCCATTG TCCTCCCCT AAGAGAAAGTG	120
AATTAGGGTA CAGAGGAAGG AAAAACAGA AGTAATAACCC CCAAAATGCA CCCCTCCTGG	180
GGGCTAAGGC AGGAATCCCC TCATCAAAC AAGACTGAAT TAAGAAGTGC TTGACCTTAT	240
GAGTACTAAG CCCATGTCTC TGTCATTGAG TTCCTGTGCT ATCCTTGCG ACTATGGATG	300
AGGACTTCGA AGGAAATGAT GATGTCCTTA TTCTTCACA ACATCACTAT CCAAGCTTGA	360
AGGAAGGAAN TATGGGCACA CCCGAATTAA NTGCAATATT TTAGGAAAAC TGTAGTGGAA	420
GTGTTNAAT TGTGGTACNT GCCCAGTATT GGATGGGGT AAAAAGGAAG GTTCCAAAAA	480
GNGNTNAAAA ATT	493

(2) INFORMATION FOR SEQ ID NO:989:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GGCACGAGCA CATCCTCACT AGTATGCCAT TATTTCTTCA TGTACTTTT CAGTCCAACT	60
GTCCCATTGG GCAGTTCTGA TACCACCAGA GAAGGCTGAC GGAGGGAGTC CTATTAATGC	120
TGGTTAGGGG TGGAAGTCCA GATAATCCAG GCAATCTCCA CTGCCACTGT GTGGTGGAG	180
CTTGTATNA CCTACTGGAG TAGAAGGTTT TGGGGTCCCT AAACAGTCAG CCACCTCTNA	240

CGTTACCCCA ATGTGGTTT GAGTGCTCG TTACTGCCTG ATGGTGGTGA AAGTCTAGTA	300
TCTCCAATTG ACCTTACTCG TGTGGGTGGG GATTAGGTCA CAGTTTTTG GTGTGGGGGG	360
CAGAGGGGGT TGCTNTTGA CAGCAGGGTA GTGGTTATTG TTTAAAAGTT TTCTGTTCTT	420
AAATAGGGTG ACCTTTCCCT GGTTCTTGG CTAGAGAGAG CAAGTTTTG TTGGAGTTCT	480
TTCTGTCTGT CCNGTTGGTA T	501

(2) INFORMATION FOR SEQ ID NO:990:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GGNGGAGATG GCCTTCTCCA CGGTGNCTGC GGATGTCCC CGNGTCTCCG NCACCCACTG	60
GACATCTGTG CTCGCAATTA TAGATGCCCT TTAGCTCCTC ATTTTGAGCA AGAGGAGCTC	120
GAGTTCTCCT TTGGCTCGTG NATGGAATCN ACAGCAGGTC AGGAGAGATT CAACAGCATT	180
ACCTCAGCTT ATTACAGAAG TGCCAAGGGG ATCATATTAG TATATGAATA TCACTAAGGA	240
NGAAGTTAGA AATCCTTNAT GAAGGGTACC ANCAACAGCA NGTGN	285

(2) INFORMATION FOR SEQ ID NO:991:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GGCAGAGCCA CAATGTAAGC ACCAAACTTC AGCACTGGT CGTACATATC TATGGAGAAT	60
GNGACAAATT AGAAATCAAG AAATTCTCT TCCTCAAAGC AGTACTTTA AACACTGTT	120
AGGACCTCTG GCCACGNAGA AGCCTCCTT NACTATGCCT CCTGTTGGC CACCCTATAG	180
ACTAAAGGGA GTATCGACCT GTATCCCATT CAAGACTCCA GAGGATCTC AAAAGCACAA	240
GACAGCAACA GAGAGATGCA CTGTCTTCA CAAGATACAG TGTGTAAGTC TTNCCAGATT	300
GNCCTTCCC ATTTTATATC CNCTCNGNAT TTCTGTAATC ACGGTTTCA CCNCCNTAA	360
TTTCACATTT GGTTCTTACA AAGGTTGGGG TATTTTCCA AG	402

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

GGCACGAGGT CCTTTTATT CCAGTCCACT GCATTCTGGT CCATTCCATT TGATTCCATT	60
CCATTCTATT CCATTCCATA CAGTTGCATT GCTTGATT CCATTCTATA TCTATAANTT	120
CAATTGAGA CCATTGCTTT TGAGTGCATT CTATATGATT CCATTCCATT CAAGTCCATT	180
ACATTTGGTT CCATTCCATT CCATTCCATT CCCTTCATT CCATTCCATT TGATATCAAT	240
CCATTGATT CCATTCCATT CGAGCACATT CCATCGAGT CCATTCCATT CGNATGCCAT	300
TCCATTTGAA TTCTATTCCA TTAGTCTCCA TTCAATTCCA TTAAANTTCC ATTCCATTCC	360
ATNCTATNCC AACTGN	376

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GGCAGAGNAA AAAGTGTCTN CTTTGGACCA GATTCATCA CTGTCACAAA GGAAAATNAA	60
GAATTAGACT GGAATTACT GAAACCAGAT ATTTATGCAA CAATCATGGA CTTCTTTGCC	120
ATCTGGCTTA CCCCTGGTTA CTGAGGAAAC ACCTTCAGGA GAAGCAGGAT CTGAAGAAGA	180
TGATGAAGTT GTGGCAATGA TTAAGGAATT GTTAGATACT AGAATACGGC CAACTGTGCC	240
AGGAAGATGG AGGGGATGTA ATCATTACTN CTGAAAATG GAATTCCAGA ACATGCTGCC	300
AGTTTTATAT TCCGGAGGTA GAAGGCGTAG AACAGGTTAT GGATGATGAA TCAGTTGAAA	360
AAGGANGCAA ACTCACCTTA AATNATCTNG GNTTTTTTN GGGCNTAACAA TCCGANTGTT	420
GATATATATT CCAGTTTTA TTATTAAANG CTGGGGACTN NAGGTTATNA AATTGCCTTC	480
CGGGATGTTT TTAANTG	497

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GGCANAGCCA GCACTTGGG AGGCCGAGGG GTGGATCACG AGGTCAGGAG TTCAAGACCA	60
GCCTGGCCAA GATGGTGAAC CCCATCTCTA CTAAAAACTA CAAAAATTAG CTGGGCATGG	120
TGGCAGGCTC CTGTAATCCC AACTACTTGG GAGGCTGAGG CAGGAGAAC TCTTGAACCT	180
GGGTGGCAGA AGTTGCAGTG AGCTGAGATC GCGCCACTGC ACTCCAGCCT GGGCAACAGA	240
GTGAGGACTC CGTCTAAAAA AAAAAAAAAA AAAAAAAAANN NTGGGGGGGG	300
CCCCNANC	310

(2) INFORMATION FOR SEQ ID NO:995:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

ATTTATTATT ATTGTTTATT TATNCTTGCA CTTGATGAAA TGTAATTAAN CGCTTTGTCT	60
TATGTGGTTT TTTAATTGTC ATTTTACTGT TTAATTCTC CATAGAGTAT ATGTATTTT	120
GNANCTCAGA GACTCTGCCT TTTCCCCTCA TAGTACACAG CATAATACTA AGCTGTTAGA	180
AGAGTTCAAT TGAATGTTAA TTCATCTGAG TAAACAAACT TGTATATGTA TTTCAAGTAC	240
CTCTACCAGT GGTAGTTGGA ATCTGTTCCA TCAGAAAGAGN TTTCTTAAAT CTGNAATAGT	300
NAAAGTGTAA TATATTCTTT GCTCACAGAA TGAAGGGCAG GAGACCTTN AAAATGGTAA	360
TGATGGTGGGA ACCACATATT TTTAAAAGNG GTGGAGGTTG TTCCGGCNGT GGTATTGNTT	420
TAANCCATGG T	431

(2) INFORMATION FOR SEQ ID NO:996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

GCCCCACCCN GGNCCGCCCG CCCTAGANCT AGTGGTCCCC CGGGCCTGC AGGNNTTCGG	60
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CAGAGCAGTC TTTGGCCTCC CAGTAAATTCA	120
CAATTCAAA CAACTTTAA CTCAAACCTTC	
ACTCTTAGAT TTTTAACAAG CTTTCACAC ATACATCATT AATGCTTCCC CTAATCTTC	180
ATGTTGTACT GGCTATTGGG CAGTTGTGTT AAAAAAAA AAAAAAAA AAAAAAACAG	240
CACTCCCCAA GCGCTTGAAT TTATTTNNNT TTGGGGGAAT AAGAGACCTT TTNTAAATNG	300
TTTTTCGATA AAAGGTAATC CNTTTT	326

(2) INFORMATION FOR SEQ ID NO:997:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GGCACANGAT TTTNTNAGTT TTTGGGTGTC TGTAAATTAA AAAGGAAAAG TAGAAATAAG	60
TAAAAACTNAG GTTGAAGGAA ATATACATAA ATAAGATAAA GCTGACCTGT AGATATAGGC	120
AGGTTATAAG AGCTTAGAGT TGTCTAAGTT GGGTGCAAAT TTNCCTCTGA NCTTTCTGAT	180
GCCGAGACAA AAAAGGCAGT CCATATTNT TACGTGATTG GGGTGGAAACC CGAGAGGAGA	240
ACATGCTGTN TTCTNTGGG ACAGGAAAGC TTGCNTGGCA CCAAGTCTGA ACCANNAACT	300
TCATTGGTGA CATAGATTAT NTGCTGGAAC ATATTTCAC ANCAGCCTGG CATAACCNC	360
TGTTAGTGTGTT TGTACATTGG GAACGGTTCA TTTTCCCTTA AGCACCATGT GTTTTGCCA	420
TGGGAATGGT CCTCNNCCCT TAAGGACANT TNCCTCGNAG TTATGC	466

(2) INFORMATION FOR SEQ ID NO:998:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

GTTCACAAAGT NGGGGAGCCT GTAGCTTTGG GTCTCANTAG CTCCTGGGGT AGTATTTNCC	60
CTTNATTCT CGCCCTGTAT ATCTAATTN AATGACATCT GTNAAGGAGA CAGTGGAGGG	120
	120

(2) INFORMATION FOR SEQ ID NO:999:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

CCTACCCATT TAACTTATAT GCAGAGTACA TGATAAACGC TGGGCTAGAG GAAGCATATT	60
GTCCTCGATT CCAAGCATAT TGGAATCAAG ATTGCTGGGA GAAATATCAA TAACCTCAGA	120
TATGCCAGAT GAACACCACC CTTATGGCCG AAAGTGNAAG AAGAACTAAA GAGCCTCTTG	180
ATGAAAGTGN AAAATGGAGA GTGCAAAAAN TTGGCTTAAA AGCTCCAACA TTCAGAAAAC	240
TAAGGATCCA TGGCATCTGN GTCCCATCCA CTTCCATGGG CAAATAGATG GGGGAAACAT	300
GGAAAACAGT GGGCTGACTT TATTTTCCTG TGCNTCCAAA TTCACTGCAG ATGGTGGACT	360
TACAGCCCTN AAATTTAAAA GACGTTTAC TCCCTTGAA AGAAAGTTT GACCCAACNT	420
GGNCCGGCTT TTTAAAAACC GGGTTTTTA CTTTGTTCA CCGGGGTNCC NTTNGTTCAA	480
GGTTTGGTTT T	491

(2) INFORMATION FOR SEQ ID NO:1000:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GGCACGAGGN GAAGGACGGC AAGGCCTACT NTCGCAAGGA CTACTTCGAC ATGTTCGCAC	60
CCAAGTTGG CGGCTGCGCC CGGGTTCATC CTGGAGAACT ATATCTNNGC CCTCAACACG	120
CTGTGGNCAT CCTGAGTGCT TTGTGTGCCG GGGAAATGCTT CACGCCATTC GTGNAACGGC	180
AGCTTCTTCG AGCACGACGG GGCAGCCCTA CTNTGAAGGT GCACTACCAC GAGCGGCGCG	240
NCTCGNTGGT GNTTCTGNNGC TGCCAGAGGC AGAT	274

(2) INFORMATION FOR SEQ ID NO:1001:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

ATGTTTCAT CATGGACAGC CATGATGATA TATTATTATC TCANCTTAA TCCTTGGTGT	60
GGTTGATTTG GGATCTGCC CTGAANCATC TNTCGAGAAA TGCTCCAACA GAGCAGNAAT	120
CTTAACANTC ATTACACAGAA ACATTGTTAA GAAGTGCCTT GAAGCTGTTT TTTGAGGTGG	180
CAGAAGACAA GGAGAATTGC AAGAAATTCA ATGAGGCCTT ATCTAAAAAT CTAAAGCTTG	240
GGNCCAGTTG TGGGTATCTC ACCTTTGTAA TCTCAGGCAC TTTGGGGAGG GCCAAGGCCA	300
GGTGGGNTTT GNTNGGNAGC CCAGGGTTT TTGAATACCC ANCTTGGGGT TG	352

(2) INFORMATION FOR SEQ ID NO:1002:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GGCACGAGGN AACTTNAGT GCAATGTTCC TCTGGCATG GAGTCTGGCC GGATTGCTAA	60
TAAACAGATC AGTGCCTNAT CTACCTACTC TAATGNGAAG GTGGACCCT CAACAAAGCC	120
GGNTCCATGG TGATGACAAT GGCTGGACCC CCAACTTGGG ATTCCAACAA GGAGTATCTC	180
CAGGTGGNCC TGCGNTTTTT AAACCATGCT GACGCCATC GCAACANAGG GGAGCGATTT	240
CCNGGGNAAA CACAGGAATG GCTACTAATG TGCAAATCCT ACAAGCTNGG NAAGTTCAGC	300
ACTTAATGGG TGAGGACTGG NATGGTGTAA CGGGTGTGG CCAAAAACCA CANGTTTTT	360
TNCA	364

(2) INFORMATION FOR SEQ ID NO:1003:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

CCTCTNAAA TGTGCTTGC TGCTAGAAAC CTAAGCATGC CGGATCTGGA AAACAGATTG	60
ATAGAGCTAC ATTCTCCTGA TAGCAGGAAC ACGTTGATCC TACGCTGCAA GNATACAGCC	120
ACAGCACACT CCTGGTTCGT AGCTATCCAC ACCAACATAA TGGCTCTCCT CCCACAGGTG	180
TTGGCTGAAC TCAACGCCAT GCTTGGGGCA ACCAGTACAG CAGGAGGCAG TTAAAGAGGT	240
GAAGCATATT GCCTGGCTGG CCAGAAACAG GCAAAACTAG NTGGTGGGAG GACAGCAATT	300

GGNGACCTGT TCCTCATGGG NTGTGAAGT NGAAAGGGAT TTGCTGGNTC TNTGGACTGT	360
TATGCCCTTG GGACCAGGGT TGCCTGGGN TTCACCCCTGG CCACAGTTAC CCANTTTTN	420
GCCACCAGGT TTGGTTTCCT TTTTGTTTC CGGATNTTGG TTCCCCTTCC CTTTGGGT	478

(2) INFORMATION FOR SEQ ID NO:1004:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

GGCAGAGGTC TTNCTTNGG AGATGGGCAG AAGCTGAAGG ACTGGCATGA CAAGGAGGCT	60
ATCCGGTAGG AACGCTCAGC GCGTAGTAAA TGGAGAACAA GGAAGACCTT ACCCCATGAA	120
CCGATGCTGA GAGAGTGGAT CAGGCATACC GNGAAAATGG TTTTNAACAT CTACGTCATA	180
ATAAAATCTC CTTGAATCGC NNTCTCCAG ATATCCGGCA CCCAAACTGC AACAGCAAGC	240
GCTACCTGGT NGACACTTNC CANCACAAGC ATCATCATCC	280

(2) INFORMATION FOR SEQ ID NO:1005:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

AGTATGAAAG TCTCAGCAA TTTATTTTA TTCAGTTAAA TATGTTTAC TCAAAGTGAA	60
CTGAAATAAA TTTCATCAAA TTGATATAT TATGAGTTA TTTAGAACAG AGACAAATGT	120
AATCCCCAAA GTTCTGAACC TTCTAACTTC AGTTCAGTTG CTCAGTTGAG TCTGACTCTT	180
TGTGACCCA GGAACCGCAG CACGCCAGGC CTCCTGTCC ATCACCAACT CCCAGAGTCC	240
ACCCAAACCC ATGTCCATTG AGTCGGTGAT GCCATCCAAC CATCTCAGCC TCTGTTGTCC	300
CCTTCTCCNN CTGCCCTTNA ATCTTCCCA GCATCAGGGT CTTTCAAAT GAGTCGGGTC	360
TTCACATCAG GTGGNCAAGT ATTGGGNTTT CAGATTCAAC GTCAGTCCTT NCAATNGAAC	420
ACTCAGGACT GATCTCCTTA GGGTGGACTA GTTGGGTCTN CTTGCAGTCC AGGGNTTTC	480
AGGGTCTTTT NACGG	495

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

GGCACGAGCG GAGGAGAAAA GGTGGTGCTC NGACCTAATG ATGTTTCAGT ATTTACGACG	60
CTCACCATTA ATGGACGCCT NTTTGCTTGC CCGCGAGAGN AATTGATTC ACTGACTCCC	120
NTACCAGAAC AGGAAGGCC CAACTGTTGGA ACAGTGGAA CTTTGAACT GATGAGCTCC	180
AAAGATTTAG CATAACCAGAN GACANTTTAT GATTGGAAC TCTTCAACTG CGTGCATGAG	240
CTGGAGCTAA TCTATCACAC ATTTGGAAGG CATTAATTAA TAAAAAGACC ACAGCAAAC	300
TGGGATTTGT TCCTGAGGAG ATTTTAATTG AAATTCAGTT TTGGGTCGTG CACTGAGATC	360
TNCCTTGTT TCTTCAGCTT CAGNAAGCGG TGGTTTCAGN TATTTAAAAA AAATTGTTT	420
AAGNTAGCAG NCCACTGTTA AGGGGTNTAA AAAATCTGGA ATTCC	465

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

CCAGGGCGGA ANATCCCTCC AAATTNANGT GGGCGATTG TGGCGCTGAN TACGTCGTGG	60
AGTCCACTGG GTTNTTCAC CACCATGGGA GAAAGGTTGG GGGGTTCAATT TNCGANGGG	120
GGGTGNCCAA AAGGGGGTNC ATCATGTTG	150

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GCNTCGTNGC GAATATNTGG NACCCAAAAN TAGACCGATG CCATCACCGC AATATTAAAA	60
ACAGCGATCA ATAAAAAGGT GTACGCCAGC TAAATTCCCTG ATTTAAATAC GTTCCCAGCG	120

GAATGCCAG CAAATTGGCG ACTNTGNATC CCGGAAACCA TCCCCGNAC GCNCNGGGT	180
GAACTTTCC GGGTTTGAAT ATTTTNGAAT AACACGATCG NTTCCGACGG CCAATAATTG	240
CGCCCTGGGG AAAGCCGGNT ACCAGCCGNC CATGGGGN	279

(2) INFORMATION FOR SEQ ID NO:1009:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

AAATCTAACAA TTCGAATCAA AGGTGCCATT AAGCAGCCAG TCAACACTTA CGCCAAGAGC	60
TGACGCAATT CCTGGTAAAA AGCGTGGTCG CTTAGTTTA CCGTTTCAA GCTGCTCTAT	120
AGACTGCTGG GTAGTCCCCA CCTTTAAGC AAGTCAGCC TGGTTAAGTC CAAGCTGAAT	180
TCTTTGCTT TTTAACCTG GAAGAAATAC TCATAAAGCC ACCTCTGTTA ATTTACCCCC	240
AATCTTCCAC AAGAAAAACT GTATTGAAAC AAACAAGTTA CATTGTATGG AAAATTACAA	300
GAAAGTTTGT TTGATGGGAG GCGGTTTGC AAACCTCTT NCTGAAACGG CTTCAAGAAG	360
AGGGGGATTT GCGGTTAAAA TGNACGGCAA ACCGGAANTG GGCAACCAAAG GCCGGTGT	420
AAACNGCAAT TCATTTCANN GGTTGA	446

(2) INFORMATION FOR SEQ ID NO:1010:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

CCTCGCTNAA ACTNTNACAG GTCGGCGGCG CACGTNTTTC TGCGNACCCTT GCGGCGCGTA	60
TTCCCGCTGA ATTGGCTGT AAGTTGCAGC AGGTGTTGG NNATGGCGGA AGGGCCTGGT	120
GAAACTNACA CCCNGCTTGA ATGGATAGCG CC GGNGAAAA TTAATCCATA CCCAGGGTTT	180
ACCCAATGTN TTCCGGTTGG NC GGAA	206

(2) INFORMATION FOR SEQ ID NO:1011:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

AATAAAGATG CAGGANTTA ATATTGCGGT GGGGTAAAAC CCGGATGANA TGGCTCATCC	60
GCTANGATTA AAGNATTAA AATNCCTGNA TTAACCGCTG CNAGGCCGTC CCTGAATNAT	120
TGCCGCTTCA CCCGTNGCCA CCAGGCAGCA AGCCATCTGG TTTTNAAGCG AATTGGGAA	180
TCGNTTCGCT GCCAGCANGG CAACG	205

(2) INFORMATION FOR SEQ ID NO:1012:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

CAAAGACGCC GCCTCGAGAA CATCAGGTTT CTGAAAGGGA TGGGCTACTC CACGCACGCG	60
GCCCAGCAGA TTCTGCTCAG CAATCCTCAG ATGTGGTGGT TAAATGATTC CAATCCTGGA	120
AACCGACAAC CGTCAAGAAA GTCCCTCCCA GGAAAACATT GACCGATTGG TGTACATGGG	180
TTTTAATGCA CTCGTGGCCG AAGCTGCGCT GAGAGTNTTC AGAGGCAACG TCCAGCTGGC	240
CGCCCAGACC CTTGCTCACA ACGGAGGAAG CCTGCCTCCC GAGCTGCCGT GTTCGCCAGA	300
AGACTCTTG TCCCCGCCAG NCACGTNCCC TTTTGACTTC GNNGAACCTT TTAGTGNCTN	360
	360

(2) INFORMATION FOR SEQ ID NO:1013:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

CCTAAAAAAA ACAAACACTA AAGAATTGGT TAGAACAGCA AAATTTCTT AAGGTATTGA	60
TTTACTCTTA ATAAAATTAC AAGAGATTTT AATTTTTTT TAGCCCAAAG TTCAACTTTT	120
ATTGCATTTT GCTGTTTCA GCTTCTCTC CCCTTTAAA AGGCCTGAAA TAATAACTCT	180
CCTTCANCTG CATTTCAGC TCCTGTGAGT TTTTCTCCCC TCAGGTTCTA ATTATTTGTT	240

GTGGCCTGAT GCTTAAAAT GTTTATCTT AAAGGTCTAA AGGGAAATGT TTTCTTGCTT	300
AACATAGTGT CCCGTGGCTC TTGGGNTTN AAANTGNTN CTATGGA	347

(2) INFORMATION FOR SEQ ID NO:1014:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

CAAGCCCCAT AGGCAGGAGG CCCCCGGGNA GCACATCCTG TCTGCTTGTG TCTGCTGCAG	60
AGTTCTGTCC TTGCATTGGT GCGCCTNAGG CCAGGCTGCA CTGCTGGAA GCTGGGCCAT	120
GTCTCCCCAC CCCACCGCCC TCCTGGGCCT AGTGCTCTGC CTGGCCCAGA CCATCCACAC	180
GCAGAGGATC TGCCCAGACC CTCCATCTCG GCTGAGCCAG GNACCGTGAA TCCCCCTGGG	240
GAGCCATGTG AACTGTCGTG TGCCGGGGCC CGTTGGGGTT CAAACATTCC GCCTGGAGAG	300
GGAGATAGAT GCACATACAA TGATTATTGN AAGATGTGTC TCAAGTTAGT NCCNTNTGAG	360
TCANAGGGGC CAATTTCCGC	380

(2) INFORMATION FOR SEQ ID NO:1015:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

CCGCCTTCGC TGGCATGACC AACCAACCAGC TGAGCACCCAC TGAGTGGTAA TGACGGAGACT	60
NTCTACCAGG AGTTCAATGG CCTGANGAAG ATGAATCCCA AGCTGAAGAC CCTGTTAGCC	120
ATCGGAGGCT GGNAATTCA GCACTCAGAA GTTCACAGAT ATGGTAGCCA CGGCCAACAA	180
CCGTCAGACC TTTGTNAACT CGGCCATCAG GTTTNTGCGG CAAATACAGC TTTGNACGGG	240
CCTTGACCTT GGACTGGGA GTTACCCAGG GAAGCCAGGG GGAGCCCTGC CGTAGGACAA	300
GGAGCGNTTT CACAACCCTG GTTACNGAAN TTTGGCCAAT GNCTTNCCA GCAGGAAGGC	360
CCAGACCTTT AGGGGAGGGA CGGCTTTTT TTGAGTNCAG GGGTTTCCA ATTGGGNAG	420
ACCTTTNTNG GGATGTTGGT ACGGGGGTTG GNCAAAATTG GCCCGAACTG GGTTTTTTN	480
AACTTTTGCG CT	492

(2) INFORMATION FOR SEQ ID NO:1016:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TNAAAANNA AAGG 54

(2) INFORMATION FOR SEQ ID NO:1017:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

CAGGGNCTNC CCGACCTCAA CCACTCCAG GNTTATGCCG TNAAGACTGT NCTGCAAAGA 60

CCACTGAGCC TGATCCANGG NCCGNCAAGCA CGGGGTAAGA CGGTGACGCG TTCCACCATC 120

GCTCTACNCAC CTTGCCCGGC AAGGCAACGG GCGGTTNCTG GTG 163

(2) INFORMATION FOR SEQ ID NO:1018:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

CCGTCCCCCTT CGANAGCAAC GTGGGGNAGT ACCGGGCGGT GAACGGAGCT GGGGCGNCCT 60

TNATGCCNAG TACTGGAACA GCCAGAAGGA CCTCCTGGAA GCAAAGGCGG GCCGCGGTGG 120

AACACCTACT GCAGACACAA CTNACGGGGT TGGTGAAAAG CTTCANAGTG CAGCGNCGAA 180

GTTGAAGCCT GAAGGTGACT GTNTATCCTT CAAAGAACCC AGCCCCTGGC AGCACCCACAA 240

CCTCCTGGTC TGCTCCTGTG AATGGTTTNC TATTCCAGGG CAGCATTNNNA N 291

(2) INFORMATION FOR SEQ ID NO:1019:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

CGAACATTT TGGGAAAATA CAGTTCCATT GTACCTGCCA CCNTNNAGCT GTAGCCAGAG	60
ACCTTTATCA AAATGGGCTT GTTTCCACAG AACAGCAGAA CGGTTGGGGG TTTGCATGTA	120
CAGTTAACCA GCATAAGACT CGTACTGGGN AAAATCCAGC TGGGAATGTG ACACAGCTTA	180
ACTGATAGCT TAAGGCATCA GTATTGGGAC CAAAGGCTGG TCAGATTGT ATCATTCTGA	240
GGACCAAATG ATGGGAACA ATAAAATTGT TCCATGNACA GTTGTTCCTC ATTTTGCTGT	300
NCCAGATGAA GACTCTTAAG ANTGACAGAA GGTGATTTT CCTGGGTGNN TCGAGGACTT	360
CCGGGGTAA TGACCNTGAT GGAAATGCCA GGGGACCCGG TTAGGTTTTT TTTTGGNGA	420
NTAACCGGGG GGTTGCCNCG TGGGACAAAC AGCNGTTNC CAGGGTTGG GTTGGTC	477

(2) INFORMATION FOR SEQ ID NO:1020:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

CTTTTTTTTT TTTTTTTTTT TTTTTTANCT TTNCAANTTT TTNAAAAAAA	50
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(2) INFORMATION FOR SEQ ID NO:1021:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

AGAGGTGTCT GTGTTGAAG TCAACATTG ATTATTGGA GGCCTACTTG CAGCATATTA	60
CCTATCAGGA GAGGAGATAT TCAAGATTAA AGCAGTCAG TTGGCTGAGA AACTCCTTCC	120
TGCCTTAAC ACACCTACTG GGATTCTTG GGCAATGGTG AATTTGAAA AGTGGAGTAG	180
GGCGAAACTG GGGCTGGCA TCTGCAGGTA GCAGCATTCT GGCTGATTT GGTACACTAC	240
ATATGGNGTT CATGCACCTG CAGCTACTTG TNAGGGGAC CTGACTTNNC TACAAAAGG	300
TTATGGCACA TTCGGAAACT TACTTCAGA AAATGGGTTG GTGCCAANGG GTCTTTATT	360

CCAANTANTT TGNACCCAG NACAGGGCGN TGGGGTCAN TATTCANACA TNTGTTCGGT	420
GGNCCGGGAG ACAGTTTTA TGGATACTTA CTGGAAGCCN GGTTTGATGT CCAGTTAAAA	480
CAGACCCTG	489

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GGGAGCCTCA GTGAAGGTGG CTGTCCGGGT AAGGCCCTTC AATTCTCGAG AGACCAGCAA	60
GGAATCCAAA TGCATCATTC AGATGCAAGG CAACTCGACC AGTGAGTACA TGTTGTTTC	120
TCTCAGCTGT GTATCTTACT TTCCTTTCTT CTTTCCCTGT CGTCTTGCTG TGTTCAGAAT	180
AGATGAACAT CTGTATGTTA ACACTTGAA CTTTGCTATT CTGAATGATC CATTGGAATG	240
TATTCCCCTC TGTGGTATTT GCTATAGTAT ATTTGAAATA TGGACTATTT ATTTTACCT	300
GTACAATTGA GAAACCCGGA ATAACGTGAA NATTAGCAA GTGTTTATGC TTATTAAGTT	360
GAAATTAAAT GGTTATAAAAG GTTTAACAG TGCTTTTGC CCAGTCCNAA GGGGNATTAT	420
ACCCATGGNG GNNGCAGATT CCATGTTTN CT	452

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

TTCAAAGAAC TACTGAAAA TGCAGAGAAA TCCCTGANTG ATATGTTGT AAAGACATAT	60
GGCCATTTAT ACATGCAAAA TTCTGAGCTA TTTAAAGATC TCTTCGTAGA GTTGAAACGT	120
TACTACGTGG TGGGNAATG TGAAACCTGG AAGNAAATGC TNAAATGAAC TTCTGGGATA	180
CGCCTACCTG GAGACGGGAT GTTCCCGCCT GGTGAAACTA CCCAGTGACC ACTTGACAG	240
ATGGAGTTA CTGGGAATGT GTGAGCCAAA GTNTGACGGT GNCAGCTGNA AGCCCTTNCG	300
GAGATGTACC CACGACAAAT TGAAAGCNCC AGGTTACT	339

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

TTCAAAGAAC TACTTGAAAA TGCAGAGAAA TCCCTGANTG ATATGTTGT NAAGACATAT	60
GGCCATTAT ACATGCAAAA TTCTGAGCTA TTTAAAGATC TCTTCGTTAGA GTTGAACGT	120
TACTACGTGG TGGGNAAATG TGNAACCTGG NAAGAAATGC TAAATGAAC TCTGGGNTCG	180
CCTCCTGGNG CGGATGTTCC CGCCTGGTGA ACTNCCCAGT ACCACTTTGA CAGATGGAGT	240
ATCTGGNAAT GTGTGAGCAA AGTATAACGGN GNCAGCTGGA AGCCCTTCGG GAGATGTGCC	300
CTGCGCAAAT TNAGAGCTTC CAGGTTTACT CGTGGCTTT GTNAGCAGCC CGTTANTTTC	360
GTTCAAGGTT AGCGGTTNCG GGGAGATGTC GTGGAGCAAA GGTCTNCCGN GGGTAAAACC	420
CCACAGNCCC AGTGTACCCC TGGCC	445

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

CACGGCAGGT CAGGAGCNAT TCCAAAGCCT GAGGACACCA TTTTACAGAG GTTCTNACTG	60
CTGCCTGCTT ACTTTTAGTG TCGATGATTC ACAAAAGCTTC CAGAACTTAA GTAAGTGGTA	120
GNAAAGAATT CATATATTAT GCCAGATGTG AAAAGAGCCC TGAAGAAGCT TTCCCTTTGT	180
GAATTCTGGG TAACAAGGAT TGACATTAAG CGAAACGGCA GGTGTCTTAC AGNAAGGAAG	240
CCCAAGCTTG GTGNCAGGGG ACAACGGCG GACTTATNCC TTATTTGAA AACAAAGTGCC	300
AAAAGATTGC CACAAATGTG GCAGCCAGCC TTTGAGGGAA GCGGTTCGAA GAGTTNTTGT	360
TACCGAGGNT AGGTTCAGTT CNTTGATTN CGNACAGACA CGTCATTTT CACCGGAAGG	420
CCCAGCCTAG TTCANTGCT GTTGNNTGTTA GGTTGTTGNT GCNTTTAAC CACTTACACT	480
TTTNCCCAAT TCACCT	496

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

CCTGGNGGAC CATGAAAGCC TTTAAAACCT CGTNATTAAT TGGACACAGT GCCAGAGTGT	60
ATGCACTTA CTACAAAGAT GGACTTNTCT GTACAGGGTC AGATGACTTG TCTGCCAAAG	120
CTGTGGGAAT GTGAGCACAG GGNAGTGCCT TTATGGCATC CAGACCCACA CTTGTCCAGC	180
GGTGAAGTTT GATGNAACAG TAAGCTTGTG AACAGGCTCC TTTGAACAAC ACTGTGGGCT	240
TGCTGGNAA TGGAGTTCCC GGAGCCAGGA CCCAGCACTT TTCGGGGGGG CACACGGGGG	300
GCGGTNTTTT AGCGTGGGAC TACAATGATT GAACTGGAT ATCTTGGTGA GCGGGTTCTN	360
CAGACTTNAN TGTGGAAATT ATGGGNTTTA TTCTGTTNGG GGACATGCC TGAAACACANT	420
NACCGGGGCA CAGGGATTGG GTTCACCCAG GTAGTTTTT CCAGAAGTTN CAAGTCAGTT	480
TTTNT	485

(2) INFORMATION FOR SEQ ID NO:1027:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

AAAAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	60
AAAAAAAAAA AAAAAAAA AAAANNAANA NAAN	94

(2) INFORMATION FOR SEQ ID NO:1028:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

CCCATTAAGG AAAGAGAGAA GAGGTGGCCA TTCACCTTAAT TCAGNAGGTG GAGCCAATNG	60
GCTAGTAAAA CATACTTTTT TCATTTCCC TTTCTNTAAT TTCCTGCGTT TCCTGTTCC	120
CACATTCAAGA ATCTGAATT AGTTCTTAC ACTCGTCCTC ATCTGCCTCA TCTGNAATCT	180

GCCTCATCAT CTGNTTGAAA TGGCTCAAGA GTTGCTTTA TTAGTGCCCA TATTGACCAA	240
ACCAAGACTG GGAATTTNT GGCTCCATCT TGATATGCTT TTTTANAAAA NNCN	294

(2) INFORMATION FOR SEQ ID NO:1029:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

GTCAGGACCA GCTGGATGAC TTGGTGGTGG AGTGTAGAGA TATAGTTGGC AACCNCACTG	60
AGTTAGNATC AGAGGNATT CAAATAGAAG CCTTGCTGAT GAAGAGCCTG TNATGCCAT	120
TAATTCAAGAA CTTCTGCCAC GGTGTGNAAT GATAACCAGAT TAGACTCTGG GGGACCTGNA	180
TGGNAGTGTC TGGNTACAGG NCAAAACACCA GAAGGGACAT GTAACGAGAA ATGTTGCCAT	240
CGTTGTTACC CACTTNCAGT	260

(2) INFORMATION FOR SEQ ID NO:1030:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

CAACAAAAAA AGATATCCTC CGGCATATGG CCCANACGGC AAACCAAGAC CCCGCTTCAA	60
TAATGTTCAA CTGAATCTCA CAGATGAGGA GAGAGAAGAA ACGGANGAGG AAGTTTATTT	120
GTTTGAATAG CACAACCTTT TAACCTGAGG GNAGTCATCT ACTTTTTTT CCTCCTTGTA	180
CAAAAAAAGG AAGGTNANTA TAAAANCCGG GTTTTGTCA ACATGGTTTG CANATAAATG	240
ACTGGTGGAA ATGNG	255

(2) INFORMATION FOR SEQ ID NO:1031:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

CTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTGGANTNC 50

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

CGGACCTGCT GAAGGACCAG AGAGGGAGCC CTGCCTACAT CAGTCCCGAC GTGCTCAGCG 60
GCCGGCCGTA CCGTGGCAAG CCCAGTGACA TGTGGGCCCT GGGCGTGGTG CTCTTCACCA 120
TGCTGTATGG CCAGTTCCCC TTCTACGACA GCATCCCGCA GGAGACTCTT CCGCAAGATC 180
AAGGCTGCCG AGTATACCAT TCCTGAGGAT GGACGGTTT CTGAGAACAC CGTGTGTCTT 240
CATNCCGGAA GCTGCTNGGT CCTTGANCCC CCAGCNGTGN CTTGGTCCG 289

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

CGGAGNCCCA GAGGCCGAGT CGGTCACCCG NACGGATCAC TGGAAAAGTC GCACATCGGA 60
GGGGATNCTC NNTGAAGATT GT 82

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

CCTGTGAATT ACCTAGAAGA GAAGGGTATT GAAACCTACC TCATCATTGC CTCCAAGCCA 60
GAGGTGAAGA AAACAGCCAC CCAGAATGGC CTCAATGGCT CGGCCCTGCC CAATGGAGCA 120
CCAGCTTCCT CAAAGTCCAG CTCCCCTGCC CTCATTGAGN ACCAAGGAGC CCAACGGGGA 180
GTNCCACAG CAGTGGTTC CACGTCGGAG AAAGCCCGAG GAGCAGGATN CCCAGGNCGA 240

CAACCCCTNA TTTCCCCAAC CCACGTCGGA GTTNCGGCTT 280

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

CGGCCTGGTT TCTGGTGGCC TCTATGNATA CCCTGTAGGG TGCGNGACAGT ACTCGATNCC	60
TCCCTGTAAG CACGACGTCA ACGGTTCCCG GCCATGCCAC GGGGGGAGGG CGGATACCCC	120
CAAGTNTAGC AAGCTGTGAA GCCTGGCTAC AGCCCGACCA AACAGGNACA NGTACTACGG	180
ATATTCCCTNA CNGTCT	196

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

CTAAAAATAN TGGNTAAAAT TACCTTGCAA GCTATGTTGT ATAAGGTGNA TATAAAACAA	60
AGNAATTNG NNGTTTAGAC TTGGGTCTAC TCCAAGANG ACCTCATNAT ATATATACAA	120
AAATCCCCAA ATCCAAAAAC ANTTGNAAAC ACTTCTGGTC CCACACATTT TGGN	174

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTNCCNGG GN	52
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(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

CATTTGGGC AATAAACCT ACAGCAAAA GGACTACAGA TCCTAAGCCG GCCCCGCCG	60
CNTGCTCGGT ACAGTTCCG TTCCCTCCTA GTCTCTGTT GCTCGCTTAA GCTGTTTAA	120
AGACCAAGTG AAAGAGTGTG GTTTGCATCC AAGAGAAAAC ACCACACTGT GATGTCATCG	180
GGNAAATGAA TCTCCAAGT CGCTGCCAGA NACCACCCAC TGNTTCGCCG GACAATGTCG	240
AAGTCCAGTT TGTNGCCGGG GGAAGGCNTG GTTTAGGGAA GGATGTTCAA ACGGTCCCAC	300
CCANGCNTGT NNAACTCTGG TTGATTCTT NCAAGAGCCA CCCAGGTTTT TTCCCAGGNC	360
ACAGGCCAGT TTNCCAAAG TTCAAGGGNC CAAAGATTAA TCCAAGGTTT CCCCAAGTNC	420
AAGGGCCAGG GNCAAGG	437

(2) INFORMATION FOR SEQ ID NO:1039:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

CGGTAGGTAA GGAAGGGGCC TTAACCTNTG CTGGTGACCA GAAGCCTGCA TTTCTGCATT	60
CTGCTTAATT CCCTTCCTT AGATTGAAA GAAGCCAACA CTAAACCACA AATATACAAC	120
AAGGCCATTT TCTCAAACGA GAGTCAGCCT TTAACGAAAT GACCATGGTT GGACACAGAG	180
ATGCCATTCT GGCCCACCAA CTTTGGGATC AGCTCCGTGG ATCTCTCCGT AATGGAAGAC	240
CACTCCCACT CCTTTGNATA TCAAGCCCTT CACTACTGTT GGACTTNCTT CCAGCATTN	300
CTNATTCCAC ATTACGGAGG ACATTCCATT TCACAAGGAA CAGATTCCAT GGTTGNNG	360
	360

(2) INFORMATION FOR SEQ ID NO:1040:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

CGGCCATGGC TTTCTGGCG GGGGTTCGC CCAGCGTCGT GGACTATTG CCTAGCGAGG	60
ACTTCTACCG CTGCGGCTAC TGCAAGAACG AGTCGGGCAG CCGCTCCAAT GGCATGTGGG	120
CACATTCCAT GACAGTACAG GATTATCAGG ATCTCATAGA CCGAGGATGG CGAAGAAGTG	180
GAAAATATGT GTACAAACCT GTCATGAATC AAACATGTTG TCCTCAGTAC ACAATAAGGT	240
GCCGACCTTT ACAATTCAG CCTNCAAAT CTCACAAGAA GGTTTGGAA ANAAATGTTG	300
AAATTTCTGG CTAAAGGGGA GGTTCCAAA GGAAGTTNTN AAGGGTGAGC CCATGGTTT	360
CCACAATGGG TTGATGTTGT NGCCGGTGG ACTTTGGCAT TGATTAATA AACTNGTTT	420
TACCGTGNNG NTCNTTAAAC CA	442

(2) INFORMATION FOR SEQ ID NO:1041:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

AAGTTTGTNT TCAGGTAAAC AACCTCGTN AGGNGNNNNG GGGTTNTNT TCNGACTCAC	60
ACTTCCATCT CCGTGTGTAG GTGTCCATCA GCGGAGAATG GTCTCCGTGG CAGGCCAAGG	120
TGCCTCAAAT TGAAGTGGAG ACCCACAGG TGGCAGCCCC TAATGTCGTC GTGCCAACCC	180
TGGGACACAG TCCGCCACGA AGCCCTTTG TACACTTGGC TGGCCGAACA CAAGCCCCCTG	240
GTCTTGTNTG GCCCTCCTGG GTCTGGCAAG ACCATGTACA ATTTTNANN GNCTTCCGGC	300
CTT	303

(2) INFORMATION FOR SEQ ID NO:1042:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

CNCGTNTGCA CGCGGGCTGC CCAGCTCTNT CCTGCCGCC TGGCCGCTGT NCTCTCCTGC	60
NTCCAGCACA GCCGGGAGCA ACAAACACTC CAGGTTGCTG TGGCCACCAG AGCCGAGTNT	120
NTAANNGCA CCCCAGGTTG TGCAGCGTCC TGCAGGGACA NTAATGCTCC TGGGCCCGGA	180
ATGCAATGTC TCNTAATCCC CTCTGTGGAT GGTGGTGGCC GGGGAGTGGC GATGGTGACT	240

GCCNTGGCTN NCCGTTGGT TGCCACCGGG GCTGTNGAGG AGACCCTGGN CCCATTGGT	300
T	301

(2) INFORMATION FOR SEQ ID NO:1043:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

ANAAGGTCCC CCCCTNGGGC CGTTTGAGGC CATGCTTTTT TCCCATTGAC TTAAAANCAA	60
TCGGGAGGGG GNNGGGCCTG CCCCCCTTNA CCCTTTCCC CCTTNCA	107

(2) INFORMATION FOR SEQ ID NO:1044:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

CAACTTTATT CATGGCAAAG AGAAAGAAAA GTAAAGACAG AATTTCCCT TCATGATGGA	60
CCTCCTTATG CAAACGGTGA CCCTCATGTT GGACATGCTT TAAATAAGAT TTTGAAAAGA	120
CNNAGCCAAT CGATTCCATA TGAATGAATG GCTCCAAAAT ACATTTNGTG CCCCCGGCTGG	180
GAATTGTNAA TGGGTTGCC ATTGAAATAA AAGTATTATC CAGANCTTGG TAGAGAAGCT	240
NCAGAATCTT TGCAGCTATG GGAATTAGAA GGAAAGCTAG NTCCTTGCT NAAGGCAGCC	300
CTTGNNGAAC CNGGATCCAG CATTTCCTCG TTGGGGGGAT TAATGGCNG TTTGGAATAA	360
TGGCT	365

(2) INFORMATION FOR SEQ ID NO:1045:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

ACCCGTGATTC CGGAGGCACC AATGGCACTN AGGAGCGGAT GTCCGTGAAT CTGGGACAAG	60
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GCTGTGGTCA CTGGGAAAGA TGGATGAGAA CCAGTTGTG GCTGTGAACC ANCACCAATG	120
ACAGCCAAAG TNTTCAAGGT TTACGNNGG GAAAGGCCGC ATTGCTGTGG GATCCGATGC	180
CGACCTGGTC ATCTGGAAC CGNGACAGCN TTAAAACCAT CTNTGGCNGG GACACANAAC	240
AGCTCTTTTC G	251

(2) INFORMATION FOR SEQ ID NO:1046:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

CTTTTTTTT TTTTTTTTTT TTTTTTTTTT AAAAAANNNN TTNTTTTCCC CAAAAAA	56
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(2) INFORMATION FOR SEQ ID NO:1047:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

CGGGTCTCCC CGACCGAGGC TCGANTCCAG GTCGAAGGGT NGCCGGAGNN ATGGTTGGAG	60
AATGTGGAAG GAGCTGGAGG ACACCCGANT ATTCTAAAG CAATCCCCAT GGCCAGATGT	120
CATCAGCAGC TGAACACGCAT CTCCAGAAAC CAGCTGAAA GACAGAAGCA GAACAACTGG	180
TTTGGTGGAG AGATCTGATA ACAAAAAGTT GGGAAACAGG TAAAATAATA ACTTGGGTA	240
GAAGTTATGC TTGTTTTCT CCAGGCCAAA ATCAACAGCT GATCTGGATA CCATCAAGAC	300
ACCTGAAATT TTATCATGAG CCAATGCTGA GGGAAAGAGAN TCCGGGNNGTT TCCNCAGGAC	360
GCCCCATTN CAGCCCTGTT TGAGANT	387

(2) INFORMATION FOR SEQ ID NO:1048:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

CCCCAAAGTC CTGGGATTAT AGGTGTAAAC CTCCATGCCC GGCGGTTTT AACATTTNA	60
AATGGTTAAA AAAATAGTAT TTTNTGAATA CATGANCATT ATATGTAATT NCCNTTCAN	120
CATCTATAAA TAAAGTGT TTGGAACCA CAGCCATGCT AATTCAATTN CATATTGTNT	180
GTGGCCACTT TTCCTATTAA AATGGTGATT TCGAGTAGTT ATGACAGGGA CTGCATGGCC	240
CACAATGCCT AAAATATATA CTATTTGCC CTTTACAGAA AAAGTTAGG CTGGGTGCAT	300
GGGCTTACGC NGTAATCTCN GCNNNTGGGA GGTCCAGGCG GGTGGGTCCCT CTGNNGTCCG	360
GGGTTCGGGG	370

(2) INFORMATION FOR SEQ ID NO:1049:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

CCACACTGTG AGNTGCCAA TTACCTGCC CCGGTGNGCT CNNCCATCGN GAGGNAGGTG	60
CNCCAGCGCT ACGTGTGGCG TTTCTGCATC GGCCTGCACT CGGCGCCTCG NTTCTGGTG	120
GCCCTCGCCT ACTGGAACCA CTACCTCAGC TGCACCTCCC CGTGTTCCTG CTATCGCCCG	180
CTCTGCCGCC TCAAATTCGG CCTCAATGTC GTGGAGAACCC TCGCGTTGCT AGTGCTCACT	240
TATGTTTCCT CCTCCGAGGA CTTTCACCAT CCACGGNAAA GGCTTCATT NGTGTTCATT	300
GNCTTCATCC CTTNGGGCA CATGGTNCCCT TCACCTGGCA TTCTCTGGC GGTTGAACCA	360
AGAAGCACAC AGTTAAGTTC AGGNNGGNTC GCAA	394

(2) INFORMATION FOR SEQ ID NO:1050:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

CCTGTAGGAG TGCAATTGGA ACCTAAGCGC TTGGTCAANA TCCTAGAGGT GCTTCGGGAA	60
CTCCCTGTCC CAAACTACAG GACCCTGGAG TTCCTCATGA GGCACCTGGT ACACATGGCC	120
TCATTCAGTG CCCAGACCAA CATGCATGCN CGNAACCTGG CCATCGTGTG GGCTCCAAAC	180
CTGCTGAGGT CTAAGGACAT AGAGGCCTCA GGCTTCATG GGACAGCGGC CTTCATGGAG	240

GTGCGGGTAC AATCCATCGT CGTGGATTCA TCCTCACACA CGTGGACCAG CTCTTG	300
GTGCTGCCCT CTCTGGTGGT GAGGTGGAGA GTGGGTGGCG NTCGTTCCA GGACCCGGG	360
CNTCAGGCAG CCCCAGGAC NTATGCCAG GCCATGNNTT GTTCACNGNN NGAGCTGATG	420
CAGTTGGCGT TGGACCCCCA CAATGGGGNC TACCTNATT TCNTCGGGTT TGCCAGAGCA	480
CAAGAGGAAG GGGTTTTTA AANGTTCAAGN AAT	513

(2) INFORMATION FOR SEQ ID NO:1051:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

CTTAAGCGCT AACGTCTTN TNTNTCCCG CGGTGGTGAT GACGGTAAAA ACTAAGGCTG	60
CTAAGGGCAC CCTNACTTAC TCCAGGATGA GGGGCATGGT GGCAATTCTA ATCGCTTTNA	120
TGAAAGCAGA GGAGGATGGG TCTGAAACGA ACTTTATTCA GAAGATTGCC AATNAACTCC	180
TAATGNCATG CAAACACCCCT GAAAGTTCCA GTCCATCTTG AAAGATCTCC CAACCTCCAG	240
GNAGCCTGAA GCTTATGAAA TGCCAACCCCT TCTTCCTCCA CCAAGTCCTT TCTTNAGGCA	300
AATCAACCTT GGGCCCGTGC GTCCCAATCC TGCATGGTT AAACCCTNCT GAAGCTTTA	360
AATTTTTTG GAAAGTGNAT TCGGGAAAGG GGNCNTTTT TTGGGNAAGG GTTTTTCTT	420
	420

(2) INFORMATION FOR SEQ ID NO:1052:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

CCCGAGAAC ACTTATCAGT GTGCCATGGG GAAACAAGCC ATGGGTACTA TAGGATACAA	60
CCAGCGAAC AGAATTGATA CTCTCATGTA TCTACTAGCA TATCCACAAA AACCCATGGT	120
TAAGAACAAA AACCATGAA TTGATAGATT TTGNGAAACT GCCAGCTGGA CAGAATGCAA	180
CANTTGCTGT GNATGAGCTA TAGTGGCTAT GNTATTGAAG ATGCTCTGT TTTAAACAAG	240
GCCTCTTAG ACAGAGGCTT TGGCGTTGC CTTGTATATN AAAANTGCTA AATGTACGTT	300

GAAACGATAAC ACCANTCAGA CTTTGATNA AGTGCTGGGG CCCTGTTGGA TGCTGCTACA	360
GGAAACNTAT TNGGGGACNG GAATNNTAGN TGCAGATGGT ATTTGTTCNA CCAGGTGAGN	420
AGTTGGAAAA CANACAAGTG GTTGTAAATN AAGTNCCNGC CCACAGTGAC TCCGATTCC	480
TGGAAGGNAG TTATG	495

(2) INFORMATION FOR SEQ ID NO:1053:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

CGANTCAAAA AGGCTGACCT CCCTTTACTC ACCAGCACTT NCCTTGGCAG CCACATGTNC	60
TCCTGCTGCC CCGAAGGACG ACAACTGGAC ATAAAGAAGT CAAGCTACAA AAAGCTCTCT	120
AAGTNCCCTGC AGCAAATGCA GCAGGAGCAG ATTATACAGG TGAAGGAGCT GAGCAAAGGG	180
GTGGNGAGCA TTNTGGCTGT GGACTGGAAA CACCCGAGGA TTACATCTTT NGTCATACCC	240
GAGCCCTCCC CGACCTCCCA GACTATCCAG GNAGGGTNGC AGGGGACAGC CCTNATTNAC	300
CCTTCCAG	308

(2) INFORMATION FOR SEQ ID NO:1054:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

CCCCCGGCCT CATNAGTACC TNTCCCCAGC GGATCTGCCA AAAAGCTGGN ACTGGCGCAA	60
TGTGGATGGT GTCAACTATG CCAGCNTCAC CCGGAACCAG CACATCCCCC ANTACTGCGG	120
CTCCTNCTGG GCCCACGCCA GNACCAGCGC TATGGCGGNT CGNNNTCAACA TCAAGAGGAA	180
GGGAGCNTGG CCCTCCACCC TCCTTCCGT GCAGAACGTN ATCGACTGCG GTAACGCTGG	240
CTCCTNTGAA AGGGGGTAAT NACCTGTCCG TTTGGGACTA CGCCCACCAAG NACGGAATCC	300
TTNAA	305

(2) INFORMATION FOR SEQ ID NO:1055:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

ATGGTCCAGT AANTNNTGAG CTGTTCTGGN TGTAAACNAG ATGGAGCCGT TTTTGTCCCTG	60
CATTTGGAAT TGTATGAGTG TGGGACAGGG AAGGTCTGTT GNTTNANNA CAAGTTTAG	120
TTAGGAGTTT TTGGGTCGTT ANGTAGGT	148

(2) INFORMATION FOR SEQ ID NO:1056:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

CAGGACTGCT GGGACCCCCCT GCACCTCCTG GCCACGGAGA GATCCTGCTC CCAGGGACCA	60
GCGTCTGGNT GGGACACAGT TCACTCCTCT NTCCACTTCA TGTTCTTTT CTTCAGCAGA	120
TGGCTCAAGT TCCTTGTTTT TNTCCTTGCT TTCTGACAGC NGTAGCTTCT GAAACCTGCC	180
ATTTTTGGTC TCCTGATGCC TGATTTCTTA ATTGTCTGA CTGTGTCTTC TAGGAAGCAT	240
TAAGTCTGAA CTGACTTATT AGGAACTTT AGAAAGTTAA ACACACAAAA CCCTTTCTTT	300
GACTCCTATC TTNAAGGACA TGGAGATACA GTTNACATAT ATTTATACAC AAGGNTATTT	360
CATATGGCAA AAACGGGGAG AAGGCACAAT TTTAAGAGCC CAATGGGGAC TGGGGTTGTG	420
TATGCATCTN TACAATGACA TGTTATGAAG TCATTCTGTT TTTAATAAAA CTTTTTAGTG	480
GNCATGGGN AAATACAAA	499

(2) INFORMATION FOR SEQ ID NO:1057:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

TACTTATCCC CCCACTATGG ATTCTGGGTN ANAAGGCTGA GGAAGGGAAA TAAGTACCGA	60
NCAGGCACCG ATNAGTACCC AATCCTNTCC TTNCGGGTCC CTCCTCGCNG GGTGGNAATN	120

TNCGTGGATT ATAAGGCCCA TNANATTNNNT TTNTACAATN TNACTAANTG TGGCTCCCAC	180
ATCTNCACTT TCCCCCGCNA TCCCTTCCTT GGGCGCCTCC TGCCCTATTT AAGTCCTTGC	240
TACAGCATTG GAACCAACAA CACTGCTCCT NTGGCCATCT GCTCCCTGGA TGGGGAGGAC	300
TTAAGAAAGC TNACCACCTT AACCAACAGAG GCTTTGGAAT TGGGNCTGGC CCCCATGGGG	360
CTTGGAGGAC CGANCCACTT GAAAGGTATC CCCTGAAAAC TTAAGNTTGA GCCCAGTATT	420
CCAAGGATTC CTCTGTTNTN ATCCTTTGGT CTTTGCTACC AGGGNTGAAG	470

(2) INFORMATION FOR SEQ ID NO:1058:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

CGGTCTACTT ATCCCCCAC TATGGATTCT GGGTNANAAG GCTGAGGAAG GGAAATAAGT	60
ACCGAGCAGG CACCGATNAG TACCAATCC TNTCCTTGCN GGTCCCTCCT CGCNGGGTGG	120
AAATNTTCGT GGATTATAAG GCCCATAAAA TTTTTTNTA CAATNTAACT NANTGTGGCT	180
CCCACATCTT CACTTCCCC CGCNATCCCT TCCCTGGCG CCTCCTGCC TATTTAAGTC	240
CTTGCNACAG CATTGGAACC AACAACACTG CTCCTTGGC CATCTGCTCC CTGGATGGGG	300
AGGACTAAAG AAAGCTTACC ACCCTAACCA CAGAGGCTTG GGAATTGGGC CTGGCCCCCA	360
TGGGGGTTTG GNNGACCGAG CCACTGGACA GGTATCCCCT GAAACTAAGC TGAGCCCANT	420
ATCCAAGGAT TCCTCTGTT TGATCCTTTG GGTCTTTGT TACCAGGGTT GAAANTTTA	480
AATGGAAACC ATTTTNTT	498

(2) INFORMATION FOR SEQ ID NO:1059:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

TCANCCCCCC AAANTGGATT CTGGGCAGTN TNTTTTGGT ATGGGAAAAA AATATTGGGC	60
TCTNACCTCC CCAATAACTG CCGTACCCCT GCGGACCCCG CTCCANGATG AGGGATTTT	120
TTGGACTATA ATGCTGGTAA GGTCTCCTTC TACAACGTGA ACAAGAAGGT GTCACACCTT	180

GCACTTTCTC TGNATGGTAA CCTTTTGNG GCCTNTCCG GCCCTNACTT GNAGTNTGAN	240
NTAACTTCGG GAAGGGAAA AGTGCCAGTT CCTCTGAATC CATCTGCCCG CATGANTGGG	300
NATAGATGGG TTTTTGGGN CCATGTTGG GGNATTGATG GN	342

(2) INFORMATION FOR SEQ ID NO:1060:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

AGGGTGCCCA GTTTACCCAG GNTGAGGTAG CTGCTTCTGN CAATCCTGAN TGCNCCACCT	60
GGTTGAGGNG CTGGGAGGTA CCCCTTTCCA AAGCCGTGTG GTCCAGGNAG GNGCCCGNCC	120
ACCTCATGAG CNTGTTGGT GGGAAGCCCT GATCCTNTAC AGGGCGGCAC CTCCCGGAGG	180
GAG	183

(2) INFORMATION FOR SEQ ID NO:1061:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

CGCTTCCTTC NTGNGGTGGT GGAGCCAGTT TTTGCCAAC TCAGCCGACC GCAAGAGGNN	60
GCTTCTGGGG GCTGNGAGTC ACTTCCGCAG GTGGAGGACC TTTCCTGACC TTGCCCCANT	120
GGTTCTGCNT TCAAC	135

(2) INFORMATION FOR SEQ ID NO:1062:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

CCTATNAAAT GCGACGCTGG AACGAGGCCT TGGTCACCAA CATGTTGCCT GAGCACGTGG	60
CACGCCATTT CCTGGGGTCC AAGAAGAGAG ATGAGGAGCT GTATAGCCAG ACGTATGATG	120

AGATTGGAGT CATGTTGCT TCCCTGCCA ACTTCTCTGA CTTCTACACA GAGGAGAGCA	180
TCAACAATGG TGGTGGTGTAG TGTNTGCTTT TCCTCAATGA AATCATCTCG GNATTTGAA	240
CTCTNTCCTG GGACAATCCC AAGTTCCCGG GTGGATCACC AAGATCAAAA CCATTGGCAG	300
CACGTTATTT GGCGGCTTCAGA GGAAGTCACC CCCGATGTNC AACACCATGG GNTTGNC	360
TTCNCAACAA GNAAGACAA	379

(2) INFORMATION FOR SEQ ID NO:1063:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

CCTATNANAT GCGACGCTGG NAACGAGGCC TTGGTCACCA ACATGTTGCC TGAGCACGTG	60
GCACGCCATT TCCTGGGTC CAAGAAGAGA GATGAGGAGC TGTATAGCCA GACGTATGAT	120
GAGATTGGAG TCATGTTGC CTCCCTGCCA AACTTGCCT GACTTCTACA CAGAGGAGAG	180
CATCAACAAT GGTGGTGGT AGTGTCTGCN TTTCCTCAAT GAAATCATCT CGGNATTTG	240
AACTCTCTCC TGGGACAATC CCAAGTNCCG GGTGGTCAC CAAGATCAA ACCATTGGCA	300
GCACGTATTA TGGCGGGTTC AGGAGTTCAC CCCCGATGTN CAACACCAAT GGGTTTGNC	360
AGCTCCCAAC AAGGNAGGNC AAGTTCCNAG AG	392

(2) INFORMATION FOR SEQ ID NO:1064:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

CTTNTNCTCT TCCCTGGAGA CCTGAGAAC CAATCTGAAC CGACAGNNAG CTGGCAGAGG	60
NAATACCTGT ACCGCTATGG TTACACTCGG GTGGGCAGAA ATGCGTGGTA GAGTCTAAAT	120
CTCTGGGGCC TGCGNTNGCT GCTTCTCCAG AAGCAACTNT NCCCTGANCC G	171

(2) INFORMATION FOR SEQ ID NO:1065:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

TAAACGGAGG AGCTGTTCCA AAGGCTGCC NGAGGATGCC GCAANTCCCC CNTAGGCNTC	60
TGTTTACCC CNTACCCGGA GCCTTCAAAG TGCTCCTGGA AGAACCCCGA GGCAGAAGCN	120
GCCCTTAANC TGGCGTTAAG ATCACGGAGN NGTGCCTTCC TGGGGCCGAT TAAANCTTAC	180
CGGTTCGGGC TGATGTTCC GG	202

(2) INFORMATION FOR SEQ ID NO:1066:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA ANAAANAAAN AANAANAAAA	110

(2) INFORMATION FOR SEQ ID NO:1067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

CCCCAGAACCC TGGATTNTTNAACCTTATG GCCTACGACT TCCATGGCTC TTGGGAGAAG	60
GTCACGGGAC ATAACAGCCC CCTCTACAAG AGGCAAGAAG AGAGTGGTGC AGCAGCCAGC	120
CTCAACGTGG ATGCTGCTGT GCAACATGGG CTGCAGAAGG GGACCCCTGC CAGCAAGCTG	180
ATCCTTGGCA TGCCTACCTA CGGACGCTCC TTCACACTGG CCTCCTCATC AGACACCAGA	240
GTGGGGGCC CAGCCACAGG GTCTGGCANT CCAGGCCCT TCACCAAGGA AGGAGGGATG	300
CTGGCTTACT ATGAAATCTG CTCCTGGAAG GGGGCCACCA AACAGAGATT CCAGGATCAG	360
AAGGTGCCTT ACNTTTCCG GGGACAACCA TGGGTGGGTT TTGATGNTGT GGAGAGTTTC	420
AAAACCAGGT TCAGTATTG AAGCAGAAGG GATTGGNGGG GCCNGGTNTT GGGCATGGGA	480
TTAGATGATT TGCCGGTTT CTGCAACCAG GCC	513

(2) INFORMATION FOR SEQ ID NO:1068:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

TCACGGATCA TATGCTGACG GTGGAGTGGT CCACAGAGTT TNGATGGGNG AAACCTCATA	60
TCAAGCCTCT TNAGAACCTG TTATTGCACC CNNGACTTCA TCAGCTTGC ACTANGCANT	120
GGNATTATTT GAAGGATTGA AGGCATTCG AGGAGTTAGA GAATAAATTC GACTGNTCA	180
GCCAANCCTC AACATGGA	198

(2) INFORMATION FOR SEQ ID NO:1069:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

CCCGGAGGTG TACCCGACCC CCCAGGCTTG GAGGCAGCCA AAGAGGTGAT GGTGAAGGCC	60
ACTGGNCCTC TAGAGGACAC CCCAGCAATG GAACCCAACC CTTCAGCAGT GGAGGTAGAC	120
CCCATCAGAA AGCCTGAGGT CCCCCACAGGA GACGTAGAAG AGGAGAGACC TCCCAGGGAC	180
GTGCACTCAG AAAGGGCTGC TGGAGAGCCA GAGGTGGCAG CGGACTTATN TGNAAGTTCT	240
CCAAGGAGAA GTACATCCTG GACTTCATCG CCAGAGAAC TCCACAAGGA ATTGGGAGGA	300
GGAGCTCAA ACTCAGCAGC ACGGATTTTC CGCAGCCATG CCTGGTTACC ATGGTCCGNA	360
TTCCCCCGAG AGGTCTTCGG AGACCTTNGT TACAAACGGC AAACGGNGAC TTTCCTCATN	420
CCGGGANTCA ATTCAACCAG TCTTGGGGGA TTATGTGGNT CAAGT	465

(2) INFORMATION FOR SEQ ID NO:1070:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

GGNCTCCGTA	GCCGCACAAA	CCAGGGCTCN	NCATGGAAGC	CAGGATTCAN	TCCCCGTGGG	60
GGTGGCTTT						69

(2) INFORMATION FOR SEQ ID NO:1071:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

GGCAGAGTNT	AGGGCCTGTN	CACAATGAGC	TTGCATTCCA	GCCTCCCATT	TCCAATCATC	60
CTGCTCCTGA	GTATTGGTGT	TCCATTGCTT	ACTTGAAAT	GGATGTNCAG	GTAGGAGAGA	120
CATTTAAGGT	TCCTTCAAGC	TGCCCTATTG	TTACTGTTGA	TGGATACGTG	GACCCTTCTG	180
GAGGAGATCG	CTTTTGTGTTG	GGTCAACTCT	CCAATGTCCA	CAGGACAGAA	AGCCATTGAG	240
AGAGCAAGGT	ATTGATTGTA	TAGTCAGATA	GTTACTTTA	AAAAATTGGN	GCATAGTACA	300
TTGTCTTTA	ATTCAAGGTT	NAAGTTTTTC	CCCTGTTACA	TNATATGTNG	TTCCCTTAAAT	360
TNTAATT						367

(2) INFORMATION FOR SEQ ID NO:1072:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

GGCACGAGCA	GCAGTGGAGA	AATTIGTTTA	TTCCTGTNCA	GGCTACTGTN	TGGNANCCTT	60
TGTCCTTGGA	ATAGGCGACA	ANCACAATGA	CAATATTATA	ATCACCGNGA	CAGGAAACCT	120
ATTTAATATT	GACTTCGGGC	ACATTCTTGG	GAAATTACAA	AAGTTTCCTG	GGCATTAAATA	180
AAGNGAGAGT	GCCCTTTGTG	CTANCCCN TG	ACTTCCTCTT	TGTGAATGGG	NAACTTCTGG	240
GAAAGAAGGC	AAGCCGACAC	TTTCCTGAAA	TTTCAGGACA	TNTGTGTTGA	GGCTNATCTA	300
GNCCCTTCGTC	CTCNAC					317

(2) INFORMATION FOR SEQ ID NO:1073:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

TCCTTCCTCG CGGCACCCNNC CTCCCCCGCG GCCTTCCTCC GCCGCCGGGN NCTCCGGCAG	60
CTTATCGCC AAATTCCCTG AAACNTCGC TTTCTTTAA ATCCCCTGCA TCGGAATCAC	120
CGGCNTGCC CACCATGTNA AAACGCAGCC GTANACACCA GCTCCNAAAT CACCACCAAG	180
GAACCTAAAG GAGAAGAAAG GAAGTTTG AAGAGGCAGA AAATGGAAGA GACGCCCTG	240
CNTAACGGGA AATGCTAATN AGGGAAAATG GGGGAGCCA GAGGCTGACA ATGANGTTA	300
GNACGGAGGA AGAGGGAAGN	320

(2) INFORMATION FOR SEQ ID NO:1074:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

GGCACGAGGA CCAGGTGACG GCGGGCGCCA TGCAGCGACT GGGGGCNGGG GGCCTNACGN	60
TGGACAGNAT CCTGCAGACA GATGATGCCA CGNTGGAAA GCTCATNTAC CCCGTGGTT	120
TCTGGAGGAG CAAGGTGAAA TACATCAAGC AGACCAGNGC CATCCTGAAN NAACACTACG	180
GTGGGGACAT CCCAGCCTTT TTGGCCGANT TGGTGGCGCT TCCGGGTTTT TGGGCCAAA	240
TTGGCACACC TGGTTTATG GNTTTGGNCC TGGGGGANAA TTTTTTTCGG GNTTTT	296

(2) INFORMATION FOR SEQ ID NO:1075:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

CAGATGATGC AGAGGNAGCN ANCTGAGCNC NTCCAGGAAG AAAGTTAAGG GAGAAAGGCG	60
GGCCCGGGAA ACAGGCTGAG GCTGAGGTGG CCTCCTTGAA ACCGTAGGAT TCCACCTGGT	120
TGAAGAAGAG CTGGACCGTG CTCAGGAGCG CTTTGGCCAN TGNCCTGNAA AACTTGGANG	180
AAGTTGAAAA AGCTGNTG	198

(2) INFORMATION FOR SEQ ID NO:1076:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

GGCACGAGCG TCGCGNCGCC TTCTGAGTGG TCGGGTCGAG GCTTCTCGGN CTAGCAGTGC	60
CCTCGCTGCG CGATCTCAGG CGGGTTCTCC TCGGCTCCGC GCAGCCGNGN CGCGNTGGGG	120
GACCCGGCGC ANGGTCACCT GCTGCCGAGG GACCCCGNGG CCCGCCCCGG TGCTCGTGAT	180
GGNGCTGATC TNCGCCAAAC TGTGGAGCCT CNNCTGTAAC CAAGAACACA AAGTAATTAT	240
AGTGGGACTG GATAATGCAG GGAAAACCAC CATTCTTAC CAATTCTTAA TGGAATGAAG	300
TGGTTCATAC TTNTTCCAAC CATTAGGAAG CAATGTTGAA GAAATTAGTT TGTGAAGAAC	360
ACTTCATTTT TCTTTATGTG GGGATTATTG GGTTGGTTCA GGAGTTCTCT CGGGATCATT	420
NNTGGGAAN CACATTATTT ACNTCAAATT ACAAGAGNTT CATTC	465

(2) INFORMATION FOR SEQ ID NO:1077:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GGCACGAGCG ATAATGCACA GCTCCGGTCT GTGGACCCTG CCACATTCCA CGGACTGGGN	60
CGCCTACACA CGCTGCACCT GGACCGCTGC GGCCTGCAGG AGCTNGGCCG GGGGCTGTT	120
CGNNGCCTNG CTGCCCTGAA GNACCTNTAC CTGNAGGACA ACGTGCTGCA GNAACTGCCT	180
GGATGNCANC TTNCGTGACC TGGGCAACCT TACANACCTC TTNCTGTACG GCAACCGCAT	240
CTCCAGCGTG NCCGAGCGNG GNTTCCGTGG GCTGCACAGN TCGACCGTTT CCTACTNCAC	300
CAGAACCGCG TGGGCCCATG GTGNAACCGG ATGNTTTCC GTGANCTTGG CCGTCTCATG	360
ACANTTTAN TCTGNTTTGC CAACAATCTA TTCAGCGGTT NCCCANTTTA GGGCCCTNGG	420
CCCCCCTNGG NTTGCCTGGA AGTAACCTGA GGGTCAAAGG GCAAACCCCTT GGGTGTGG	480
AATTTCGGG GAAGGTCAAT TTTGGGGG	508

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GGCANAGGNA GTAAACAGAT AACAGGTGGT GGTACCTGGT TGGGGGAGGG GGGCGTCAC	60
TGCCATGTCT TNTTTTTTTT TTTTTTTTT TTCCCNANT	99

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

GGCAGAGCCT TGGTACTAAC TCATCCTCAG GTTTNATAAC TAATGGTGCC TTCTTNATC	60
CATCAAAGTT ATGACTGANT GTGGCACCGG GGACAGTTAG TTGCTGTCCT AGAGTTAATT	120
TCCTAGCTTC TTGTGTTACA NATNGGTGGC AGCTAATGCC TTAAAGGCAA AGGGGCCATC	180
TTAACACCAC GGGGTCTAGT TGTTGGGNAT AAATATGGCC ACTGGGGTGA CGGCCATGAT	240
NCCTATAAGT TGGGGTCAGA GCCCCCTATG GGCCATTGTT TTTTNGGGTN CAGGAACATT	300
NTGGGGAAGG CNTTAGTTAA TGT	323

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

GGCACGAGGG ACAAAATATAC AGCTGTTGTA AAGATGATTG ATTCTGGAGA CAAGCTGAAA	60
CTTGACCAGA CTCATTAGA GACAGTAGTT CCAGCACCAAG GAAAAAGAAT TCTAGTTTA	120
AATGGAGGCT ACAGAGGAAA TGAAAGGTAC CCTAGGAATC CATCANTGNA GNAAGACTTT	180
TTNCAGCTAC TATCGTGCAT TGGNAACTGG GCCCTTGAA AAGGGACGCA GAGTTGGAAG	240
GGAATTCAAT GATGGAAGGA CATTCTAAA CTTGNCTGA GTTTGGAAA ATTTGTTAAA	300

CANTGACATT GAAAATCTTG AAAGCATNCA AATTGGGTGT TCCGNCCAAG GGCATTNATG	360
AAGGACTCNG ACTGTGGTTT AGGGGT	386

(2) INFORMATION FOR SEQ ID NO:1081:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

GACCGAGGNC NNCCTGAACC CCCAAGGACA ACCGAGAGTN GATGACCCAA ATCATGTTG	60
AGACCTTCAA C	71

(2) INFORMATION FOR SEQ ID NO:1082:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GGCACGAGGT GAAACTCATC ATGGCAAATA TGCTTATNTG NATATATCCT TTGCCATACA	60
TGNCTGCAA ACTGTAATGA AATGTTATT ATAAGACTCG TAAGGCATGT NTNATTAGAC	120
TGGGACACAC AAAAGCCCNT GAATTATCTA GGCAAGCAAT CCTCTAGGGT CCAGATGTAG	180
TTTGGTAATG TGGGTGTTCA GTGATCACTG NTACTTGCAT TGANTGGATT TTNAATTGCG	240
TATGCCTGTG TTGAANTAGT NATTAG	266

(2) INFORMATION FOR SEQ ID NO:1083:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

GGCACGAGGT TAAACANCCG ANNCTNNGCN GCAGGTTGCC CNCNTGGGG CTGCTGGCTG	60
CTGCNTTCC GGCAGGAGGT GGTGGCCGCG GTCCCACGAG AGGGGGTATT TTNCGTCAGC	120
CAAGATGGGT TCCAAAAGGA GAAATTGAG CTGTAGTGAA AGGCATCAGA AATTAGTAGA	180

TGAAAAC TAC TGCAAAAAT TACATGTCCC AAGCTCTAAA AAANCGTCCA ACAGTCCAAT	240
TNNGGGTNTA NAATTG	256

(2) INFORMATION FOR SEQ ID NO:1084:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

TAAGTAACAC GNGGTGAGGG TTGCAGATGC AGTTNCCTGT TTTAATCGTA TAGACAGGGC	60
AGCTCTACTG CGGAGATGGT CAATGTCCCT AAAAGCCAAA GAACCTTGTN TTAAGAGGTG	120
TGGTAAGCAT CACCCTTACA AAANTAACAC AGTATGAGAA AGGGCAAGGT TTCCCTGTTA	180
TGCCCAAGGA AAGAGGTGCT ATGAATTGGA AAGCAGAGTG GCTGTGGTGG GCAGACAAAG	240
TCAGTTTCC AAAAGAAGGC TGGTGCAGTT TGGNCTGTNT CCCCACCCAG NTTTGCCTCT	300
TGATTTCCC ACATGTTNNNT GG	322

(2) INFORMATION FOR SEQ ID NO:1085:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

CTACATCCAG TCCCTNCCAC AAACCCCAGG AAGGATTCA CTCAGCTGTT CCCACGGGCC	60
ANCCCCCAGG GTNAGTNTNA AAGCCCGCTC CCCAGGGGCC TCTNAGCGTA TCCCAAAGGG	120
CGGGCTCTCC CAGCCCCCTGG TGTNAGGCTC TTGGCTCTNC CCCTGCAGCT GCGGACCTGC	180
TGGAGAAGAT GCTGGAGCTA GACGTGGACA AGCGCCTNAN GGCCGCGCAG GCCCTCACCC	240
ATCCCTTCTT TNAACCCTTC CGGGACCCCTG AGGAAGAGAC GGAGGCCAG CAGCCGTTTT	300
AATGATTCCCT TAGNACACGG AGAAACTTNA CAGTGGGATG AATGGGAAGC NTTAAGANCT	360
GGGGGCCTCG GGGTTCCCTCG CCTTCGNCTG CAGGCT	396

(2) INFORMATION FOR SEQ ID NO:1086:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

GGAGCTCTCA GCATACCGTG CAACAGTTCT GGGAAATGCC AGTNCAAAGT GGGTGTNATT	60
GGCTCTATAT GTNACCGATG CCAAGATGGA TATTATGGCT TTAGTAAGAA TGGCTGCTTG	120
CCCTGCCAAT GCAATAATCG GTCTGCCAGT TGCGATGCNC TCACAGGTGC TTGTTAAC	180
TGCCAGGAAA ATAGCAAAGG TGATCACTGT GAAAGAATGT AAAAGAAAGG NTTTTATCAG	240
AGTCCTGATG CCACTAAAGA ATGTCTTCGC TGCCCTTGTG CCAGCAGTGG ACATCTACAG	300
GCAGCTGCTC CTATTAAAAT TCGAGTGGAA TTGGGNGCCT GGAATGTGGA ACCAGTGGTN	360
AAAGANGGGT TACATAGGGC CCGAACTGGC ATTAAATNTG GNAAATGGGT TATTTACAAT	420
TTTNGACCAG CATCTGTTGG AAAGTGCCCA T	451

(2) INFORMATION FOR SEQ ID NO:1087:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

GGCANAGGAA GACCTACATC GCCAGCCAGN GNTGTTCTGG AGGCCACGGG TCAATGACTT	60
CTGGCAGATG GCGTGGCAGG NGAACAGCCG TGTNCATCGT CATGACCACC CGAGAAGGTG	120
TAGAAAGGGC CGNAACAAAT GCNTCCCATT ACTGGGCCCG TAGGTGGGCA TGNCAGCGTG	180
NCTTGATGGG CCCTACTACT GTNAACCAAN TTTCGGGGGA GCATGTACAC AACCGATTNA	240
CAAAACTNCC GTACCTTACA GGTCTGCCCG GTTTGGACA ATTNCNNCG	288

(2) INFORMATION FOR SEQ ID NO:1088:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

CGTCGAGATC ACTTTAAAGA AGCCATGCC TTTGCGCGNG TTNTGTAAGT AACAAATAACA	60
TTCGGAAGTN TGAAATGTTT GCCCAGACCC TTNAGCAGAG TCGGGGCTTT GGCGAGCTTN	120

AAATTCCCTT NNAGGGAAAC CAGGGTGGAA GCTGGCCCCA GTNAAGGGCA GTGGAAGGCCG	180
GGCACAGGTG GCCAGTNTAT ACACAGNAAG ACAATGAATG GTAACCTGT NTGGTTNAAG	240
TGGTGGTGGC CAGCGTGCCA GTGAAGCTGG ACCTGNCCCTG GT	282

(2) INFORMATION FOR SEQ ID NO:1089:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

ATCAAGACGG GCAACAGGGT ATCTTGGGAA GTACTTNCT GACATCATCA AGGAGGTTAT	60
GTCAGACCTG GGAGGANAGC ANNTACCAGA NTGCAAGAGC TTGCGGCTCT GCCATTTACT	120
GGGCCTCGA NGGGTGGATT GGGGACAAAG CT	152

(2) INFORMATION FOR SEQ ID NO:1090:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GGCANAGACT GGACTGGTTC AAGCGGCCCG ACGGCTTCCT GCTGGTGCTG GAGCGGCCCG	60
AGCCGCGCAG GACCTCTNCA ACTTTATNAC GGAGCGCGGC GCCCTGGAAC GANCCGCTGG	120
GCGNCCGTTT NCTT	134

(2) INFORMATION FOR SEQ ID NO:1091:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

GAAAATACGA GGTTAGAAAC TTAACCATTG AAGAGGAGTA AGGCTACTTA AAGCGTTAAA	60
AACTAATTGG GTAAGGTATG GTTGACCCAG CTACTTCATT TGCCTTACGA TGTATATTCA	120
TTAANCTAAG TCACTCACCT TCTCTGTGNA TGTTGATGGT TTGGTACAGT AACATGAGA	180

TATGATTAAN GGTGATTCA GGTGATTCA AGTGTCTGCC TAAGTAAATC TGTGTTTCA	240
TTTTTTTTC TAGTACCAT A CAGCTTGGG GGAAAGACCA TGAAAAGAT GCTTTGNAA	300
CATATTGTGA ACACAGTTT CCATCATGCC CTGTTNCTGT GGGTCCANCG NTAGCTATGG	360
ACCATTTTN AATGCGTGTG GAGNAATTN NGGGGGTGAA GTTNCAGA CATTNATTA	420
GTTTCCGGGA AGTACNCCNG GCNCCNNTAT TATTCA GACC NGTTTCGGG AACCNCTNG	480
NCACNTGTTA AAGGTTGGG GTTT	505

(2) INFORMATION FOR SEQ ID NO:1092:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GGCAGAGGGC ACTGGGAAA ACAGAGGAGG AGGCAGTGAA GCACTTCAA GTAAAGTTA	60
ACGANNCCCT CCGTGAAGAC CTGGCAAAAC CAAAGTAAAC TGGCTGGCCC ACAACGTGTC	120
CAAAGACAAC AGGCAGTAGT GGCTCCTCCC AGCTCTGGC CCAAAAGGAG GCGGCTNCGG	180
GTCGTGGGGA CCAAGCACAT TGGTNCTAAA GGGGCTGAAG AGCCTGAACG GCACCTTAAC	240
GGGCAAAGAA ACCGACATGG CTGCCTTTG TTTACACTGG TTATTTGATT TCATGANCTT	300
TGAAATAGTT TANGTGGCT AAACAGCCAT AAACGGAAAC GGCTNCTTT ATGCANCAGG	360
GGT	363

(2) INFORMATION FOR SEQ ID NO:1093:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GGCAGAGGNA GCAGCTCACC CCCTGGGGN CCCCCNAAGC CGGGGGCCA GCTGGACAGC	60
ATGCTGGGGA AGCCTGCAGT NTGACCTGAA TCAAGCTGGG GGTGCCCCACA NTCGCCAAAG	120
GAAGTCTGCG GGGCCTGCAA GAAGCCCATC GCCGGCAGG TTGTGAACCG CCATGGGAA	180
GACGTGGCAC CCCGAGCACT TCGTCTGCAC CCACTGCCAG GAGGAGATCG GATCCCGGAA	240
CTTCTTCGAG CGGGATGGAC AGCCCTACTG TGAAAAAGGA CTACCAAC CTTTTTTCC	300

CGGGCTTGT	ATTATTGNAA	AGGGCCCCA	TCCTGGTNA	AATGGGTGAA	CAGCCTTTA	360
ACCGGACGTG	GGAACCTGAA	AAATTTTTT	TGTNGNAANA	TTTTGGG		407

(2) INFORMATION FOR SEQ ID NO:1094:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

ACTTTNTTGG	CCCCAACCT	AGGNCCCTGGG	GGATCCCCTG	ANCCCAC	TGG AGAGTNCA	60
GGGCTGGCCC	CTGTCCCCAA	AATCCCAGGC	TCCCCATT	TTT TCCCAGGTGT	CCTGCTTTT	120
AATCTCATCT	TCATGTTGAG	GCCGTTTAT	TTGACCCTCA	AAGAGGAAGA	CCAGCTTCTA	180
GGGCTGTCCC	CGCCCCAGGA	CCAANAGTCC	TGCAGGGCTA	AAGTNTCCCA	CTGTGCCATG	240
TTAACACACT	GCACAATTAA	CTCCAGGGGG	TGCCGCTCAT	NNTTGAAAAT	TNACAGTCAA	300
TGCTTGAAGT	CACGACATTT	TTTCCAGAAG	ATGGGCNTTA	AGGNTCTCGA	AGAAGGGGGC	360
ATTTCTTAAT	CCCTTACAAA	NTNGTTTGG	GGTTNTNGGT	GGAGGTCGNT	CTGGTNTCAG	420
NAGCCCTAAT	TTTCCTCCCC	GGACCTGTCA	AGAATT			456

(2) INFORMATION FOR SEQ ID NO:1095:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

TAAATAAATA	AATAAATAAT	AAAATGAATG	AGGAGCCAGG	TGCAGTGGCT	CGTGCCCTGT	60
GAATCTAAC	ACTTTGGAA	GGCCAAGGGT	GGAGAACATCAC	TTGAAGCCAG	GAGTTCTAAA	120
CCAGATTGGG	CCAACAAAGTG	AAGAACCTCA	TCTTTACAAA	AAGTTAAATT	AGCCAGGCGC	180
GNTAGAGTGT	ATCTGCCAGT	NCCCAAGTAC	TTGGGAAGGC	TAAGGCAGGA	GGATTCACTT	240
GAGCCCCAGG	AGGCTGAGGC	TATAGTGAAG	CTNTTGACCG	TGNCCATTGN	ATTNCCAGCC	300
TGGGGNAACA						310

(2) INFORMATION FOR SEQ ID NO:1096:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

CAGGTTATAA GTTGAGAAAA CCACTAAGGG AAACGCCAT TGACGCCAT TCTGAATCAC	60
TATTTTCCCC GTATTAACTG GTCGGGAAGC TGCTGCGNTC AATATTGATA CGCTTNGTGC	120
ATTGCNCTGA AAACACAATT GCACCATTCC GTTTGAAAAC CTCGACGTTT TGCTGCCGAG	180
GGAAATACAG CTTGATAATC AATCGCCGGA AGAGAAACTG GTGATAGCCC GTCGTGGCGG	240
TTACTGTTT GAAGCAGAAT GGCGTGTNN AGCGGGTGT ACAGCAGCTT GGGTTAACG	300
TTTCGCAGTT GTTAGGGCGC GTAATGTTA TTCAAATTCC GNCCAGNTTA NCNGCNGGA	360
ACCCATCGTT TGCTGTTGG TGGGACTGGA GGAGGAAAAA TGGGTTGCTG A	411

(2) INFORMATION FOR SEQ ID NO:1097:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

GGCANAGGGT ATTTACCTAC TGTAGACAGC TAATAAGATG TGTGTATGGA AGACTGAAGA	60
CAGTCTGAGA GATGCATCTC AACAAAGGCCT AAGTCTCCCT TCCTCTGGGA ACTGTCCGGT	120
AGTGNCTAGT TCACTGGGT CCTTGCTCTG AGGCTGGTGG GAAACTGGAT TTCAGGGACA	180
CAGGCTGACC ACACAGGGNG CTGTACCGNA CCCCTTCCAA CTGGGAACTC CCCTCGGTTT	240
CTCACACTGT GGNCAGTTAG TGGGTTGGG NAGGCTCTAG GCAAGGGGGA TGGTAGTAG	300
GGTGGTTGAG GATNGGTGGT TGANTATGGA CAAAGGTACG NGTTATGGGT TTTCACCCCA	360
GAAATCCAC NANA	374

(2) INFORMATION FOR SEQ ID NO:1098:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GGCANAGTGA TTAACAGATG CAGGCCTATT CAAATTNCT ATTTNATGTC AGTCTGGTA	60
AATTGTAATT TTNAAGATAT TTGTCCATT NATCTAATTT TCCTAATTTC TTGGCATGAA	120
GTTGTTCGTA TTTNAATCCT TTTNACGCCT CTAGGATCTG TAGTGAATGT CTTTGCCTCA	180
TGTTGCTCAA AGAACCAACT CTTTGCGTT TGTTGAAGTN ATCTGNTTGT TTTNATGGAT	240
TCTGATTCCN TAAGAATTTC CNTGCTTGCA TTTAGT	276

(2) INFORMATION FOR SEQ ID NO:1099:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GGNANAGTGC ACGTTGGCGC TACCGGACGG AATGCTGTAT CCCCAAAAAA GCCCGTCGTG	60
GCAGCGCAAG AGCTGGACGG CCTCTAAAGC TTCCNGNACG ACTTCTCCAA NAACCAANGC	120
CGGGGNNTCA	130

(2) INFORMATION FOR SEQ ID NO:1100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

TGTATAAAATC CTTATTTTAT TAACAGNATA CTATCATAAA TAGTATTATA ATGCTGNAT	60
TTCAGGTAAG NAAATAGCTA AACTNCAGTA CACTCTACAG TAGCAACTCA GGACAGCTGG	120
TTACAAGCTG GTTGTNTTAG GACATTGGTT ACACGGATTC TTAGACACTT TAATGGCTGC	180
GATAACTGTN ACTCTCCATG ATCCATGTTT CTTTTATGCG CATATNATTG GACGCACACT	240
CATTCAGAGT CCTCCGAGAG GGGCACCCAT ACACGGCAGA NGTGTTCATC TCCAACATGA	300
AAGTGACCAG CTCTCATCCT CGTCTCCCCA ACACCATAAC GTCCTCATCC CGCCTCCAAC	360
CCACACCAGG NCAGAAGCCCT TCAGAGGGTG TTTTCATCCA GGGAACCACT CTCGAACCTG	420
AAGGTTTNAC TTTAGCGTTT AGCNAACCCA GGGCGGGTGT GTGTGTTCC CGTTTGT	480
TTCTG	485

(2) INFORMATION FOR SEQ ID NO:1101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GGCACGAGGG NCCCCTGTGC AGAGACTGCT TATNTNCTGG GGAACATAAA GACGGAGCCT	60
TGCAAGAACG CCCCCGGCT GTNCCGNCAA GGCTATGCCT GTCCCTACTA CCACAAACAGC	120
AAGGNCCGGC GGCGGAGCCN CGGAAGCACA AATACAGGTC CTTAGGCCAG AGGAGGCCAG	180
CCACGGGAGG GAGGAGTGGC AGGAAAGGG TCAGGCAGAG GCTGCTCCA CTGGCTCTCC	240
GGGAGGTGNG GNNGTTGGTT CTGGGGATTA CAGGATCGCA AAGCCCAAGG GCCCAAGGGG	300
AGGGCATTAG TTNAGGATTA GTTGGACAAT TAAGGAGNCC CAGTTTAAA CTTNCTTNCA	360
ATTAATTTNG GGG	373

(2) INFORMATION FOR SEQ ID NO:1102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GGGNTACACG CAGGCGCCAA CCAAAGTGGC CAGGTCTTCG GCCTGGGCC GGNAGATATA	60
TAACCCCAAG TACTGCCGA ANGGAACAGT GGCGATGGG GTTCCCTCGG GNNACNGGGA	120
ACTGNCCGGG NCCCGGGGA AGGTCCCTGA ANTATCCCCC TTNATNACCA GGAGGAGGCC	180
GGCTNACTGA GNGCTCCAG CACGTTTCT CCCAAATGC GTNTTCCCA TCTGGGATTT	240
TGGGGNTTTT CATGTGTTT AAANTTTTT TTTTTTTTT T	281

(2) INFORMATION FOR SEQ ID NO:1103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GGCAGAGGGAA CCTCTGGCAA GTNTNTCCCT TTCTGGGGC CTCACCTGTT TCATNCGCAA	60
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ATGGGGATGT NCCACCTGAA CCCCACCCAC ATCTNCAGGT GGTGAGAGCA GATGGAATGG	120
CACTTTGCAA ATCCCCACCA GCTGGTAAAG GTGAATAGCC TCACTCTTCT GCTTAAAGCC	180
GTCAGTGNGC TGCTNCATCA CACTAGANTA AAATGGAAAC TCCTCACCAT AGGGATCCAG	240
NCTTTGCNCC AACTTTTGA ACAGCATCTT CCCTGGGATT TTTCCANCNC AAAATTGG	298

(2) INFORMATION FOR SEQ ID NO:1104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

TGGNTTAANC GANTTANAGC TGCTAGCCAG GAACATGGAC TGANGTATCC AGCGCTCATT	60
GGGAATTTAG TTAAGTCCC A GGTGGAGCTC AACAGGAAAG TCCTAGCGGG ATCTGGGCCA	120
TCTTNCGGAG CCAAAGANTT TNAAATCTTT TGGGCTTGCC TTTGGCCAG TAGGGAGGGC	180
NGTCACGGAG GGNTTTTCCT TG	202

(2) INFORMATION FOR SEQ ID NO:1105:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GGCANAGTTT CTCCACAAAA ATATAATTNT NAATTAANGT CTCAAATACA ACTATTTAAT	60
CAACCACTGA TTACTCATAT NGTATACATA TATAAGGGAT ATGACAGAGT AGAATTTNAA	120
TAAANGTAAA TAACTAATTA TAAAATAGGG GTCTTATTTG AATAAACAAAT TTTGAATGCT	180
ATCACTGCTT ACCTGANAC TNCTGCTCAT TTTGGGCCCT CTGGGATCCA AAAATTCCAA	240
AGNCCTTGGG CNTTGGGAA CCCNCCCCAG GGTTGAGAAG TCTTA	285

(2) INFORMATION FOR SEQ ID NO:1106:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

GGCACAGGGA AATGTGTGCA GCAAGGTTGT CCTCAAGGGG CTCTTGTCCA CGTGNCCTC	60
TACCCATGGT CCCCCACAGCG GGACCAGCTC CACACACAGG GAAAGANTGG NAAAGGAACA	120
CCCAAAGCCA ACCTGGCCCT GGGAACCTCC CCTTCCTGGT TTTGAACGGC TCCTGNAAAT	180
TGGNTCANTN CACACCGAAA GGACTTTTTT GGAAGGNAGC GCACCAANTT TTTTNTTCTG	240
GGAAAGATGG TGGTAAGGCA GAGCTTGAGT TCCATTGCTT ATGGGAGGGG AGAGATTAGN	300
CCCTTGCACA GAGCCTTCCT TCGGGGGTTN CCAGGGGNAN TNG	343

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

GGACAGTAAG ATCTTAATCA TCCANAGCTT CTTTAACCCC AACATCGTGA GAATTCCATG	60
AGGTNTACGA AACAAACATG GAAATNTACC TGAATCCTGG AGTACGTGCC AGGGAAAGGAG	120
ACCTTTTGA ACGCCATCAT AGAAAGTTG AAAGTCCCCG GAGCCCGATG CTGCCCTCAT	180
GAATCATGGG ACTTATGCAA AGCCCTCGTC CACATGCACG ACAAGAGCAT TGTCCACCGG	240
GACCTCAAGC GCGGAAAACN TTTTGGTAAG TNTTGATTT TTGATGATAT GGGAGAGGGT	300
NTTTTTAGAA TATGGGGTTA AATTGNTN	329

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

ACTGGGTTGA TACAAAGGAT TGGTCTCAAA GCTCTGAAAT TTTTTCTNCT GCTTTCTCTA	60
GTCTGTNGTA TTTNAAAATT CCTATAGTAA ATTNNNAAT TCCAGAAGT	109

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

GAATAATTTC CNCATCGNAG ACCCACACCG GGCAGCCAAA TTAANCGGGC AAACGCAGCA	60
NATTTNNGGC GGTNAGATCG GTATCGGTGC TGAACAGTGA ATGTGGCATA ACAAACTCCA	120
GATAAGTNCT TTTTNATGAT TAGGCCACAT CATAAAAAGA NTAAAAAAATA TCGATTATG	180
TCGAGTCTAT GCAAAATTGN TATGGATTAC CGGTTGCGA GAGAGCGCTA ATGGCCGCCG	240
TTAACTTACG TCATATTGAA ATTTTCATG NGGTTAATGN CCGCCGGAAG CNTTGACTGN	300
GGNGG	305

(2) INFORMATION FOR SEQ ID NO:1110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

NCCTCTTGGC ATGCCTGTCC TAACTTNTNG TAACATCAGG CCTGCCCGA ATCACCTGTN	60
CGAGCCACNC CAGTGCACAG CAGGAACCTGG TAAAGTGCCT GGNCTGCTTC TNCCCTTNCT	120
CCCTTTCCAT CT	132

(2) INFORMATION FOR SEQ ID NO:1111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

CACGGNATTA ANAAACGGTG ACGCGGGTAG CACCACTTCA AAGGCCTCGC NACGGTTAAT	60
TGCNACCAGT ACACGTTGCT GATT CANCAC GCGGACAAAT ACCACCACGT TATCTTCCGC	120
ATACAGCACC TNANAGCCGC CATGACGTAG CGCCTGATTT TTTTNACGCA GCGCAATCAT	180
TCGCTGGTAC AGCNGGAATA ACGCCGTATC CTGCTTTCC ACCTGCNAGG GGAACGGTTT	240
ACGGCAAAC GGATCGTTT TGCCATCCAG TCCTACTTCA TCACCGTAAT AAATGGGACG	300
GTACACCAGG GCCAGGTGGA ACAGGNAGGT NCACCGNNCA NGGCAGGC	348

(2) INFORMATION FOR SEQ ID NO:1112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

ATTTNNGATT GTNCAANACA GAGAATCTCA TCCCGNACAA GATGTAGGAG .GAAGAATTAT	60
CCAGGTCAAT GGACTTGGTG AATTCCGATC CACCTGAAC NTGCCACAGT GAGTCCGAG	120
TTCCTTAGGC TTNNTGGTNT AGNNG	145

(2) INFORMATION FOR SEQ ID NO:1113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GGCCATTNAA ATTNCCTCATC CTGCATGAAA TTCCCCTGG TGTAATNAC CTGCACAATA	60
TGACTCCTCC TTTACTTCAT CATGACTTGA AGACTCAGAA TATCTTATTG GACGATGAAA	120
TTTNATGTTA AGATTGCAGA TTTGGTTTA TCAAAGTGGC GCATGAATGT CCCTCTCACA	180
GTCACGAGTA GTCAAATCTG NCACCAGAAC GAGGGACAAT TATCTATATG CCACCTGAAA	240
ACTTATGNAA CCTGGGACAA AANTCAAGGG GCCCAGTATC AGGCACGGTT ATATATGAGG	300
CTNTGNCAGT TTTTCACAT CGGNAAGT	328

(2) INFORMATION FOR SEQ ID NO:1114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

AGGTGACACA GGAGTGGCCT TNCCCTTCGA ATCTTCCTG GGCAACTACT CCTGTGCTGC	60
CCAGGGCACC CAGGGTGGNC AGCAAGAAGT AAGCAGGGGA AAGGCCAGG GAATGGGTG	120
AAGTAAGGGC AGGGCCAGGN CAGGGAAGGG AAGGTGGAGA GGGTGGGCTT TTGGGGTCTN	180

TTTCCCTTTC CTTCTCTAA GCCCCTGNTN CAGCCCTGGG GATGGGGTCA AGACTGGGGA	240
ATCAAAGCAA GGCCCTGTGG GGCAGTTNTG GGGAGGGGGC TGAGTNNTCG ANAAGAACAG	300
TTCCAGTTAG GGGTNAACGG CCTTCCTTGA GCAATNGTTC TT	342

(2) INFORMATION FOR SEQ ID NO:1115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GGCANAGGTT TACTTATCAG TCAGACCCAT TCCGGTGGGC CTCGAAAGGT ATGTNCATGT	60
TTGGAGTTTG CTTGGTTTTN TTCTCACCTG CTTTNACCC TTTAAGAATT TNATATGGTA	120
TACATTGTAG TAGAAATATT AGATAATGNC AGGCAAGCAA GCATCAGAAT GACCTAAAAT	180
TCCAGTACTT TGAGTACAAG GCTTTAAACA TTTTAGTATA TACATCTTC TGGTATATGT	240
ATGTGTGTAT ATATATATAT ATATGTGCCN CACACACACA TATATCTTNT TATAAAANTT	300
TATAATCTNT ANT TT	315

(2) INFORMATION FOR SEQ ID NO:1116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

AGGCACAACG TTTTNANCAG CTTTATCGCC GCTATCAGCA ATGGNCGATG AGGCCGNAA	60
CAACACTATC TTCCAACCTTC CGCCCCGGCA CAGGCTGCC AGGCCGTTGC GAACTTTATA	120
AGGACACGAT AATGAACGAT TTTNAATAAT TATGAAAGTG TGGTTGTAA ATTGGNAGCC	180
AGCATCTNTT TGGCCCGGAA ACCCTGNNTN AGGTTCACCC AACATGCCGA GCACGTGGTT	240
AATGCGCTGA ATTA	254

(2) INFORMATION FOR SEQ ID NO:1117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

CNAGGGGCC	TNAGGNTCCC	TCCTGGCCCC	CACGGAACCC	GTGCTNCTNT	TAACTCCTAG	60
GAGATGGTTT	AGAAACGTTT	CCCCCACTTT	GACGGCATTG	NAGGCACCAG	GNGCAGCTCA	120
AAGTAATGTT	CATCGGAGGC	CCCCAACACC	AGGAAGGACT	TTTCACTTCG	AAGAGGGGTT	180
GAAGGAGGTT	GGGTTTNATT	TGGTCTNCCT	TGGNTTTAGG	NCCTTNGGG		229

(2) INFORMATION FOR SEQ ID NO:1118:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

GGCACGAGGG	AGACCCGGGG	GAGAACCAAGG	CGTCCAGGAC	GCGCGTTGNA	CCACCCCTCAA	60
CACGGATATC	AGCATCCTGT	CCTTGCAGGT	GAAGACCTGC	TNCCGGGGTN	CCCGGGCCCG	120
GNGNCGGACA	CTCCCGGGGT	TTTCTNGTCC	TGTGCACTAG	GTAGATCCGT	AGCCCAT	177

(2) INFORMATION FOR SEQ ID NO:1119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

TGGGCCATN	TCCTCCTCCN	TCTCCTCCCT	GCNATCTTC	CTCTCCTCAA	ATNTCCCTGC	60
AGTNTGAACC	CCGGCCTTGA	AGGCTGGGAA	GCAGGGAGGC	CAAGAGAAGG	AAGCTGTGAC	120
TCCGCCTAGC	TCCTGGTTGT	TAAGCACCCA	TGGTTGCCA	GGTTTGNNAAC	AAACTCTGGC	180
GCTCTAAAGG	CTGATAAAAGC	CCCACAGCCT	GCACGTTGG	NGCCTGGGCC	TCCAGCCCTG	240
ATAAAGCTGG	ACCTGTNAGC	ACCATGGCCA	CACCTGCTGT	AGGNATGAAG	CGGCCACCCG	300
TNTCCCTGG	GCCATTCCCA	NTNAAGGGTT	CCTGTTCCCC	TGTTGCACAG	NCAAGCCCTG	360
GGCCACCATG	NCTTAGGCCA	ACCCTTCCTG	GNTGAAGGAA	CAAATGGNNG	TTGGCCATGG	420
GCAAG						425

(2) INFORMATION FOR SEQ ID NO:1120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GGCACGAA	GAACCCCG	NAAAGTCTCA	GGATGGNAGT	TCAGATTGG	TAAGGCATCC	60
CCTAGTTNCA	GCTTCCTGGC	GGCCTGCTCC	ACACAATNGC	CTNTGGGCC	ATGGCCTTNA	120
TCC						123

(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

TTTAANCAGC	TCAGGGGGTT	TNATTCCAA	GTAGAAGGCC	GGGAATGGTG	GCATTCCTCC	60
CANAAGTGCA	CANTGAACTA	TAAACTNTT	TGTGGTAGAT	AGGANTGAAC	AATTATCCGG	120
TTATCTNGTT	TCCCTTGCCC	AGAAATGGTT	CTNTCCCAGT	GGAAATTGTG	CCCCGCTCTG	180
CCAGGACTGG	ACACTGGTC	ACAAAANTGG	TAGCAGAGGA	TGCTGACAGT	GGTTCTAATG	240
CCTGGTTTTT	CCTACCACAT	NTCCCGGGCG	TTTGAACTCT	GGTNTCTTT	AGAATTTCA	300
GCCAATATTA	GGTNAGCTTC	CNTAANTG				328

(2) INFORMATION FOR SEQ ID NO:1122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

CACCATTGAT	GGATACTTNG	GTTGATTCCA	TGTCTTCCT	ACTCTGAATA	GTGCTGTGGC	60
AAAACCTTTC	ATGGCCTCCG	GAATCTCCTT	CCTTGGTCCT	GCCACAGTNC	CAGCAGTTTC	120
CATATTGTTT	ATTATTGGA	ATTACAGCAC	CAAAGTNCCT	GTTAAAATGT	AACTNCTACT	180
TTGGGAAGAG	ACCTGATTCC	TCATGACAGG	CATTAATAC	CTTAGTTAG	GCTAGTTAT	240

CTGCTTGGCC CTCNAGCACG GGGAGCCCTT GGGAAATAGAA GGAAAGCAGA TAATGTTCC	300
CTGGGGTCAG TATTGGGTTG TTACCTGGGG AAGGAANTGG GAAANCTTGG GGGGTTTCGA	360
GGGGGGNCCC NGGTACCCTT TNGCCT	386

(2) INFORMATION FOR SEQ ID NO:1123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

CCCAGACGGC GGCAGTCGGG CTTNCCCTTG GAAGTCNAGG CTCGGTTGTC TTTTGGAAAGC	60
CATGGAGAGT AACTTTAACG TGNGCTACTA CGTGGGGCAC AAGGGCAAGT CCGGCCAGAG	120
TTCCTGGAGT TTAAGTTTCG ACCGGAGGGG AGTTAAGATA TGCCAACAAC AGCAATTACA	180
AGAATGNTGT NATGATCAGA AANGAGGCTT ATGTACATAA ANGCGTGATG GAGGAACGTGA	240
AGAGATTAAT TGACGACATN AAATT	265

(2) INFORMATION FOR SEQ ID NO:1124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

GGCAAGAACG AGCGCCTTAC GAANGGGAC AAAAAGGGAG CCATGAAGNA AGTGGNAAAT	60
CCATTTCTA AGAANGATTG GTATGCTGTN AAAGCACCTG CCTATGTTCA ATATAAGTGA	120
ATATTGGAAA AGAACGCTCC TCACCANGGN CCCACAGGCN NCCAAAATTT GCCATCTGAA	180
TGGTTNTTCA CGGGTCGTGT C	201

(2) INFORMATION FOR SEQ ID NO:1125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

GGAAGAAAAC CAGAAGGGCA CACTTNAANC TAATTGGGG TATCACTAAC CTGAAGANAA	60
AGAGAAAGGG GGAGAAAACC TAGCAAACCA CCATGTCCTA TGGGAAAGTT TGCANNATGC	120
ATCGAANATT NTNTGGTGGG GCTCCNCCTC CTNTGCCATC GGGGNTTAAT ATTNCCCTT	180
ACTTTNCCCA ATGGGGAAAC AAAGTTGCT TCNAAAAACC ANCTCAGCGG TTTGGTGTGG	240
TTTTTNCTG GAATCGTGGG AGGTGGCCTG	270

(2) INFORMATION FOR SEQ ID NO:1126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

GNCGCAATT ACCTTGCCA AATAATTACC TTTATCTAC AATTTNCCT GTTTTTGGT	60
TCTTCAGAT CTCACTTGTA TAATGNCTTC TTTGNTAATT TTGTTATATT TTCCTTTCTA	120
TTGTCATAAG TTGGGATGAC TTAANTTANC TNCAGTCTTT GATTGTTATA GGTACTATGG	180
TATNGCAGAC CATAAANATC CT	202

(2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAAANTTTA GATANTACAT AATTATTGCT GTCCANAAAA TCTTAAAATA TATGNATTCC	60
ATGAGACAAG AGATGAAGTA TGAGGTNAAG AATACTATGT CTAAGCTGNA AAGGTACCTC	120
ATTAAGTTAT AGACAGNANT AAAATGAGGA GGGAGTATGA AACATATGGA NGT	173

(2) INFORMATION FOR SEQ ID NO:1128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

GGCAGAGCAG CAGTTCTGA AGAAGGCGNT GCAGGGCTG CCANGGACT TNCTGGGNGC	60
TGCGCTCGTN GCGGTGTGGG AGCAGCTCAT GTTACATCAA GGAGGGACCT CATCCTNNCC	120
GCACTACCAC ACCTTCTGAC GANCTTCATG CATGCCAGG GNGAGGNTGT CAAG	174

(2) INFORMATION FOR SEQ ID NO:1129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

GGCANAGCTT TCCTCAGAGA CCACATCACT ATTCCATATT TAAGCAGGCC AGCATCGTGG	60
AAAGCNCTTT TCGGGCATCT GGGGCTCCAG AACCGCAGTA TCAACCTTCT TTCTNATGAC	120
TATGGAGATA TTGTTGCTCA GGAGCTTCTC TACAGGTCAG TGGAGCTTCA AACTTCAGCT	180
TATGAATGCT AGGAGAGTAC ATTGTTTCTG GACTGTTGT ATCCTTTNN CTCTCGTTT	240
TCAGCGGTGC ACTGGTTAA GGTTTGCTCC AGCTTACATG TGTGNTNTCC TCGTCTNCCT	300
TTT	303

(2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

NGNGCACGCT GCCCCGNTNC CCCACTTTNA ATGCAGGCTG GCATACCACT GTGAACTCAG	60
GATCTAAATT TAAAACTTCA ATTCAATTAA ATTTCAAAAC AAAAGCANTG TAAATATTTT	120
NCCCTATCCC ATTACCCCTGN TTTGANTCAT TACACATTGT ATACATATAT CCANT	175

(2) INFORMATION FOR SEQ ID NO:1131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

CAGCTCAATG TGTAAGCATT TTGGTGCCTG TCCACTAAGT TTCAGGGAGC CTCATTCTTC	60
CTTCACTCAG GGCAGCATTG GCTCTGAGAG AGGCGGCAGA TTCACAAGAG TAAGTAGACA	120
GTCTATTGAG GTTTAGGTTT AAAGTCTTCC TCCAGATACT CCAGATTGAA TGTACTAATT	180
AAAATAGCAA CTACAGTGTT GGAGCATTNA GAATGCTAAT GAATGTTTA ACCCTTGGA	240
AACCTGATGC ATTCCCATAG GTTCATATGG TCCATTCTCC AAAACACTGG GCATTGGTTA	300
GAATGGAGTA GACAGTAGAT GCTTAGCTTG AGGTGGGAGT GAAGCTGGGT TCCTCACCN	360
TTTTNNNN	368

(2) INFORMATION FOR SEQ ID NO:1132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GTCCTCTCCA AACTGAACCC AGAGAACATG GAACTCGAAC AACCTGGGA GNCAACATC	60
CGTAAGCAGT CAGTCGCCAA TGCCTTCATC ATCTGTGGCA CCTTGNACAC CGTCAGCAGC	120
TACACCTCAG CAGATGCTAC CGTCAACTTT GCTTATGAAC ACAGGCACAG GTATCAGCAA	180
GACCCTGACC ATCCCATTCA AGAACCGCTA TAAGTACAGC AGCATGATTG ACTACAACCC	240
CCTGGAGAAG AAGCTCTTG CCTGGGGACA ACTTGAACAT GGTCACTTAT GACATCAAGT	300
TTTCCAAGAT GTGAAAAGNC TCCAAGTGTAA CAGGCATGGG CAGAAGGGGG TTGNTCAGGG	360
TNTTGGGGGG AGCAGGTNNA GGG	383

(2) INFORMATION FOR SEQ ID NO:1133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

CAAAATGGGA TTTNTTCAAG GNCTGGTTT AGAAAANTCA GCACAAGGCA TCACTGAGCA	60
TATCATAACCT ACTCCTAAAG CAGACTCTAC AGGACTTGGT TATTCTNTTT AGAACGGTC	120
ACTATCAAGC CTCCAGAACCC CATCCCTTG ACCTGGAGGA ACTTTAAAAA CCTGTTCTAG	180
GTAGGTGGAG TGGCTGCTCC CAAAAAATAA AGCTNGGGNG GCNCTGCATA ATTTGAGTT	240

CTTGGAACAG TTTAAAATTT NGGGN

265

(2) INFORMATION FOR SEQ ID NO:1134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GGCAGAGCTC GCGTGNCTG TGGCCGCAGC TTGAGTATGC TCAGGCTTCA GAAGAGGCTT	60
GCCNTGAGTG TCCTCTGCTG TGGCAAGAAG AATATCTGGT TAGACCCCAA TGATGACCAA	120
TGAAATCACC AATGCCAACT CCCGTCAGCA GATCCGGNAA GCTGATCAA GATGGGCTGA	180
TCATCCGCAA GCCTGTGAAT GGTCCATTCC CCCGCTTGAT GCCGGAAAAA CACCTTGGCC	240
TGCCGGAAAG GGCNAANTNA TGGGGCATAG GTAAAGCGGA AGGGTACAGC CAATGCCCGA	300
TTGCCAGAG AAAGGTTCAC GTGGGNTGAG GAGGAATGAG GATTTNGCA CCGGNTGCTT	360
TCAGAAGTTA CCNTGNATT TAAGAAG	387

(2) INFORMATION FOR SEQ ID NO:1135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

GGCAGAGCGG CANGAGTGNG CGCTCCTGCT GGGGGTCACG GGAGTCGGGA AGANTGNCTG	60
GTGAACGGCT GCAGGAGGTG AGCTCACGGG ATGGGAAAGG CGACCTTNTG ACCNGCCTAG	120
TNCACGTCCC ACGTTGTAA TGGACGCCTC TGNACCCAC CCAGCTCTCT NCATCCTGTG	180
TGCA	184

(2) INFORMATION FOR SEQ ID NO:1136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

AATNTTTGGC AAAGCAGTGG AACATATGTT TGAGACAGAG GATGGTTCTA AAGATGAGTG	60
GAGTCCAATG GTCTTAGCAC GTGCACCTNT CATGAACACA TGGTTTACA TTACCTATGA	120
AGAAAGNNCC TGTCTTGTGN CATGTGCCAA CTCTTAGATG ATTACAAAGA AGGCGACCTT	180
CGCATTATGC CTGATTCCAA TGGAGTCACC TCCAGCAGAA AGGGAACCAG GGAGAAGTTG	240
TGGACAGCCT GGTAGGCAAA CAAGTGGAA TATGGCGAAA GAAAGATGGG NTCGNAAAAG	300
GGACTNGGCA TNGTCATTT CATCCAAGGT AGGAAGGNCC AAG	343

(2) INFORMATION FOR SEQ ID NO:1137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GGCACGAGCA ACAGCCTCGG NNNTACTCTG TCTGTGGCGT ANATNTCTTN ATTCCTTTAC	60
TCTCCTAATA AACTTNCTTT CCCTGTACTC CAAAGACTCG CCCTGAATTC TTTCTAGCAT	120
GAANTCCAAG AACCCCTTT TGGGGTCTGG ATTGGAACCTT NTTTCCTGTA GCATCTTCT	180
GGTGNCCACT GAAGGGACTG NAGTGCAGAA AACCCCCACC CAAAGGCTTA NCTTTGGTA	240
AGTGGTGGGG GCCAGTAACA TTTTTCTAGT GNACCCTGAG GGGACGGTTA CTGAAGAAC	300
CCCCCGGACC CAAAGGGAAA TAGGAGTTGC AGCACTGGTT AGGGCCAANT TTGGGTAAGT	360
GGTGGGGGTT ACCAGGTTAA AGGATGGATT GGGTTAGAG GCCCAANTAG GGGAGTCAGA	420
GTCTTCCTA AGACAGATGG GTCAAGGCCG TNTTGTAAA GGCAGGACAC TGACCTACTT	480
TGGTTAAAGN CCACTTAGGN GG	502

(2) INFORMATION FOR SEQ ID NO:1138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GATCAAGTAA TGAAACTACA GAATCTNTTT GTAGATGATT CAGGTCGATA TTTGGCTATT	60
CAATTCCATC TGGAATNTGC ATATGTGTTT TNATATTATN ATGAGTACAG AAAAGCAAAA	120
NATCAGTTGG ATATTGCTAA GGACATCAGC CAATTACAAA TTGATTTGAC AGGTGCTTTG	180

GGAAAAAGAA CACGGTTCCA GGAAAATTAT GTGGCACAAC TGATTCTAGA TGTAAGAAGG	240
GAAGGGGATG TCCTTCAAA TTGTGAATT ACTCCAGCAC CCACTCCTCA GGAACATTTA	300
ACCAAGAACATC TTGAGCTTCA ATGATGACAC CATTCTGAAT GACATAAAGT TTAGCAGATT	360
GTGAACAGTT CCAGATGCCG GATNTGTGTG CTGAAGAGAT CGCTATTATT CTTGGATCTG	420
CACTAATTTC TCAAAGGATA ACCCAGTGCA CACATTAACt GNAGTGGGGG TTTCTGGGCA	480
TTTACATCA	489

(2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GGCACGAGCT CGTNCGTATA ATAATTTAAT TTGGGTTTGT TGGTATAGAA ACTGTATNTN	60
CACAATAATG ATAAAGCCAC TCAGGCTCAT CTAGTCATTT CCTGGATTTA TGTGTGTAGG	120
AGTACATAAA AATANGGGCA CTGATTCGTT TTGTACTTGT CTAAAATTGT TATTNTTCAG	180
TTGTTCAAAG GTACACAAAA TGCTTTTNC TTTATAAGGT AANAAATACT TGGNGGTTAT	240
AAGANNTAAC TCTTAACTAG CTTACTTTGA GTGGCTTGA TATGTATTTN CTCATAATGG	300
AATTCATGAG CTTNCCTTCT TTCGCTTGGC CAAGATTTT TTTTCCCTT GAATTCCCTT	360
CTCCGGTGTGTT ATCTAGGATG TTTGCATTAC AAGCAGGCCG CTTTACCCCCC TTTGTCCGTT	420
GTCACAGGTG AAAAGCCATA CAAGGGTACC CGGGGAGGCT GCGACTGGNG GTCCGGCGGT	480
CCGGATGAGC TGACCCGCCA TAC	503

(2) INFORMATION FOR SEQ ID NO:1140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

AAAAAAAAAAA AAAAAAAAAAA AAAAAAAAAAA AAAAAAAAAAA AAAAAAAAAAA AAAAAAAAAAA	60
AAAAAAAAAAA AANNAANNA GGGNGG	86

(2) INFORMATION FOR SEQ ID NO:1141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GGCAGAGGCA CAAAAACACA CACCAGAACG TTTCATAGCAG CCTTATTAT AATAGCCAAA	60
ATCTGGAAAC AACACAAATA CCCATCAACT GGTGAGCAGA TAAACAAAAG AAACAACATA	120
AATAACCCATC AGCTNNTGAG TAGATAAAGA AAACAGGGTG TTATCCATAC CATGGAAATA	180
TTGTTCAGCA ATAAAAGGGG AAGAAATACT GNTGNTTGCT ACATCACCGA ATGANCTCG	240
GAAAACATAT GGCTGGAAGC CAAAATGGAA AAACAACATA TTGTATGATT TTCCATTATA	300
TGGAATGGCC TTTATATGGA ANGGGAAGGG CAAACTTTG GAAACATAAG CCNTGGGTTG	360
NCCCAGGGTT NGGGGTTTGA ACNGGGTTG ACTGCAAAT	399

(2) INFORMATION FOR SEQ ID NO:1142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GGCAGAGNCT CACTGGCCGA CAGTTGCCTG CTGGGAATT TGCTGGCGGA CTTCGTTCGC	60
GGNCAATCCT GNACGGACAA TATTCTGCTG AAATCGTTAG CGGGATCCGT NTGCTTCGCC	120
GCGTTGATAC CCTGACCGAC TCCCTGNCCC GAAGTGCAGA TCGCGCGCAN TAATTCCGT	180
GGTGATTTCG GCCGCGTNTC GATGATCAGG CTCGACGTGG TTGTGGGATC ACTTCCTGTC	240
GCGCCATTGG GGCANAATTC ATCCACAGCA ACCGCGNAA GATTTTTTG CCGCCTGTTA	300
GCAGGTAATT AACGCCGTNT TTGCCCCATT TTGTGGAGG CGTTTCCAG AATCTGAAAT	360
GNCCTGGTTT NTGGNCNGAG CGTTGGATGG GAACGTTACT NCGGAATTCC TTTTATCGC	420

(2) INFORMATION FOR SEQ ID NO:1143:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

AACNANTNAC GCAGGNACCA CNAAAATCAT GTTCCACGTG TCCAGAATGC TGCCTTACAC	60
CCCTAATAAC CAGCAGCAGC TCCTCCGGAA GCGCCACATT GGCAACGAAC ATTNTGAACC	120
ATCGTNTTNC AGGAAGCCTG GNCAGCAAGC CCTTNTGCC CACCACCATC CGCTCGCACT	180
TCCAGCACGT NTTCTAGTG GTGCGGGCAC ACACACCCCTG CACGCCACAN ACCACCTTAC	240
AGGGTGGCCG TGAAGCCGCA CCCAGGGACA CCCCTGNTTT CGGGGCCAGT TCTGCCTGCT	300
TGGGGANGGC CCCTTCGNA GCCAACGGNG ATTTTCGGGN CTT	343

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

AAGCCACANA ATTATCATT TTTNTTTTT TGTTAGGGTG GGTCTTCTTT TTTNNNTTCC	60
CTCTCTCTTT TTTTAACAAA TGCCTTCTTA TAGAAAAACT TTCTAAGAGG CAACAATTAA	120
GNAATGGGAT ATTTTGAACG AATCGGCATG AGTGTAAACAG NTGNATAACC TGATCTGTTT	180
GTTTTNAAG NATTATTAAC CAAGTGGAAA AATTCCAGNA ATGANTAGTA ATTTACACTA	240
AACATGCTAT ATAAAANGNT TNAAAGTCNT GATGCTGTGG AAGCAATCTN GTGCTATATT	300
TCTACCTCCT CATTGTCTTA ATTATTGGGT AGTGGGG	337

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GGCAGAGGGA AAATCATTTC CTTTATCTTC TCCACTAAAT CTAACAGCTT CATTAGTTCC	60
TTCTTTAAGA CAGAAGTAAC ACATTGTAAA GAAAATGTAC AATAGATTGC NCTCCAAAT	120
AGCATCTATG TTGTAAAGTN TTGCAGATGG CCTTGGGAAC ATCTGGTGNA ACAGGAATT	180
GTTGAGCCTA TGTNCATTGT GCATGTGCAG TGAAGGTCAA CTGACAGAAG GAGAGCCAGA	240

AAATAAAAAA TAANNAANCT GNGAGGAAAG ATTGAGTTAT TTGATGGACT GATTGNCTCG	300
ACACCTCTGC TTCAGAGAAA TGCCATTTG CCAAACGGAT GGNTCCNCTG GTTATCANTG	360
NAAGGTTAGG GCATTTGTC TGTGGGNCCN GNTACAGAGG TTGAATGTT TCAGGGTAGCC	420
CTGGTTTCAN NTGGGTTAGA ACCTCCGGTT TGCTTTAAG CTGGGGTG	468

(2) INFORMATION FOR SEQ ID NO:1146:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

GGCANAGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAANN AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAAANN	87

(2) INFORMATION FOR SEQ ID NO:1147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

TTTCCTGTTT CTGAAGCNCA TTTTTGTTA TATTTATAA TATATCAAA TATAGATGGT	60
ATAAAATAAG TCCCTTCTCA TGTCTCTCCT TTAAAATTGC ATTAGCTATT TATAGATCTT	120
TATTTTCCA TATATATGTN ATAGTAAGTT TGAGAATTAT TCAAAAAGTC CTTCTAGGAA	180
TTTNGAATTG GAATTGATTG AATTGTAGT TACATTTGG AAGAATTAAC AGTTTCATAA	240
TGCTAAGTCA TCCCAGTCAT GGAAGAGGAA GATCTTTAA ATNATTAAAT TGAGCTTTCC	300
CCCAACCTCA TGTAAATAGT TTTGGGGCAT NCTTTGTTAG ATAAATAGGC AAATACCTNG	360
TTTTGTTGG GGGNGTTCA C	381

(2) INFORMATION FOR SEQ ID NO:1148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GGCAGNGTNA CGAAATACAG NTCCTCCCCA GATGACGCCA TTTTCCAAAG CTTNGCCGG	60
GATATACTCT TCTTTCAACC CGGCCATGGT CTGACCCCAN TNGNCCACCA T	111

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GGCAGAGAAC GCCCTTCAAG ACATGGACAA ATTTAGCTTG AAAGACAGTG GCCGTGGTGA	60
CAGTAAGGCA GGAGACAGTG ATTATAATTG GGGGCGAGAT TCTCCAATAG ATAGGCTGCT	120
NNGTGAAGGA TTCAGCGACC TGTTTCTCAC AGATGGAAGA ATTCCAGCAG TGCAGCTATG	180
AGAACTCTGG CACGGAGGAG TGCANGTCC TGGGACACTC TGACCAGTGC TGGATGCCAC	240
CACTGCCCTC ACCGTCTTCT GATTATAGGA GTAACATGTT CATTCCAGGG GAAGAATTCC	300
CAACGNAACC CCAGCAGCAG CATCCACATN CAGAGTCTTG AGGATGACGN TCAGCTGCCA	360
GATTCCGGTG AAAAGAAGAA GAGTTTTTC CACNTTGGN AAAGGATTCC CCAAAAGNTT	420
GNGGACATTG GGGTTACCN NG CACATCATT T	451

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

GGCANAGGN AATGTGATAT TGGAAGAAAA ATAGTCACAT ATATCAATGG AATATACTAG	60
AGAATCCACA GATAAAACCA TAGAAATATG CTCAACTGAT TTTGACATAG ATGAAAAGTA	120
TTTGTATTAT TACATTGAT TGATCTTGCC TCACAAAGATG GATTTTAATT TNCTTGTGG	180
CACATACCN TATCTTAGT CTATCTTCA CAATGCCGT TAATGGGATC TTAGGCATAT	240
AANTATACAT TGAACCTAAA ATACTGTTGG NNNTGATTAT AAAAGTTTT CAGGGGGGAT	300
AAGTTATNAT TATNGGTTGA GAAGGAGGAT G	331

(2) INFORMATION FOR SEQ ID NO:1151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GGCANAGCCC CCCCTTTTTT TTTTTTTTTT TTTTTTTTTT NNGGGGGGGT TTTTTTTTTT	60
N	61

(2) INFORMATION FOR SEQ ID NO:1152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

GGCAGAGTTT NAGAACACAA ATGTTAACAA TATAGCCAAT ANGTACAGTC TGACACAGCTG	60
GGTTGGACTG ATAGCTGTCA TATGCTATTG GTNACAGCTT CTTTNAGGTT TTNNAGTCTT	120
TCTGCTTCCA TGGGCTCCGC TTTCTCTCCG AGCATTTCTC ATGCCCATAC ATGTTTATNC	180
TGGGAATTGT CATCTTGAGG AACAGTGATT GCAAACAGCA CTTATGGGGT TGACAGAGAA	240
CTGATTTTTT TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCANAAG GTGTTTTTCG	300
TAAATAAGGT TTGGCCTTCT GATCNNGGTG TTCCGGGGGC CCTCATTNTT TGGGGTTAGT	360
NCACCNG	367

(2) INFORMATION FOR SEQ ID NO:1153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

ATTCATACCA TACTAGGCTG ACTCACAGAC ACAGTACAAG TGGTGAAGAT GTAANGAAAT	60
TGGAACCATC ACACATTGCT CCTAGGATTG TAAAATGGTG GAGTCACTTT GGAAGAAATC	120
TCCCAACGGC TTCCACAGN GTCTGANCTA AATTACNTT CCCACCAGCA GTGTATAAGT	180
NTTCCCTTTC TNTGCAACCT CACCAAGTATC TGTAATTGTT GACTTGCAG TNATAGCCNT	240

TCTGACCATT GTGA

254

(2) INFORMATION FOR SEQ ID NO:1154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

GGNAGAGGGG CAAAGACTTG GGAACCTTAA AAGCTGAAGA TTCTTAAGAA GCTACAATGT	60
ATATAATTTN TNGTTTATT TNATTGACTG GTTCTCATAG CATAACATATG TATGAAAAAC	120
TGAGTACTTA TCTCTTNNTA ATATTCTAT ACCTCCATTA CCCGTGCCCG ATTTGAAGAA	180
CTGAANTGCN GNCCTGTTCC GTGGNACCCCT GG	212

(2) INFORMATION FOR SEQ ID NO:1155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

GGCANAGGNA GATTCCATGC ATTGGGTCCA ATTTACTACA GAGNTTCAAA TGGAGCGATT	60
TTAGTTTATG ACATAACAGA TGAAGATTCT TTTCAGAAGG TAAAAAACGG GTCAAAGAAT	120
TACGGAAAAT GTTGGGNAAA TGAAAATCTG TTTATGTATA GTTGGTAATA AAATAGACTT	180
GGNAAAAGGA GAGACATGTT TCCATTCAAG AAGCAGAGTC GTATGCAGAA TCTGTGGGG	240
GCAAAACATT ATNCATACTT CATCCTGTGA ANGTNCAACA ATNAAAAACC AATTATGGG	300
GCTGCTTTN GTGCACACTA GCCTAG	326

(2) INFORMATION FOR SEQ ID NO:1156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

GGCANAGNTG CANATACTAG TGGAAACTGG GAAGAACTGG TGAGGGACTT GCANTTNGCC	60
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CGTAAGAAGG CTCGAGAGTC CTATGTGGAG ACAGAACTGA TATTGCACT GGCTAAAACA	120
AACCGCCTTG CAGAGTTAGG AAGAATTATC AATGGACCAA ATAATGCTCA TATCCAACAA	180
GTTNGTGACC GTTGTATGA TGAAAAAATG TATGATGCTG CTNANTGTT GTACAATAAT	240
GTTTCCAATT TTGGACGTTT GGCATCTACC CTGGTTACAC CTGGGTGNAA TATTCAAGGTC	300
AGCTGTTGGA TGGNGGCTAG GGAAAGCTTA ACAGTNANTC GNACCTGGGA AAGAGGTCTG	360
	360

(2) INFORMATION FOR SEQ ID NO:1157:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

ATAAGAAGGG TGGCGAGANG AAAAAGGGCC GTNCTGCCAT CAACGAANGG TNAACCCGAG	60
AATACACCAT CAACATTCAC AAGCGCCATC CATGGAGTGG GCCTTCAAGA AGCGTGCACC	120
TCGGGNCACT NCAAAAGAGAT TCGGNAATT TNCCCAGTNA AGGAGATGGG GNACTCCAGA	180
TGTGCCGCAT TGACACCAGG NTCACACAAA GCTGCTGGG CCAAAGGAAT ANGGTATGTG	240
CCCATACCGA ATCCGTGTGN GGCTGTNCCA GAAAACGTAAC TGNAGGATGG AAGATTCAACC	300
AATTAAGCTA TATACTTTGG GTTANCCATG TAACTNTTTA ACCATTTNA AAATTTTACA	360
GGACANTCAA TGTTGGGTGA NGAATTAATT CGTTGATTGT CAGTT	405

(2) INFORMATION FOR SEQ ID NO:1158:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

TGNATAGCCA GAAAACTGNG ANAACAAAGGG ANCAGTGTGT AAGGNACTTG TGCACATCAC	60
TGACTGGTAC CCCACTCTCA TTTCACTGGC TGAAAGACAG ATTGGTGNGG ACATTCAACT	120
AGATGGCTAT GATATCTGGG AGACCATAAG TNAAGGGTNT TCGGTCACCC CGNGTAGATA	180
TTTTNCATAN CATTGACCCCC GTATACACC	209

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

ACTGTNTTTA TGGACTAGGA ACTTANTAAA GATGAAAGAG TTTCTNCCCT TGAAGTCCTC	60
CCNGATAGAG TTGCGACATC TCNAATCAGC GATGCACACT TGGGCAGACA CANTNATTGG	120
GCAAAGCAGT GGAACAT	137

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

GGCAGAGTGG CTATAAACTT TGTNACTGAA GAAGACAAGA GGATTCTCCG TGAACATTAA	60
GACTTTCTAC AATACTACAG TGGAGGAGAT GCCCATGAAA TGTGGCTGAA CCTTATTGAA	120
ATTCCCTGGGA ATGAGAAGTT TTGGATGCAG TGCTCGCTGT TGCTGGAATA GGCGGATCAC	180
AACGTGCATT GTGCCTCTT TGTTGGGGA ATATTGAAT CTTGTCTCAA TGCTCATGAA	240
CGGATCAGAA ATACAGNTTT TGANTAGCAA AGNANCCTTA GCCGNAGNCT CCTTGTGAAG	300
GGAAAAGTCCA TTGGGCTTTA TNCCCTTTA AGAGTTAGA CTGTTGGGG TGGGTTTTAA	360
AAGATGGGGG TCTGTGAAAA TCCTTCNTT NNTNAGGAAA TTT	403

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

GGCANAGTGA TCACTCATCT AGATATCTCA NACTCTGAAA TAATATAATT NACTAATTG	60
GGAATTTATA AGTTAAATTT ATAAGGTTTT TAACAAATAT ATTTGTAATG GAATTATTTG	120
AACTTNCCA AATGAAATTG CATAAAGNAT GTGAAGGNTT GCAACAGTTT ATATTAAT	180

TTTTTNCTGG TTTGCAATAC TTGGGTGCC TGATGAAAAG AAATTCTCA ACTTTAGTCT	240
CTTCCTGGC ATTGTGTTCA TACCACTCCA TATTTAAAAA GTTGGACCNG TACTTTGGG	300
TTTCACCTCT TTAAATGGNT GNAAAAGGAN GCCCNCCAGG TAATTTT	348

(2) INFORMATION FOR SEQ ID NO:1162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

TGTTAGTGGT GGGNAGGTGT CCTGTNAGCC CCCTCCAAGG AATTCAACCAC CCAGCGAGGC	60
CACTAAAACC TCCAGAGTAA GTCAATCAGC CATACTAAGG NAAAGTCCTA AGGGGGACAG	120
ACAAGGTGAG NAAGAGGAAT CCTGTGGGCT GGAGGCTGCA GGNAATTAAG CCAAGTAGGA	180
AGGAGAGGAA TCCCAGCGGG AGGNAATGGG GGGAGCAGGG GCTTGGGAAG ATGAGGACAG	240
GCTTTAGTGN ATGGTTTTG NGGGAGACAG CTCTTNAGGT GGGAGAGCCA GGAGGTTAGG	300
GGGTTNAGAC AAAAGTTAGG AAGAGGGTTT TCAAAACCNC AGGGCCCCCA CAAGGGGGGA	360
GGTTCCATGA GCCCCNTGAA GTTGTNTTN CACATTNTTT CCCGTTACAG TTTTTTTTTT	420
GCGCAANACT TTTGGTTTT CNTCAATTT TTCAA	455

(2) INFORMATION FOR SEQ ID NO:1163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GGCAGAGGNA TGAACAGTAC CAAACAGCAG TTTTCTCTC ATGGTCTGG AGCCTGGAAG	60
TCTGAAATCA GGGTGTCAAGG AGGGCCATGC TCCTTCTGAA GGCTGTAGAA CATTCCCT	120
TGCTTTNCC TAGCTCTGG TGGTTGCTAG CAATCCTGG GCATTCCGTG GCTTGTGAAA	180
TGTNTCTCTC CAGTTCTTGC CTGTATCTTC ACATTGCCTT CCTTACTATG TTTACAACAT	240
CATCGGTGGG ACTTGATGGA AGAAGGAAAG GGGGCTGTAT ACAGTTTTG AATCCAGTAG	300
GGTCTTACCA GAGAGACTCC TTCAAGGCTG GGAGGCTCAG CAAGTGCCCA TGTTACAGC	360
CCTGGTTGA CAACCAGGTT GGTTTTAAG GACCATGCAG NATTTNGGNG CAATTCCNC	420

TGTCCCTTGG CNAAGGCCAG GGGTTGGTGA AAAAAGTCTT CATTTCGGG TTA

473

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

TCGAAATCTA ATTGGGGCG CTGACATCAT TGTGATCAA TACAACGTTA ATGACAAGTT	60
TTCATTCCAT GAAGTAAAGG ATAATTATAT TCCAGTGATA AAAAGAGCAT TAAATTCACT	120
TCCAGTAAAT TATTGCTGCT GTTGGTACCA GACAAAATGA AGAGTTACCT TGTACATGCC	180
CACTAATGTA CCTCAGAAC A GAGGGAGCTG TGTTTAGTTA CAACTGTAAG GGGNTCCAAC	240
TTNCAAANNA ACTAGGNGGC AACCTATCTT NGGAACTTCC ACAGGCCTTG GATGGACTTG	300
TTACATAGGN AAAGTTTTT TGGGAGGGAG TGTTTGGGT TNTTTTATGG ATTTCAAGNC	360
TTTAAANTCA GAAGGACAAG TGGAAAAAAA TGGAAAN	396

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

GGCACGAGGG AAAAACAGAA ATCAGCGATA CATAGGATGT AAATATACAA CAGAGNAAAA	60
TCAACAAAGC TGAGATTGG TTCTTAGAAA AGATAAATAA AATTAAGAAC CCTCTATGAA	120
ATGAGGACTG ATCAAGAGAA AGAAAGAAAA CACAAGTGAA CANTATCANG AATGAGGAAG	180
AGGNNTATTAC ATTGTNTATC AAAAAGTTAC TGAGGNTTAT TCAAAAGCAC AAAANCAAGA	240
CATTAGCATT TTGTNATGGT GAATTTGACA TAGTTGGGT TAAAATGNNG ATGNTTGTG	300
NGAGGCAAGC TTACCAAAT G	321

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

GGCANAGNCA GGATTTGATT CCACGCCATC TGGTGCTGGA GGCTATGCTC ATAACCAC	60
CTGCATTCTG ACCTCTGTAA CATGCTCATG TCATTACCC GCTCAAAAGC CACACGTGG	120
TCCCCACTGC TGCAGGGACG GCATACTACT GTNTCTTATT CATCTTGTA TCTTCAAGCC	180
TAATGCATCA CTGAACTGAA ATAGCAAATC GGCGGAAC	240
AAGNAATGTN TCTGTGCAAG GGATGTTCCG TGCGTGGCCA ACGTTGCTG GGTGGACANA	300
AAAGATTGAA CCCACCANTG GGAAGCCAGC TGGGCTTCAGG TGNTTGATNC	360
CGGAAAGCAT CCAGGCCAAT TAAGCGNCCG GTTATGGCCC TGTTATTGGG TTGNACAGG	420
GTTCACATTG CTGGAAGTTT GCTGAGCTGA AGGGAAAGGT TGATCGNCGT TTTGGTAAA	480
GGTGGN	486

(2) INFORMATION FOR SEQ ID NO:1167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

GGCAGAAAGG NGAATGGCTT AAGGCCGGNA GTTTNAAACC AGCCTGGGNA ACATGGTGAG	60
ACCTGTCTC TACAGAAAGA CGGAAGAATT GGCTGAAAGT GGTGGCACAT GTCTGTGGTT	120
CCAGCTACTG GGGAGGCTGA GAACCGGAGG ATACACTTGG GACCTAGNAA GTTCAAGGCT	180
GACAGTGAAG CTAATGAATA CCTTACCACT GGCACTNCCA GCCTGGGAAG ACAGAAGNCA	240
AGCCCCTTT TNCTCTTACA AAATTAAAAT TAAAAATCCC CCACAGTNCT TTGANGGGAC	300
TAATGACTNA TGCTTTAATT AAATTAGGGT GGTTTTAGG TNAAATTTTT AATTTTNGGT	360
TTGGGA	366

(2) INFORMATION FOR SEQ ID NO:1168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

TTCANAGTCA AGNAATGTGT CTGTTNAAGG AATGTTGTC GTGGCAACGT TNGCTGGTGA	60
CAGAAANAAT GAACCCACCA ATGGAAAGCA GCTGGCTTC CA TGCTCAGGT GNATTATCCT	120
GAACCATCCA GGCAAANAA GCGCCGGNTA ATGNCCCTGT ATTGGATTGC CACACGGCTT	180
CACATTGCAT GCAAGTTGC TGAGCTGAAG GAAAAGNTNG ATCG	224

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

GGCAGAGGNC ACATNATGAT TNATTCTTCC TTTTTTAAG ACAAAAGTTT CCCCTTTAA	60
CCCAGGAGGC AGAGGTTNCA GTGAAGTCGA GATTGCCCA CTGNCACTCC AGCCTGGTG	120
ACAGGGCGAG TCCCACGTTT NAAAAAGAAA AAAAAATAAA CAGCAGAAC AACAGCCAAC	180
ACCGACATCT CTATTGGTTC AGCTTACACA ATTTGAECT GAAAATTAA AAGTTGNGCA	240
AACTTCCAC TTGATGGCTG CCAAAACCAG TTCAGCTGCA GNCAAGACCN GGGTTTCAAT	300
GGGAATTGT TAAACAAGTG GGGTTCTTT AGGGTTGCTT GCAAATTAA TTTNTTGGTT	360
TTTGCCTT GAAAGGGATT NNCCAAAAAC CGGCAATGGG CTTTGGNTC CCAACCCNTT	420
GGGT	424

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

GGCAGAGCTT GACTTAGAT AACCGGTTGA CTATGTCCTT AGGTNATGAT CTTTTNCAA	60
TGAAATTNT CAGGTGCTT TTNAGCTTCT NGTATTGGA TGCCTAGGTC TCTAGCAAGG	120
CTGGGAAAGT TTTCCCTCAAT TATTCCCTCG AAGATTTT CAAGCATTN TCCTGCCTCA	180
NCCTCCTGAG TAGCTGGAA TTACAGGCAC ACGCCACAAT GNCCCGGCTN AATTTNNGT	240
ATTTTAAGT AGGAGACGGG GTTTCGCCAT GCNAGGCTGG TCTCGGAACCT TCCTGGACCT	300
CCATGATCCT GCCTGNNTT NAGGCCTNCC CAAANGNTT GGGATTACA GGGNTTNAGG	360

CCACCAAGGN CCGGGCCAAN TGTGGTCCCN TTTNAAGGGG GAAGGTTACC CTATGTGGAA	420
CTGTTGNTNG GGTAACAATT TCTTGGTTAT GGCAGGCCGG GGAAAACCTG CAGGGTTNTA	480
GGGGAAAGTT NTNGGGAT	498

(2) INFORMATION FOR SEQ ID NO:1171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

NTGTNCGCCT GNGGGTCATC TTCTTCTTTC ATGTGTCAAC TGCTCNTCTG AGCAAAAAGT	60
GCTTGGTGTA TCTTGGTCTG GGGANTTATT TGGAAGACAT TATTGTGGA ACATAATGGC	120
ATANCATTAA CATACGTTCA CCTACTGACT TTGAGTATGA ATGTGTAGGT TGTGTATATG	180
TGTGAATATA TATACACCAC GGTGTCATTC TANGTGTGG AATAACTGT TCANACAGTA	240
GTTACCTNTT CCCTNGGAAT TACNATCTG	269

(2) INFORMATION FOR SEQ ID NO:1172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

AATTGGGCA NNANCNATTA CACTTGATA TTGCACATGA NATGACACGG GGTCTTTGT	60
GGACCCTAGC AATGACCAAG GGCCCTGCAC GCACCCAAGC ATGTNCCCTC CCGAGTAGCT	120
GGGATTACAG GCATGCGCCC ACCATGCCA GCTAATTNN TTTTGTGGT TTTTTGTTG	180
GTAAAAAAGT GTTTGTNTGT CTCAAAAAAA AGTTTTGGA ATNACCTTT TCACCCAAA	240
TGGGACACAA GTNAAGGAGA ATGCATTCCCT CTGTNGTTT TGTTGTTGG TTTTTTTTT	300
TTTTTGCCCC NCCCAAGNTN CCC	323

(2) INFORMATION FOR SEQ ID NO:1173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

GGCACGAGGT TGGAACTCAG GTAACAGGTA AGCTTCAGG ACTGAANTAA CAGAAAATCC	60
AACTCAAATT GGCATGAAAA CGATAACAAA AAGGCAGGGA GGGCTCTCAG GTTGATTAA	120
TGGTTCGAAG ATCAATGAAA GATCCAGGCT TTCACTGTCT CTCTGTTCTG CCATCCTGGG	180
TATTTGGCTT CTCCAAAGGC TGGCTNTNTC CTCTTGGTCA AGATGNCTGC CCAGAGGAAA	240
CCTNAGCAAT GGTTTTGGT TTGTNACCTA GTGGGG	276

(2) INFORMATION FOR SEQ ID NO:1174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

GGCACAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA NAaaaaaaaa AAAAANAAAA AAAAANNNN AAAAAA	106

(2) INFORMATION FOR SEQ ID NO:1175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

CCTCTCCTCC AGCNATGCC CTCACACACA CAGGCACGTG GACAGACACC GAGTGCAGCC	60
CTCNTACCTG GGGCCTGCNT CTGCAAGCAC AGTCCCCCTCC TGTATGGACC CTGGCCTACC	120
NACCAAACAC TACATGGNAG CCACTGTCCT TTTCGAGCAC CCAAACGAGG ATCTGCCTGT	180
TCCCGAGCTT CCACGTGTT CCCAGGNCCA TTNATGGGG CCCCCGGGGC CGCTGGGGGT	240
TAGGGACCGA GGCAATGCAT ACCACAGAAG CCCGTGCCGG GGCTTTCCN TGGGGCCACA	300
TCCGTGNTTN NAATNGCTTC CTGGTTAATT CACACAGNTT CAGGGATGCG GNCCNTGGGG	360
GGGAAGGNA ACAGNCCAAC CTTNGCCATT GGGTTTTANT NCAAGACGGG GGTTAGCGCN	420
TAAAAGCCTT CCAGTGCCTT TGCTTNCCCC TTNCTTCNTA AGCTTAGGCA GGCTTTTTT	480
TCCGGTNAG	489

(2) INFORMATION FOR SEQ ID NO:1176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GGCACAGAAG AAGCCTCTGC NACCCTCCAG GACCTGGTCT TTAATGAGTG TGGGATCACG	60
GATGATCAGC TCCTTGCCTCT CCTGCCTTCC CTGAAGCCAC TGCTCCCAGC TNAACAACCT	120
TAAGCTTCTA CGGGAAATTC CATCTCCATA TCTGCCTTGC NAAGATGCTC CTGCAGCACC	180
TCATCGGGTT GAGGCAATCT GAACCCACGT GCCTGTGATC CTGTCCCCCT GGNAGNGTTA	240
TGAGGGAANT CCATGGGTAC CCTCCANCTG GGAANGGGTT GCCTGATCTG CATG	294

(2) INFORMATION FOR SEQ ID NO:1177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

GGCAGAGCTC AAGCNNTCCA CCCGTCTCAN CCTTTCAAAC TGCTGGGATT ATAGGTGTGA	60
GCCACTGCAC CCTCAACAAG TGTTTTAAG GACTTCTTAT ATGCTTTAA GGGAGAAATT	120
ATATTCAACC AAACAGACAT GGATGTNTGG CGCTTCTGC AAAACAGGGA GGTAGGTGAT	180
GATTATGTAG TTGCAAATGA AATATAATTG GCAGCTGTGN ATTAACACTT TTGNAGGGAA	240
AGATTCTTGG TGCTCTAGTA GCTTCTAAAT AAGGAGATT GATGTAATTG GGGAGTNCA	300
GAGGAAGCAA GACCTGAGAT CTGATGCGGA GAGGAAAGGA TGCTCTGCGC CAGAGGGAAT	360
TGCNTTATGC AAAGGGACCN NGGGTAAGAG GGAAGGNTGG NAAATTATG	409

(2) INFORMATION FOR SEQ ID NO:1178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

GGCAGAGTNA ATTTAGCACT AATTATCCAT GATGATATCA TATTTCANCA GAGCCCCATG	60
ANCATAAAAA AGGTTAGCAC TGTCTCAAAT TTTAGCTCGG CAGGGAAAGA TTAAAAGCCT	120
TTTAACAAGT AAAACAATNA ATTGAAAGT CAGAGGTGAC TGANTAACAG AGCAAGCAAT	180
GGTAAACTGC AGGTTNAAAT TTGAGTAATG GAATAGGTCC TTCTTAAAGG GGGAAAATC	240
CATCTGGAA TAGGATTACC TCTTAAAATT ATNATTNAT TTTNTGGGG TTTATTAATN	300
TTTGCCTGGG GATTAAAGTA TTATGGTTTT AAAAAACCGG GGCTTTGGA ACCCCTGTG	360
GTTAATTNGG GTCTTTTNT TACCGGCCCT TGGNAAAACC CAAANCCAA CCTTGGGCAA	420
TTTTAAATTG GGGTTCCAN CCCTTCCGG GAAGGCTTT TAAANTTTGG GAAATTTCNC	480
CCCTGGAC	488

(2) INFORMATION FOR SEQ ID NO:1179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

GGCACAGGTT TTTTTTTTTT TTTTTTTAAA AAAAAAAACC CTTTTTCCC TTTTTNNAA	60
AAAAAAANCGG GTAAAN	76

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

GGCANAGAGA GGGTGCTGTA CATTGACATT NATATTCAACC ATGGTGACGG CGTGGAAAGAG	60
GCCTTCTACA CCACGGACCG GGTGATGACT GTTTCCTTAT CATAAGTATG GNGAGTACTT	120
CCCAGGGAAT GGGATCCTAC GGGAAATATCG GGGCTGGCAA AGGCAAGTTA TTATGCTGTT	180
AACTACCCGC TNCCGAGACG GGGATTAATG ACGAGTCCTA TGAAGGCCAT TTTCAAGCCG	240
GTCATGTCCA AAGTAAATGG GAGATGTTCC AGCCTAGTGC GGTGGTCTTT ACAGTGTGGC	300
TTCANACTTC CCTATTCTGG GGGATTCGGT TTAGGTTGN TTTCAATCTN AACTATTCAA	360
AGGGACCACG GCCCAATTG GTGGGNAATT TNTTCAAGAG CNTTT	405

(2) INFORMATION FOR SEQ ID NO:1181:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

ATACCACTGC ACCCTCAGTG ACAGAGTGAG ACCCTGTCTC TCGAAATAAA AATAAAAAC	60
TTGAAGTGGAA TGAAAAGATC TAATATGAAA GGTGAAAATA TAAAGCTAAT GNATGTGTAA	120
GTATGAGCAA TAGATTTGGG GACTTTAACG TGGGGAAGGA CTTCTTAAAT ATGATTACACA	180
AAGCACTTAA CCATAGGGGG AGAATGGATA GATTTGTCTA CATCAAATN GAGGATTCT	240
GTTNCNCGGA NGCTCCCCAC AGNTTAAGTT ACCAGAC	277

(2) INFORMATION FOR SEQ ID NO:1182:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

GGCACGAGGN AAGCACAGAC TTCGGATGTA CAAAACAAAG ACTTTTCATC AACTCTTTA	60
GATATGCTAG AAGAGCTAAA GGAAACCATG GACAGAGAAC AAAAAAATTA GGAAAGCAAT	120
GTCTCATCCA ATACAGAAATA TCAATAAAGA GGTTGAAAT TTGTTGGAAA AGGAACCCAA	180
TTNGAAATTT TTGGAGGTTG AAAAGNTTTT TTAACNNAAA ACNTGAAAAT TTCCCTTAGG	240
GGGGTTTTCC	250

(2) INFORMATION FOR SEQ ID NO:1183:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

GGCAGAGTCG AGTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
TTTTTTTTTT TTTTTTTTNN CNNNAAAAAA	90

(2) INFORMATION FOR SEQ ID NO:1184:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

GGCANAGCCT CAGTGAAAAT ATTTCTGCAG CTATCCAAGC TAATGGTGAA ATGGTTACAA	60
AGCAACCATT GATTAGAACT ATGCGAACTG TAAAAAGGGA AACTTTAAAG TTAATATCTG	120
GTTGGGTGAG CCGATCCAAT GATCCACAGA TGGTCGCTGA AAATTTGTT CCCCTCTGT	180
TGGATGCAGT TCTCATGGT TTATCAGAGA AATGTNCCAG CTNGCTAGTG GAACCCAGAA	240
GTGCTTAGTA CTATGGCCCT AAATTNGTCA ACAAGTTAG GGGGGGNCAT ATTNCC	297

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

AACCCTACAA ATGTAAGAA TGTGGAAAAG CTTTCACCG ATACTCAATC CTTAGTACAC	60
ATAAGAAAAT TCATACTGGG GAGAAACCCC ACAATGTGG AGGAATGCGG AAAAGCCTTT	120
AACTGGTCCT CAACTCTTAT TACACATAAG ATAATTACA GTGGAGGAAA AACCTACAA	180
ATATGAAGGA TGTGGCAAAG CTTTGAAACC AGTCCTCACCA CCTTATGNGN ACATANGAAA	240
ATTCTAGTA AGAGNAACCT TTACAAATGT GNAAC	275

(2) INFORMATION FOR SEQ ID NO:1186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

GGCAGAGTCT CAATGTTGGA CCTAAGATAT TGAAGACAGG CTGGAGTCCA GAGCCTTCAT	60
TCAATCTCAG ATTATGAAA ATAATTACTG GATTGGATTA TCATATGATG AAAGGGAAAG	120

TAAGTGGAAA TGGGATTGAT AATGGCACAT CTCCTGGGAT TAATTCTACA ATAATGC GTT	180
TTTCTTCTGG GAGAGGAGAA TGTGCCATT TTGACCTCAA CAAGAATGGC AACTATTGAT	240
TGCATTCAAA CGTACAATTG TATCTGTGGG GAAGAGGAAT AGGACTCTAT TTTCCCTCTGG	300
ATTNCGGTGT GCGCCCAAGA AGGAAAAGGG TGAAAATGG GNATGTTTT CCCTTTTTT	360
TGTTTCCCC CNTAATAAAAT TTNCCGGATT TATTAAAATC CATTGGCTT TTAAACCGTG	420
GGGGGCCTTA GGTTNAATTC CTTTCAAAAA GGTTAAAGG TTGGAACCCG GGGNAGGGNA	480
AAAAGGGAAA ATTTATTTT TTGGG	505

(2) INFORMATION FOR SEQ ID NO:1187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

GGCAGAGGGA ACAATATCCT CCATGAAAAA CTGCCCACT GTGTGAAGAG GAATTAAATG	60
CATATTCAATC TTCCCTCCCTT TAATACGCNG CAAACCAACA TGTTTCTTTA CAGCTTCTCC	120
TGGGGAAAGA GAAGTAACCA CTGAGCTTCC AGGTTGTGAA GATATAAAAC AGCTGTTGTT	180
CATTTTGTT GGGAGCTATT TTACACTCAT GTTCATGGCC CCAGATAACA AGATCAATGA	240
AGTCATCCAA AAATTGTTCT GGGAAATGAAG TTAGTACTTC CATGTTTACT CCTGTTCTG	300
ATGGAATCAC AATTAAGTTA AACCANGAGT TCNTCATCTT CCNTGGTCT TCAACATGTN	360
AACTTTTTA TTGACAAACN TTG	384

(2) INFORMATION FOR SEQ ID NO:1188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

GGCAGAGAAG GAGAAGTCTT TACCTGGGGT CATAATGCTT ATAGCCAGCT GGGCAATGGG	60
ACAACTNATC ATGGTTAGT GCCCTGTCAT ATCTCTACTA ATCTGTCAA CAAACAAGTC	120
ATTGAAGTTG CCTGTGGTC TTACCATTCT TTGGTGCTAA CATCTGATGG AGAGGTATTT	180
GNNTGGGTT ATAATAACTC TGGGCAGGTA GGATCTGGAT CAACAGTTAA ATCAGCCAAT	240

CCCTTGGAAAG GTCCACTGGC TGCCTACAAA ATAAAGTAAG TTGTGAACCA TTGGCATGTG	300
GGCAGATGTG CTGCATGGC ATTAGTAGAC ACGGGGGGAG GTCTATGTTN TGGGGTTTAC	360
AACGGAAACG GGCAGCTTGG ACTCGGGCAA CATGGCAACC AGCCAACNCT TGCAGATTGG	420
CAGTTTGCAA GGGCTTCNTG TNCCANGGT ACGTCCATT CCAATTTGT GCGTGTATTT	480
TTAAGCTTNG T	491

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

GGCANAGGTT CCATATAGAT ATTGCAGATA GAAGTCAAGT TGAACCAGCA GACTACAAAG	60
CTGATGAAGA CCCAGCATTA TTCCAGTCAG TCAAGACCAA GAGAGGCCCT TTGGGAACCC	120
AACTNNNAAG GTACTGNATG CTGACCTTTC TGAACAGGCA GAGTCTTGGG CAACAGAAC	180
CTTGACAGGT CCTGAGTCTT GAAAGAGCTG GTGACGTTA AAGTGAAAAA ATAGAAATGG	240
GCACAAAAAT AGTTTTATTT GCGATTAAGG ACTTACAGCC AGTTGCAGTT GGCCAGCAAN	300
TCTGTGCTGC ATTAACAAAC AGAACAGNGC CAGACTGTTA ATTTTCAGNA TAATGCAGTT	360
CCATTAANCT TTAAAGGGAC AAGTGGTTA GTCNTGGGG TTNNNATGTT CTCTTTGAG	420
ACCTGAAGCG TATAAAATNC CTTTAATGA GGTTTAGTT TAAATTNGTC TTATTAAAAC	480
TGANCAGTTC	490

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

TGGATAACAA ATCCCTACCT ATAGCCATGT GGAAGCAGCT TGTCACTGTA TTTTAACGT	60
GTAACAATTA TTGAAGCGA AAATAGNAGT TGGGTCACTCT TTGAACACCT ACCTTTATC	120
AATGAATATT TTTAGACTGT NCTTCAGTAT CTGAGTCAGA GTTTATTGTA ATTTGTTATT	180
TACACCAAGG TGGCATCTTA GTCTACCTTC AGTGAGACTT GCGTTTCAGG GGAGGGCGT	240

ATGTNCATCC TCGGTCTCCG TTATGTAAAC GGTCTGATCT GTNAAAATAG TGGTAGCACA	300
TGCCACGTGG GATAGTTGGT GGAGATGATA GATGGAGTTT AAGCACAGGG CCCAGCCTGT	360
TCAGCAGTAG CTACTATTAN TGTTGCCAT TTCCCCTGCA ACTGAGGTGA GAGGTTTNC	420
NCGAGTTTA AAGCTGACTG GGCCCACAGT TAAACGGTAA CAGACCAGTT TTTTCAGGGT	480
GTCAGCCC	488

(2) INFORMATION FOR SEQ ID NO:1191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

GGCACGAGGA ACTGCTTGAG AGCTTTCTT AATTGGAAA AGAACGCCCG GGTAGATGTT	60
GGCTTCATGG TTTCTAAGCT GCTTTGACC ATACAGTTAT GTCCAAAAAC AGAATTCAA	120
CCTAGTGAAA AATTGGTGA AGACCTAAGT GATAACACTT GGGAAATACAT ATTNCCATT	180
GATCTGCTCT GCTGCCATCA GAAATGGATC TGGACGCATG ATAACATCAT AAGTAAGGAG	240
CTGTGGCCTG TGATGGATAA ATGGATAAAA TACAGAAAAG GACATGAAA CATTGCGTAT	300
ACTCCTGATA TTATTATAGC CTCCAATTAC TGAGGCTGAT TGGTCGTTA GGCAATTGG	360
GTGGAAAGA AGGGTTTCC ATCTGCTGTG AAAAAATATT AAGTCGGTT ATTGGTATGT	420
TTATTACAGC ATGCTCACGG TGAAGGTTAT TACCCNTGGG GGTATACCAAG TTTAGCAGCC	480
CGTGTATGCT CCTTTGTGAC	500

(2) INFORMATION FOR SEQ ID NO:1192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

GGCACGAGGT TTTCAGAGAC ATAGAGGATA GCAAACAAGC TCAATTGTTA GCCTTGGCAG	60
TAGTATACTT TATCTCTGTT CTTATGGTCT GCAAGTACAG AGACATTTG GTAACCCCAA	120
AATGAAAGGC ATAGCCAGTC ATGTACAGAA ACTGGCAGTG GAAAATGAAG AATGTATCAC	180
TCTCTGAAAT CACACCAGCA GCATTCAGCA CTTTGAACCA CGGCATCAGT GGGAAAGGAAT	240

CTGNAAGGCA CATCATCTGC TTGGAAGGAG GGACTCAGGC ATTGGGGAA GAAACAGCCA	300
CTGGTTAGG AAGCCATGTG GGAAGTAAC CNTCACACAG NACCTTCCTG GTGTCAGTN	360
GCAGGNCCCA GTTGCATTCA GCGAGGTGCT ATTTTANTCT TTC	403

(2) INFORMATION FOR SEQ ID NO:1193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

GGCACGAGNA AGAACGTTGC CTTATGCATG CTAATGTTAC ACTGCCAAG CCATCACATG	60
ACCCAGCTGG GTGCTAGAGG TACAAGCACT TGGNTATTAG GGGTGCGATT TGGGTACCAT	120
CCAGTATAAC AGAGTGGTT ACCACCTTAT ACACATTGTA TATGATTCT TGCAGTCAGT	180
TTTGTGGAAG GGAGTGCATT TTATTCCATT TTGTTTGTC TACAGTGGAA TTTTGTGTT	240
ATAACTATCT TCCTCCTTT AAAAGTTGGC AACCTATAATA TTACTTCA TATTGGAGA	300
TAATGTTAG ATTTTACCCAA AAAAGTTGGC AAAAATAGTN NGGANTTNCC CTTATGGCCT	360
TNCACCCGGG TTTCTACTAA TGTTAAAC	389

(2) INFORMATION FOR SEQ ID NO:1194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

GGCAGAGGNA ATTCATTGG GNACAGCAAC CATGGCAGCC AATCTCCCAG GAATGTGGAG	60
GAGAGGATGN TTGCAGTCAT TTAAAGGTGG AAAGGCTTT GTGN	106

(2) INFORMATION FOR SEQ ID NO:1195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

GGCAGAGCCC AAGCACAGTG ACTCACGCCCT GTNAATGCCA ACACTTGGG AAGGCTGAGG	60
TGGGAAGATT GCTTGANTCC AGGATTTAA GGCCACCGT GGCAACATTA AGACCCCATC	120
TCTACCAAAA AAAAAAAA AAAAAAANG GNCCCCN	158

(2) INFORMATION FOR SEQ ID NO:1196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GGCACGAGCG TTANCGNCGC NTNCGGTGAG TCAGTCGCC CAGTGCACCA ACTGCGTGCA	60
GGACGACACG GCCAAGGCCA AGATCACCAT CGTGGCAGGC GTGCTGTTCC TTCTCGCCGC	120
CCTGCAGCCT TGCNTCGGAG GCCAGCCCAC CCCCAGAAC CAGGTAAGCC CCCGCGCTGG	180
NACTGGGCAG GCTTCCCCAG CAGCCACGGC TTTGCAGGCC GGGCANTCGA CTTTGGGCC	240
CANGGGCAA ACTGCATGGA CTGTGAAACT TAACCTTTT GGAGCAAGGG GGCTTGGTT	300
ACCGNCNATA ATTNACCAA CCCGTTGGAG NCCCATTGGG GCCGTTGNCC CCAATGTTG	360
GGTTTGGGNA AGGGACCGGN AATCCTTGGGA AGGGGCATTT GATATTTTT CAATAAAAG	420
CTTTGGTTT TTGNATTGGN AAAAAAAA AAAN	454

(2) INFORMATION FOR SEQ ID NO:1197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

ATGAGCCCCC NCGCCCGGCT ACCTGAACCT CTTTGACAA GTNCTGATAT GAAGGCCCCA	60
TATCAGCTGG GGCCACGGCA GCAGCCCATG CAGGNGGGC AGNCTGGNG TGGCTGGCCA	120
GGGNAGGGCC TGGGTGGGN CTTCAAAGCT GGTGGGNATG CGGGTGGGTG TGGGGCCACA	180
AGAAGGAAGA GGGGTATCCA GGGTGCCTCC AGTTCCCTACG TGNAGGAATG GTGTCTCCCA	240
AGAGCCATGG TGGCCTCCGT GGGGACAGTG AGANTAGAGG CTTGTNAGGN GGCCCTTTCA	300
CTTGGCNTNG AAACTCACTG GGT	323

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

GGCACGAGGT TTTCTCATAT ACATGATGGT GTATGTAATG GTTAAGGTAT ACAAGGTGGT	60
TTGCCCATGA AAGTCTATT AATCTCTAAC AGACATGAAG AGTGTATTAA ATAGAACCTT	120
TCCCCAAAAT GTTGTAGGGG AAAATGTCCC AGTTCCATGT GGAATTGTCA GAACAAGCCT	180
CAGCCTCTTC GAGGATTCA AAGTGGCTTT CGTCTTTAA GTTGATGTCC TATCTCTCTC	240
TCTGTGCTCC TTTTTTTTN AACTTTGTGT GCTTGGAAACA NGGACCCCTT GCCACTTTNA	300
AAGCTGAGTN ATTNAT	316

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

GGCACGAGCT CGGCCTNTNT TNCAAGTTTC TCCAAGGGGC TGGCGGCCGC CAAGACTTGC	60
GGGGTNTAGG GGTGCTGCGG GCGGTCGAAG ATCTCGTCGN GGGCACCCAT TTCCACCACC	120
CTGCCCTCGC TCATCACCGC CACCCGGTGG GCGGATGCGT TCCACCGCCG CCAGTCGTGG	180
GGAGATGAAC AGGCAGGCAA AGCCTNACTG CGCCTGCAGN TTCGGATACA GCTTCAAGAA	240
ATCTGGCTTC TGGGATGGTC ATGTCCAACG CCGAGATCGG CTTCATCGGC AATCACCAGT	300
TCGCGGGTGT CCGCACCAAGN GCCCGGCCAA TGGNCACGCN TTNGACGCTG GTCACCGGAC	360
AANTGGTGCN GGGAAAGGGT TCGACAAATT TTTCCGCCAG CCGATTGTTC CANCAGGGTT	420
TTTGGCCAAC CGTTCAAGAC GTTTNGGGGN TTTCATGCCC GGGGAAATTG GCGNAGGNNTT	480
TCGGGGAGA TT	492

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

GGCACGAGCT TGTATTTGTC TACTGACAGC CCCTTGGTAC TATTTAGGTT GGGGGAGGGG	60
ACCTAAAATA AATAGACTTT AACATTTCCC TTGGGTGCTA ATCATAGTTG GAAGTTGAAT	120
TTAAGGTGAT TATTTGGGTG ACAATTAAAA ACCTAAGGAA ACCAGAAAT CTTGGTAGTG	180
GAAGAAATGT GTAAGGTAC CCCAATCGGT AGATTTAAT GAACGTTGTG GAATGTTGGG	240
AGAGGGGATG TTAAGTTGAA TGCAGAATT CACTAAGTAC TTAGTGTAAAG TTTAAGGAT	300
GTTNGCTNNT TTNATCNAA GGAATTCCAT GTAATGCCC CAAAGGGCAG TTTTACNGG	360
TTTTAAAAAA TTNGGAATTA ATTTTACCA TGACCATTCT TGGAAATTCC CAGGNAGTTT	420
TTNTGTGTAG GGACCCTTT TNAAAATTN CCTCCGNTT TTTAAGGGG GAAATTAA	478

(2) INFORMATION FOR SEQ ID NO:1201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

CCAAGACAGA CTGCAGGTTA CGGCCTGACA TCAGAGCCAT GGAAAATGGA GAGATAGATC	60
AAGCTAGTGA AAGAAAAAAA ACGACTTGAG GAAAAACAAA GAGCAGCCG CAAAAACAGG	120
TCCAAGTCAG AAGAGGACTG GNAGGACGAG GTGGTCCAT CAAGGTCTTA ATCCCTACAA	180
TGGAGCACAG GACTGGATTT ACTCTGGCA GCTACTGGGA CAGAAATTAC TTCCAATTG	240
CCTGACATTT ATTTAAAATG CATACAAGTC AGGGTGTTC GCTAATCTAC AATAAGTCTT	300
TAAANCCAT GTTTTTAAAA TTTTTTTTC CCTGGGTTTC TNACTTANCT TTTTAAAAAA	360
AAATGGGNAA AACCCCTCCTG GGGTTAACNG G	391

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GGCACGAGGA AATTCATTG GGAACAGCAA CCATGGCAGC CAATCTCCA GGAATGTGGA	60
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GGAGAGAATG AATGGCAGTC ATTTAAAGA TGAAAAGGCT TTGGTGACCA GTCAAAATTC	120
AGACTTACTG GATGATGAAG AAGTTGAAGA TGAGGTGTTG TTAGATGAGG AGGATGAAGA	180
CAATGATATT ACTGGAAAAA CAGGAAAGGA ACCAGTGACA AGTAATTAC ATGAAGGAAA	240
CCCTGAGGGA TGACTTATGA AGGAAACCAG TGCCCTGGAG ATGAGTTGC AAGACATTCC	300
CCAGTTGAGG TTTTAAAGGA GGGNAGGATT TTAAAGTNG GACTTTCTT GCTCTTAGGT	360
TCCATNTTAA GGGCANTTTC ACCAGTTGG CCNTCCAAAT TGAGGGGAAT TTGGGAGGTT	420
TATTCCATTN TTCTTNAAG G	441

(2) INFORMATION FOR SEQ ID NO:1203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GGCACGAGGT GGAATAGAGA AACTTAATGA GTGTTAAC CAAGCTTTC AAGAGACCGT	60
TTCCCAGGCA CATACATGCG GGGCGTCTCA ACATCCTGTC ACCATTGTNC TTGAACTCAC	120
TTCTTCAACA CCACTCATGT GGACTCTATG GAAATAGGTG ACATAAGCCA GACTTCCCT	180
CATAATGCCT GTCCACAGTT TTTGCTAAT ACATAATAAC TGATTAAGAA AGACAATGTT	240
TCCAGTAAGG ACAGTGGTGA CATATTAAG TAGATGAGTA ATGAACCTTG GCTTGTAAAGT	300
GTCCTTCTG CAGAATAGGG AGGGAAGAGT TAAAGCTGGT ATCCCCTCGG GCTCTTAGGC	360
ACCTGTTAAA CCCCAGGCC AGGGGATCCT TCCGTCCTGT CCCTGTGAGT GCTTCAGCCC	420
AGGGACACAC AGAAGGGCA TGTTCATGG GTCCGAAGGA CCCGTTAGT TTCATGTGGA	480
TTTCCAGACC TGATTGCA	498

(2) INFORMATION FOR SEQ ID NO:1204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

AGAATATTGG TAATATATTG CAGAAAGTTG TGTGCAGAAA ATTGACAATN ATTTGGCCTT	60
TAGAAAAAAC TTTTACTCTT TCAAAAGTTA CTATTTAAA GCATGGTATT ATTTGCATT	120

ACAAAATGGT TTTATTTCT TAGTGGTGAG ATAGAGGAGA AATTGTACC TGCTCTCTG	180
AATCTGAAAA GTTGTTCAGC ACTTTACAT TACTCCCTG TTTCTTCTA TTGGTTGAGT	240
GTAANTGAAA AGTTTCCCAT TNACCATGCT GGCTTGNAATTGAGACCN NATGTTGAAA	300
ATTT	304

(2) INFORMATION FOR SEQ ID NO:1205:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

GGNANAGGCG CGGCAAAGGG CCTCGTNAGT NGTGTTCAGN TTGCCCTGG GGATCTNCTG	60
TGTCTTCAGC GCCCAGCCCT GCGTGTTCCT GGTGAAGCAG TTTCACATCA GTCTCTCCAG	120
ATAGCACTAC GAATGTATTC CGCTTCTGAA ACAGGATCCC ATGCCAGTTT GGAACACTTT	180
CCCAATCTTA GTTCAGAAGT GGCTTGTATG ACCTGTTCAAG GGGTCACATG AAGGTCTCGC	240
CATTTCTGG GTCCTCTTCA GAGGCCNGAA AGTTCTAAAG TTCTGAGTCC CCGGCCAGGG	300
TCCTTTAANA CCTTGGNCAC AGAGGCTGTT TGGGCAATGT AGAGGCTGNC TCTGTGTGTG	360
GTAAAGTAA ACTGGAATGN GGACATGACG NGTTG	395

(2) INFORMATION FOR SEQ ID NO:1206:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

GGCACGAGNG AAAAGTCGGT GCGCTGGTCC TGCCTCATTA ATCCAGGGGT TGCAGTGCTT	60
TGAAGCCAG TCGTTGTTGG TTTTTNTGAT GNAAATACCT GTNAAGATGA GTGGNCAGGG	120
N	121

(2) INFORMATION FOR SEQ ID NO:1207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

GGCACGAGGT TGTGTGGTGT TTTGGACAG ACGTTATTT CTTTTTGTA GAGTAGCCTG	60
TTTGTAAAGTT TAAAGTGTTC ATTGTTCTCC TTTGCAGCAT CATGCCAGC CCAAGAACCA	120
GGAAGGTTCT TAAAGAAGTC AGGGTGCAGG ATGAGAACAA CGTTGTTT GAGTGTGGCG	180
CGTTCAATCC TCAGTGGTC AGTGTGACCT ACGGCATCTG GNATCTGCCT GGAGTGCTCG	240
GGGNGNACAC CGCGGGTTG GGGTCACCT NCAGGTNCAG TGTCCTGCCG CTCTGGGTTTC	300
T	301

(2) INFORMATION FOR SEQ ID NO:1208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

TGGCAAGCTG GGGCCCGGCC TGCAGGTGCT GGACGCGTCC TGGTACTCAC CAGGCACCCA	60
AAAGGCTCGN AAGAGTACCT CGAGCGCNAC GTACCCGGCG CCTCTTCTT TAANATAGAA	120
GAGTGCCGGG ACACGGCGTC GCCCTACGAG AATGATGCTG CCCAGCAAGG CTGGNCTTCG	180
CCGAGTATGT GGGCCGCCTG GGNATNCAGC AACACACGC ACGNGTGGTG TATGAATGGT	240
GAAACACCTG GGNCAGCTTC TATGCTCCCC GGGTTGGTG GATGTTNCCG TGTGTTNGC	300
CACCGCACCG TTTTCAGTGC TTCAATGGTG GNTTCCGGA ACTGGTTGAA GGAGGGCCAC	360
CCGTGAACNT CCNAGCCTTC AGNNCCAGAA CCGGCCTTT TCAAAGCCAC ATGGGACCGT	420
NNCTGNTTCA AAACNTAGAG TCAGTGTGG AGNAACTTGA ATTTAAGAGG TTTCACTGG	480
TG	482

(2) INFORMATION FOR SEQ ID NO:1209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

GGCAGAGCGG GGGTCTNGGG AGCGCAAGTC CNTGGCAAGC CGTCTTCTGC TCAACAACGG	60
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AGNCAAGTTG CCCATCCTNG GGTTGGGAGC TGGTNGTCCC CTCCAGGNCA GGTGNNNCTGA	120
GGACGTGAAA GATGCCATT GNACGTCGGG TACCCCCACA TCGACTGTGC CCCATGTNTA	180
CCAGNTTGAG CNTGAGGTGG GGGTGGCCAT TTCAGGTGCA GCTCAGGGNG NAGGTGGTTG	240
AAGNGTGAGG TNGCTTCTTC ATCGTCCAGC AAGNTGTGGT TGCACGTTAC CNTGGAGAAA	300
GGGCCTGGGT TGAAAAGGAG CCTTGCCCAA GAGNACCANT TCANGGGACC CTG	353

(2) INFORMATION FOR SEQ ID NO:1210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GGCANAGGTT NTCCCTTCGC GNCCCAAACC ACATCCTGGA GCGCACTCTC CAGCGTGGCT	60
GGNAGCGNGG ACT	73

(2) INFORMATION FOR SEQ ID NO:1211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

TCCAGCCTNA CTTCCCTGGGC ATAGAGTCCT ATGGNATGCA CGAAACTACC TTCAACTCCA	60
TCATNAAGTG TGNACGTGGT ACATCCGTAA ANGACCTATA CGCCGTCACA GTGCTGTCTG	120
GNGGCACAC CATGTACCN	140

(2) INFORMATION FOR SEQ ID NO:1212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

AAAAGAAAGT TTCCCCAGAC AAGATGNTTN AANTGCAAGC ANAANTTGAT GAGGAGAGAA	60
AAGCACTTGA AACAAAGCTC GACATGGAAG AAGAAGAAAG AAACAAGGCT AGAGCTGATT	120

TAGAGAAACG GGAAAAGAT CTTCTTAAAG CCCAACANGA GCATCANTCT TTGCTGGAAA	180
AATTATCTGC CCTGGAAAAG AAGGTAATT TTGGTGGGGT TGACTTGTG GCCAAAGCTG	240
AGGAACANGA GNANCTCTT GAAGAACATCA NCATGGAAC GGTGGNAAGG AGGAAAAGNG	300
CAGNGCAACT TNGCAGAGAT CTTGAGGAAA AGAGCAAGNN CGCTTGGATA TTGANGNAAA	360
TATACCCGTT TGCAAGTGGT AGCNCCGGGN AAGTCCCAGA AGTTAAGGAA GTTTGGCCCT	420
GCTGATGGTG CAAATCCNGG TNGGTTGTCT CCACCAGACC TTCGGGGNAT T	471

(2) INFORMATION FOR SEQ ID NO:1213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTNGGGGG GGNTTTTTT TTTTTNNC	58
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(2) INFORMATION FOR SEQ ID NO:1214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

GGCAGAGCGG CACGAGNCCT TGCACCTGGN CTTCGCGTCT CAAAGGTGGG ATGCAGATCT	60
TCGTGAAAGA CCCTGACTGG TAAGACCATC ACTCTCGAGG TGGAGCCAGT GTNCACCATT	120
GAGAATGTCA AGGCAAAGTA TCCAAGGNCA AGGGAAAGGGC ATCCCTCCTG ATCCAGGCAG	180
AGGTTGATNC TTTGGCTGGG NAAACACTGT GTANGATGGG ACGCACGGTG TCTTGACTAA	240
CAACATCCAG TAAAGAGTTN CACNCTGGCA CCTGGTG	277

(2) INFORMATION FOR SEQ ID NO:1215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

NTGCGGGGAC TNGCTGGAGC AGCGGTAGGG GGAGCNGTA GANCCGCTGC GTCCCTTCAC	60
AGTCCGGAGC CCGGCCGTGC GCTGNCCGTA GGGAACATGA CACTTTCCA TTCCCGAAAC	120
CGANTCCCGC AGGGGGTACA GCGNNNNGTCT GCC	153

(2) INFORMATION FOR SEQ ID NO:1216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

GANNNCATCA ACAAGGAAAAA TANCACTAAG TTGAACATTG TAAACCTCCA GATCACGGAA	60
GACCCTGGCG AGTATGAATG TAATGCCACC AACGNCATTG GNTCCCCTCT TTTGTAACTG	120
TCCTNAGGGT GTGGNGGCAC CTGGGCNNNA CTNTGGCNTT NNTTGGGAAT TCTGGCTGAA	180
TTATNATNNNT TGTGGTGATC ATTGTTGTGT ATGANAAGAG GAAGAGGNCA GATGAGGTTC	240
TGAACGATGA TGAACCAGTT GGACCAATGG	270

(2) INFORMATION FOR SEQ ID NO:1217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

GGCCTTAAG GCTTNACCCA ACGTNATCAA TCACCGATT CCACGGTAGC AGACGCGCAT	60
CCTGAAACAT CATTGCTTG TTTCTGTAN TTTAAGCCAG CGGTGTGGTG CCCGCAAACA	120
CATCGCCTGN GGTTGGCGTT TCCANACCTG CCAGCAGGCG NCACAGGGGT ACTTTGCCA	180
CCACCGCTGC GGCCCACAC CGNCACAAAC TGACCTGCCG GAATATGTAA AATCCAGTTG	240
GTTCCAGGGA CGATATTTTC CGCGTNAATG TTTGCTTTAC TGCATTGAGC AACAAATGGTT	300
TGNCCCTGGT TTCAAACGGG GCAGTTATTN CATACCGTGG GCCTCCTTTC AAATGATTAA	360
GCCGGGTTTC CCAACGGNAA CCCNNNGG	387

(2) INFORMATION FOR SEQ ID NO:1218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

CCAACCTACG GTTGNTTCGT NCTTTAACCC CTACACGTTT CCCATTATGC CGTTGGNGAT	60
GAGTGGGANG ATTGTTGNT TCGGGTTAA ACTGTTGTGC CCGT	104

(2) INFORMATION FOR SEQ ID NO:1219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

AGGGAGAAAN TGGCCAGATG ATGAGCTGCA CATGTTTGG GAAACGGAAA AGGAGAATTC	60
AAGTTTGANC CCTCATGAAG GCAACGTNTT ACGATGATGG GAAAGACATA CCACGTAGGA	120
GAANCAGTGG CAGAAGGNAA TATCTCGGTG CCATTTGCTC CTGCACATGC TTTGGAAGGG	180
CAGCGGGGCT GGCGCTGTGA ACAACTGCCG CANACCTGGG GGGTGAAACC CAGTCCCGAA	240
GGCACTACTG GGCCATCCCT ACAACCAGTA TTCTTCAGAG GNTACCATCA GGGGACCAAA	300
CACTAATGTT NAATTNNCCC CATTNGAGTG CTTTCA	336

(2) INFORMATION FOR SEQ ID NO:1220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GGCACGAGAG AAAACTCATT CTGGAGAAAA ACCCTATGAG TGTAGTAAGT GTAAGAAATC	60
TTTTGTGCAC CTGTCTCCC TGATTGANCA TTGGAGAATT CACACTGGAG AAAAACCATATA	120
TCAATGTAAG GNCTGCAAAA AGACCTTTG TCGTGTGATG CAGTCACTC TGCACAGGAG	180
AATTCTACT GGTGAAAAAC CCTATGAATG CAAGGAATGT GGAAAGTCCT TCAGCGCCCA	240
TTCTTCTCTT GTTACTCATA AGAGAACACA CAGTGGGGAA AAAACCGTTT TAAATTGCAA	300
GGAATNTGGG NAAAGCCTTT CAGTGGCGGA CTTTTCCCT TGTTTACTCC NTANGGGAC	360
ACACATTGGG GNNGAACCCCT TTACNTGGCC TGCCCTNGGG GAGGGCCTTT AATATTCCT	420

CCCCATTTT 429

(2) INFORMATION FOR SEQ ID NO:1221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

GGCACGAGCC ATAGTGGTNA TCAGTGCCTC TNATGATGAC GTGGGTGAGA ATGCTCGTAT	60
CACCTATCTC CTGGAGGACA ACCTNCCCCA NTTCCGCATT NANGCAGACT CAGGNGCCAT	120
TACATTACAG GCCCCATTAG ACTATNAGGA CCAGGTNACC TACACCCTGG NTATCACAGN	180
TCGGGNCAAT GGNATNCAC AGAAGGCAGA CACTACTTAT NTGGAGGTGN TGNTCAATNA	240
CGTGANTGGC AATGCTCCAC AATTNTGGC CTNCCACTAT ACAGGGNTGG TNTCTNAGNG	300
NTGCCCCANC TTTCACCAGT GTCCTTCAGT TCTCAGCCAC TTGCCNGGCT GCTNATGCCA	360
ATGAGTCCGT GTNCAGTACA CTNTCCAGAA TGGTGTATAG ATTGGGTGTG GTAGGTNTTT	420
AA	422

(2) INFORMATION FOR SEQ ID NO:1222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

GGCAGAGTGA AGCCTCCTGA CCTCCAATAC GGTGCACTCT GGTGAGGGAC AGTGGGTGGG	60
GTGGGCCAAG GAGGGGCCAC AGGGTGGGG CAGATGCTGG AGTGTCCCTC ATATGCCTGC	120
AGACACCCGG GAACTACATC TGTGAAGTTC TGCGCCCGGT CTTTCCGCAC TAGCAGCAAC	180
CTTGTCAATCC ACAGACGTAT CCACACTGGA GAAAAACCCC TGCAGTGTGA GATATGCGGG	240
TTTTACCTGC CGCCAGAAGG TTTCCCTGGA ACTGGGCACC AGGGCAAGNT TGCAGAGACG	300
GTGGGTTGCC TTGCGNTTTC CCCTGTGAAT TTTTNCGGGN AAGGCTTTN AGGAAGNCCA	360
GACATTTTT GCAGCCCACC TTGGCAAAT TTAACCCNGC CTGTTTTAG GCCCTT	416

(2) INFORMATION FOR SEQ ID NO:1223:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

GGCACGAGGN TGGCTTTGC CTGTAGTCCC AGCTACTCGG GAGGCTGAAT GAGGTGGAAA	60
AATGGCTTTT TTTTTTTTTT NNNNGNG	86

(2) INFORMATION FOR SEQ ID NO:1224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

GGCACGAGAA ATTATGGATT CTTTCAAAGA GAAAATGGAG AATATTGACT ACAGCAACGA	60
GGAGCACATG ACCCTGCTGA AGATGATTAAATAAAATGC TGTGATATCT CTAACGAGGT	120
CCGTCCAATG GAAGTCGCAG AGCCTTGGGT GGACTGTTA TTAGAGGAAT ATTTTATGCA	180
GAGCGACCAG GNAGAAAGTCA GAAGGCCTTC CTGTGGCACC GTTCATGGGA CCGNGGACAN	240
AGTGGACCAG GCCACAGCCC AGATTGGGTT CCATCCAAGT TTGTGCCTGN TCCCAATGTT	300
TGAAACAGTG ACCAAGCTCT TTCCCCATGG TTGNNGGNNG TTCATGNTG	349

(2) INFORMATION FOR SEQ ID NO:1225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

GGCAGCCGAG GTGGCAATGC TACACCTCAT TTTTATGCG GGTTCGCCAG GGCAAGCCCG	60
GCACTCGACC GATAGTCAT GAGGATTATG TCAGCCACCA GCGCACGCNC ACCACCAGAA	120
CCACGACCAG AATCAACCAG ACCCAGTGCT TCAAATGCTG GTCGAGATTG TGCCACCACG	180
GNGCAATCAC CTGACCACCA GCGTAACCAA TAGTGGTAAA AATCAACGCC CAGGCAAATG	240
TGCCGAGNAT TTTCAGCGGC AGAANATTT CGGCGGCACT GGTTGGNCAC CATTCAAGCGT	300
TGGGCCATTC ACCCGAAAGC CTNACTNAAN GGGGTTACCA TGACAAACAG TTACGGNTGG	360

NGTTGGNTNA GTTTTGNGN CCCGTCATT TTGTGCNGNT GTTTGGGA AACGGNGTTA	420
ACATGCCTTG TTTCAGTTAG TTAGATTCTT GCCGTNATNT TTGTCAGGC GTTGNACGGT	480
CNGGCCAGGT TAT	493

(2) INFORMATION FOR SEQ ID NO:1226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GGCACGAGCC ACAATGGCTG AGCACTTCCT GACGTGCTG GTAGTGCCTG CCATCAAGAA	60
AGATTATGGT TCCCAGGAAG ACTTCACTCA AGTNTGGAAC ACACCATGAA AGGGCTCAAG	120
TGCTGTGGCT TCACCAACTA TACGGATTT AAGGACTCAC CCTACTTCAA AGAGAACAGT	180
GCCTTCCCC CATTCTGTTG CAATGACAAC GTCACCAACA CAGCCAATGA AAACCTGCAC	240
CAAGCAAAAG GCTCACCAAC CAAAAAGTAG AGGGTTGCTT CCAATCAGCT TTTGTGTGAC	300
ATCCGAACTA ATGCATTCAC CGTGGGTGGT GTGGCAGCTG GNATTGGGG CNTGNGNTGG	360
NTGCCTG	367

(2) INFORMATION FOR SEQ ID NO:1227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GGCANAGAGT TAACGGAGGC AAGTTGGATG TCGGGAATGC TGGGGGAAAN TTTTTGGAAG	60
AGAACAGGAG CCTGGAAGGC TGAACCTGCA GAAGCTAAAG NACGAGCTGG CCAGCACTAT	120
GNCAAAAAGT AGAGAAAGCT GAAAACCAGG TTCTNGGCCA TGCGGAAACA GTTCTNAGAG	180
GCCTCACCAA GGNGTTACGN ACCGATTTNC TGGAGGAGGC AC	222

(2) INFORMATION FOR SEQ ID NO:1228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GGCAGAGCTG CAGGGCCCC AGGAGCATCC CTGNTCACCC CTCTGCNCCC TCCCCACCAG	60
AGCTGAAGAT CCCTGAAAAC GCCAACGTCT TCTATGCCAT GAACTCTACT GCCAACTATG	120
AACTTTGTCC TGAAGNAAGC GGNCCCTCAC CAAGGGAGTG AAAGGTCAAG CCACGGTAGG	180
CCAGCTTCCA CCCTCCCTTC GCATGGAAGC AGAAAGGGAC TCAAGATTGC CAAGGGCATC	240
TTCCTGAGGG GCATCCTCCC AGGGTCTGGC TGGCTGGTTA GCCAAGCACT TATGGGACCA	300
GAGTGGGCC AGGCCAGTTG GGGGGCCTTT CTTCCCAACT GNNCAGCCCA GGGTACCCCA	360
GATTCANTT TCANCCCGGA ANTTTT	386

(2) INFORMATION FOR SEQ ID NO:1229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

TAACGGCGTC GAAACCTATT TTNAAGTCTA TGTTAACGGT CAGTATGTGG GTTTCAGCAA	60
GGGCAGTCGC CTGACCGCAG AGNTTGACAT CAGCGCGATG GTTAAAACCG GCGACAACCT	120
GTTGTGTGTG CGCGT	135

(2) INFORMATION FOR SEQ ID NO:1230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

GGCAGAGCGA AGTTTTTTTT TTTTTTTTNA GGNGGTTTT ATTNAAGTN CTTNTTTTT	60
TGGGGT	66

(2) INFORMATION FOR SEQ ID NO:1231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

GGCAGAGNAA CGAACATTAA ATCTGCTGAT TGGCAAGAGA CAAAGACCAA TCCATTAAAG	60
TTTGATATT GAATGCATTT NACCCTACAC TGGCTCCAGC CACAGGGAAC TCCTGTTGTG	120
GGGGGACTAA CCTATCGAGA AAGGCATGTA TATTGCTGAG GAAATACACA ATACAGGGTT	180
GCTATCAGCA CTGGGATCTT GTTGGAAAGTC CAATCCTCAG TTGGCCACCT CAGAGGAAGA	240
GGCGAAGTCT TACAGNTAAC CTGGNCAGTA GATGTGNATT GCTTCCAAGN TTTGGTCCAG	300
ACAAGNGAAG GGGGGCATA TTTGTTCTTT GGGCCAACCT NCCTACTTCC CAGTTTCACC	360
AGTTGGATTC AGAAAATTCA AGCACGTGTG NAGAANTTN GGNGACA	407

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

GGCAGAGGNA CGAACTCATG NAAAGATACT GTCCTAATTG CGTATTGGTC ATCATTGATG	60
TGAAAGCCGN NGAACCTAGG GCTGCCTACA GAAGCGTACA TTTCACTGGN AGNAAGTCCA	120
TGNATGATGG GAACTCCAAC CTCGAAAACA TTTGAACACG TGAACCAGTG AAATTGGAGC	180
AGAGGAAGCT GAGGAAAGTT GGAGTTGNAC ACTTGTACG GGATATCAA GACACGACGG	240
TGGGGCACTT NGTCCCAGCG GATCACAAAC CAGGTCCATG GTTTTNAAGG GGCNTGAAAC	300
TTCCAAGCTT CTGGGTNTTC AGGNCTACC TGGNAAAAG TCGCCACAGG CAAGNTGNCC	360
CTTCAACCAC CAGTTCCNTT TACCAGTTGC AGGACGTTTT TCAACCTGTT GCCCAATGTT	420
CAGCTGCAGG GGTCNTCAA GGCTTTACC TGANGGCCAT GGCCATTGTG GTAGTTTATT	480
GGCNCGTTAT C	491

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

CAGGCCTTG CGCCTTCATA CTGCACCGAG TTTTCCCCAT CAATGGCTT NACCACGTCT	60
TGGTAAGTTC ATACGTNAGA ACCCAAGCAT CGATCTGCGA ACTTTAACGCC AGCACAGAAAT	120
ATGCACGTTT TGAACAGGGA TGATTTAAA TCTCGATATA GTCTACGGTG NAACCCCGTC	180
CATCACCCCTA TGAGAAAGAT CCCGCTTGCT GTTGAAGAAC TTACGCCACT GTNTTCTCCC	240
CAACTGGGCT GAGCGGCTAA AGAAACCAGA GGATCTCTAT GCGTTGGACA TTGGATTTCAG	300
TGCGGTGTTG CAGTTGTTA CCCNTNGGAA AAGGNNGTT TAGGGGGGNT AAAAT	355

(2) INFORMATION FOR SEQ ID NO:1234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

GGCANAGNNG GAGTAGGAAA ATCTTGCTTG CTTCATCAAT TTACAGAAAA AAAATTTATG	60
GCTTNTTGTC CTCACACANT TGGTGTGTTGGT TTTGGTACAA GAATAATCGA AGTTAGTGGC	120
CAAAAANTAA AACTGCAGAT TTGGGNTACCG GCAGGNNCAG GAGCGATTAA GGGCTGTTAC	180
ACGGGGCTAC TACAGAGGTA GCTATCGGGG AGCCCTTNAT GGTNCTAT	228

(2) INFORMATION FOR SEQ ID NO:1235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

AGACTGCCCT CATCCACGAT GGCCTAGCAC GTGGNAATTNC NCGAATTGCC AANGCCTTAG	60
ACAAGCGCCA AGCCCACCTT TGTGTGGCTT GCATCCAACNT TGGTGTGCC TATGGTATGG	120
CAAGTTGGTG GTGGCCCTTT GTTNCTNNNC ACCAAATCAA CCTAATT	167

(2) INFORMATION FOR SEQ ID NO:1236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

CCAGGNTTGC TGATTTGGCG AACGGTAGCA ATGATCATCA ATGAAGCCCT TGAATGCGCT	60
TCAAAAAGGC GTGGCCTCTG AACAGGATAT CGATAACCGNC ATGGTNCTTG GGGTGAATT	120
TCCATATGGC CCACTTGCCT GGGGAGCGCA ACTTGGCTGG CAGCGNAATA TTAAGGCTCC	180
TTGAAAATCT ACAGCATCAC TATGGCGAGA AACGCTATCG CCCATGTTCA TTGCTGCGCC	240
AACGGGGTTT NCTGGGAGAG CGGTTATGAA GTCATAAGGC CTGGCAAAT GCCCATGCAA	300
TGTATGAGAA CGATGCCTGC GCCAAAGNTT TGGCNGGACC ATTATCTTCA ATGGATGAAG	360
GCTTGCTGT TAGTGGACCN GNACCTTCAT TGCACAATGC TTAACGGTTC NTCAAGTTGC	420
CAGGGGGGCA GTATTTTCA TGGGTGATAN NGCTTGCNA CGCTGAATAG CCAGGGTTGC	480
ACNGTACCAT T	491

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

AACCACTGGT ATCACATGGN CATGAACTAC CGCGGGATGA TCANTATGCT GATCTNCTGC	60
GGTTGTTTCG GGCAAAGCGG TGGCGGCTGG GCACACTATG TCGGCCNGGN AAAAACTGCG	120
CCCCACAAAC CGGCTGGTTG CCACTGGCCT TTGCGCCTCG ANTGGNAACC GACCACCGCG	180
CCAAATGAAC AGCACCTCGT TTTTCTACAA TTCATCCAG CCAATGGCGC TTATGAAAAAA	240
GTCTCTGCTC CAGGGAGTTN ACTTTCACCG CTCGCCGATG CCATAAAGTT ACAGCGGTCA	300
TCTGATTGAT TTCAACGTTG GNGCCCGAGC TATTGGGCTT GGCTANCTT TTGNGCCNTG	360
ATTGGGGGGT TAACCCGTTG GGNATTNAAA GTTGAAGCCG ACAAGGCCGG ATTTTCCCC	420
CACAG	425

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

GGCANAGGTG ACGTCCGNCC AGTACACAGC CCTGAGTTGG GATGTTGAAT TTNTCGATCA	60
CGCCATAGAT GGTATCCAAC ACGCGGCTTA AGTTTCCAC GTCGTCAGTC ACCGGGTTAN	120
CGCCGATCAC CGCATCGCCC ACCCGAAGG AAAGCCCTTC GTAGATTGC GCGCGATAAC	180
TTTGCACGTC GTCACGGGTG TCATTTGGCT GCAAACGGGC GCTAAAGGTG CCCGAAATAC	240
CGATGGTGTT ATTGGCCTT TTGGATTACC GGCATTTCT TCGCGCCGTA GGATTCAAGGT	300
CCCGCGTTGGG AGCAAAATCT TTCGTTANCG CCGGGGACCA TTTCCGAGGT TCANCCCTT	360
TGCGGGTNAA AGGCAATGTC GTTCCACGTT GGTTTCANCG TTCAGCAACA TATTNAAGGA	420
TTCGTNGATG CTTCCATTAA TAANCTGGTT TAAGGCCTTT GTTAAAANGG TCC	473

(2) INFORMATION FOR SEQ ID NO:1239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

GGCANAGGNN NAAATGGATT GATTATGTCA AGGNGCCAGG CATGGTAAGG AGCAAAGAAG	60
GTTCACTCTG GACAGCACTA AGGAACTTTG GTTTAGGAAA GAAGAGCTTA GAGGAACGCA	120
TTCAGGAGGA GGCCCAACAC CTCACTGNAG NCAATAAAAG AGGAGGAACG GNACAGCCTT	180
TTGGACCCTC ATTTCAAGAT CAACAATGCA GTTTCCAATA TGCATTTGCT CCATCACCTT	240
GCGGAGAACG CTTTGAGTAC CAGGATAGTT GGTTTCAGC CAGCTGCTGN AAGTTNACTG	300
NGATGNAAGT NCACATTACT TTGGGGGG	328

(2) INFORMATION FOR SEQ ID NO:1240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GGATCCCCCG GNCNGCAGGA ATTGGCACA GGTCAAAGNC CACGGCGAGT ACACGATGGA	60
AGCAAACAAG GACTANAAGG ACTATAAGNA CGATGAGCTG CCAGCCAAGG AATGACCCAA	120
ATTCCCCNCT GCAGCCGGG AACACCCCTG CAGCTGTTG AAGGGTCGGA GGAACCGCCG	180
CAGTAGNNTA GNACGCCAA AGTGGTGGAG GAGCAGGAGT GCCANGGNNGC ACTACACCGT	240

GTGCCAT

247

(2) INFORMATION FOR SEQ ID NO:1241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GGCANAGGGA CCTTCCCACC TCAGTCTCCC AAGGTGCAGG GATTATAGGC GTGACATCTN	60
TCTGGCACCA GCCCCAGNAG CTTTCAATG AATGTGTTCT ATGTGGGAAG TGGGTATGTN	120
GTGGATTTT GTAAAGCTTA TCCTNTAGAT TTCTTGAAC CTGNGATGNM ATATCTCTTC	180
TCAGTTTGG AAAATTCTCA GCCATTATCT CTTTACACAT TTCTTCTGCC ACATTCTTC	240
TGTTATTNCT CCTTCTGGGG GCTNCAATT ACANATNACG NTA	283

(2) INFORMATION FOR SEQ ID NO:1242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

AGATGAACGA NCAGACTCAG GCGATGTGCT TTATGGCAGG CGCAAACCTCG ATTTTTTACG	60
GTTGCAAACG GCTGNACCAC GCCGAATCCG GAAGAAGATA AAGACCTGCA ACTNTNCCGC	120
AAACTGGGGN TAAATCCGCA GCAAACCTGCC GTTNTGGCA GGGGGATAAC GGAACAACAG	180
CAACGTTTG GAACAGGGCG TGATGAACCC CGGACACCGA CGGNATTTT ACAACGCGGC	240
ACATTATGC NGCTGGCAA GNNGAAANTT TAAACGGGGG	280

(2) INFORMATION FOR SEQ ID NO:1243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

NCCGACCNTA ACCATATCGG TAANTTTAAN CTTATCGGCC TTAAGCCACT GCCCAACCAC	60
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ATAGCTGGTC ATAATTTAG TNAGGCTCGA GGGTCCATT TTN 103

(2) INFORMATION FOR SEQ ID NO:1244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

NATTCTAAA GGNCTCAAGT TCAACCTCAC GGAGACTTCT TAGGTAGAA ATTACCCAGA 60

NCTTCCANCA CCTTCCTNCG CCACCCCAA TTCAGTCCAG GGANTGAGCT CNAGCTGA 118

(2) INFORMATION FOR SEQ ID NO:1245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

TTGGCACCAA AATNCTGCAC CTAACCGTTG NACAGGCACG TGGCTTTAAT GCTAACACG 60

AATGGAAAAC CNTTTTTAA TGGTNTGGTT GANTTCATGA CCTCNGGCC GATANGANGT 120

TTCCGTGNCT GGAAGGTGAA AACGCCGTT AGCGTNACCG NAATCTGCTG GGCGCAACCA 180

ATCCGGCAAA CGCACTGGCT GGTACTCTGC GCGCTGATTA CGCTGACAGC CTGACCGAAA 240

ACGGTTNCCA CGGTTCTGAT TCCGTCGAAT CTGCCGCTCG GAAATTGCT TATTTCTTG 300

GCGAGGCGAA GTGTGCCCGN GGACCCGTTA ATAATTCGT AATNGCCGNT GCAAAGTNGG 360

TTTCCGTGCG GCCAAATTN 379

(2) INFORMATION FOR SEQ ID NO:1246:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

AAAGGAACGA CCTGGCTTNT AAGCAGGACG AAGGGCCCT AGACGGCAGG CACGGTCAA 60

AGTCCAGCCC CTTAACNAG GTGGTGTNTA AAGCCTTTT CCGCTTCTTC CGTGGAAAGAT 120

TGTGGGAACA TGACTCTTG TTCCTAACGT CGGGCGAGCN TAAGGAGAGA ACCCTGCAGC	180
GGGAGGCCTT CCGCAAAGCT GTCTCCTCCA ANAGCCTCCG NNACTTCCTG GAAGGTTTT	240
CATGGAGGAC TTCAAATGTT TTCGGGGCT TTCATTCCAG GAGCGGAAAG TTGCGNCCGG	300
CAGGTATGGC CAAAGGGTCT GTTTNNAGG TTCCGNAGGN CCCAGAAGTT ATTTGGGAA	360
AACAATTCCC CCA	373

(2) INFORMATION FOR SEQ ID NO:1247:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

TTAATTCAANG CGTACCACATCG TACCGAAGTA TGCCTCCCGA TCAAAACCAA AGCAGGCACC	60
GTGTTTGGAA TATTCTGAGC GTTCCAGGCA GGAACCTCCG CNAGCTCCTG GNATGGNCTT	120
CACTTAGTTT AGCGGCCGTT TCCAGTGAAT AATCCGGTTT CCGGCGGATG TAACACATTC	180
GGCTGGCGCG CGCTTTCTGG TAGATTCGGG ATTGGGNCGA GTAGCGCAAC CGAAAGCGCA	240
TCCAGCGGCG TTCATCAACA CCACGGGCAG CAACCGATT TAGGCAATCC TGGGCCACNG	300
ACCATGTACG GTTCAGAAAT CCAGCTTTG TTTGGTCGTT TTCGGTTTG CAGGCGGACC	360
NTCCNTCTGG TTTNTTAACG GNNTTC	386

(2) INFORMATION FOR SEQ ID NO:1248:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

ATCTGGNAAG GCGATAAAAAA GCCGATGCAG GGGCGGGNAG ATATTCAAGGC TCGTCGACTG	60
AAACTAAAGA NCTGATGCCC GATGTGGAAC TGAATGCAGA AGACGCTGGG GGAAATGAAA	120
CGGTGACGCG NNACTACGCG GTAGCGTNAG ACTGCGGTGG CGGCACCTTT AGGCAACANT	180
AACGGCAACC TGGAAACTTT TGATGAATGA CGGGCTGGTG AAGCCGCAAC CTGATGGGAG	240
ATTGTTGGC TGAATGTCGG CAACTTACAT TGTCGGTGCG ATATTTGGTT GATGATGAGG	300
TGCGGGTGAA ACTNCGNCGG CGGGGAAATT CTGAAATAAT TGCCCACGGG GTTGGCGGN	360

GCCCCCAAAA TTTTTGCTT TTCGNTAACT GAGAACNCGT TTTGATTNAA TNTTAACCCG	420
GAAGGCCA	428

(2) INFORMATION FOR SEQ ID NO:1249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GTTCATCGAA GGGAAATCGCC CCGACCATCA CCGGATTTTT AATGCCCTGC CCTTTGGCAT	120
CGGCAAACAG CGCGGCGAGT TTTTCCTGGN AGGAACTGT GCGGGCGAAT CCCCGTTCCA	180
CAGCCGGTTN CATCGANGCG GGCGAAAACA TCCTGAACGT GCGTGAAAAC TGCGGGTANN	240
GCAGACATTA ANGGAAAAAA	259

(2) INFORMATION FOR SEQ ID NO:1250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

TTTGCCTGCA ANGAAACGTG AACTCGCGAA ANTGGNATAT TTGCTAATCT ACTCGCCGCA	60
TTTTTAATTG ACGACATAAT CCAGCCATCG CTGATTTGCC CCCCCAGAAG TGCCGGATCC	120
GAAAAGAAGA ACTGAACTCG TTGTGGAGAA TAACAAAAAT GGTCATCTGG AGCTTACAGG	180
TGGCCATTCTG TGGGNACAGT NATCCCTGAA CAGCCTACAA AACGCAATTG AAAGAACGCG	240
AAGGGCCTCG TGCTTGAACG NGGGCACCGA GGCCTCGCAT TGTTGCAGAT GGTTCCAACC	300
CTTGAAGTTA AGCGCTTTAT GGGNTAAATT CCCCCGCATA TNCCGGTTTG TCCAAGTTCA	360
NGGATGGGTT AAGGGCANCN GG	382

(2) INFORMATION FOR SEQ ID NO:1251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GGGCACAGTG TNCTGAGATC TGAGTCAGTA TCATTNATAT AAATGTCCTT CATAATGTTT	60
AGCACAGTGG GTTATCCGTN ANCCCAAGTA TCCTGTGAAT AGTCAAATTG GCTTTGTCCT	120
GTGTTGGAA TATGGNGGAA TAGTGAAATC CATGTGGTTA TGTCCCTTTA TGTGCCGGAT	180
GAAAAAAACT GATTAANCAG ATGTGTGTAA TTGCGTTCCC AAGTTCCAGA TAGCAAGGGA	240
TTTATCGAAT CCAGCTCATT TCTGAGTATA CACAGATTCA ANGAAGANTT GAGATATTAA	300
AGAGNTACCN ATATTTGNAA AA	322

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

AAGCTTATCG ATACCGTCAA CACCCTGAAA NAAGTGGCTG CCCAGGTTNN CTGAATCAGC	60
AACTGGAAAC TCCCCGCTTC CCCTTCCCCT ACAACACGCC AACCTCTAAA GAAGTGTACT	120
TGTATCGGAA GATCTTGAA AGAACTATTG CCGNTTCCAA GNGCCGNTGA AGTGCCTGCC	180
GGCCGGTCCT TCCATCGCTT GTTCTTCCGC TAAAGCGAAT NCGNTTGGAA ATGCAAGCGT	240
TTCAAGAAAA ATGGGACGGT TCCGTCTGGT NCGCGNGGTT GGTGTTCCAC CAGTCGGCG	300
TATTAGGTTA AGAAATNCGG NAACCGCCCC CGGTGGAATT CCGGGGTCCG GTTACCCAAT	360
TTCGNCCTNT TAGTTGAGTT CGTTTTTACA TTTNCATTGG GCCT	404

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

GGCAGAGCCA AAGTGCAGAT ATTACAGGTG TGAGCCACTG TNCCTGTCCA TTTCTAAAGT	60
TATTTTATAA ATAATTAACA CAAGTAAACA ATGAAAAACA ACCTTATTAG AAACCTTAAT	120
AAGAATTCAA CCATAGCAA CCCAATTTT TTTATCCTGT AAGTCCCTG GTTTGAAGA	180

CACATACATA TTCAAAATGA GAAAAAGTCC TTTGGANTAT AATCATCANT TGCTATATAC	240
AAACCTGTAA ACATATACAT TATATAAATC CTGATTNCC CGGTTTAAAA TGGAATCTCT	300
TAATATGGTC CGGGGGTTAN CCATNANTTC TGGGTTTTG GCATTTNAAT TGTTCAAAG	360
GGCCGTATTT TTGGAAAAT TTGGATGGGC TAGNATTTT	399

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

GGCANAGCCA AAGGGNCGGC ACAGCACGGT GCAGCGCTCC AAGTCCTTCA GCCTGCGGGN	60
CCAGGTGAAA GGAGACCTGC GCCGCCTGCC AGAAGACCGT GTACCCCCATG GAGCGGCTGG	120
TGGCCGACAA GCTCATTTC CACAACCTTT GCTTCTGCTG CAGACTGTCA CACCAAGCTC	180
AGNCTGGGCA GCTACGCCGC GCTGCACGGG GAGTTCTACT GCAAACCCCA CTTCCAGCAG	240
CTGTTTANGA GCAAAGGCAA CTACGNACGA GGGGTTGGC CGCAAGCAGC ACAAGGAGCT	300
TTGGGCCAC AAGGAGGTGG ACCCCGGCAC CAAGACGGCC TGAGGGCTCT TTTAACCTTC	360
CANCCCTTT NNGGAAGGTC TTGTAGCCGN CAGGGGAAAG TTGGGAAGGA GGTTGAGCTT	420
GGGGTTNNNT TGGGGGNCC AGTTGGNAAG GGGTTAGGGT TTTTCAGGGT AGGGGNCCAG	480
GNAAGGTTTT TTCCAGGATT	500

(2) INFORMATION FOR SEQ ID NO:1255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

CGANATGCCG CCACCGCCAC CTGCCCTTN AGCGCATCTT TNACCCCAAC CACCGCCACT	60
TCGGCAACGN CCGGAATGGC TGGAGATACT CTNTTCAATC TCGCGCGTCC CCAGCCGATN	120
TNCCNGCAAC GTTAAATTAC ATCGTCAGTG NCGCCCGAGA ATAAAGTGAA TAACCGTCAG	180
CNTCACGGAT GCCCCAGTCA AAGGTGGCGT ACACCGNGCG GGAAAACAGC GACCAGTAAG	240
TTTCACAAA CGGGCCGTCG TCGCCCCAGA TGGTCTGAAT ACACCCCGGC GGCAGGGCCC	300

TTCCACCACC AGCATCCCTT TTTCGTTGAN GCCAAAGGTT TGCCGGTGGA TTTCATTAAG	360
CAATGCAAGT TATAGNCCTT ANATTGGNAA AACGGGGNTT TCCAAAGGGT TGGNCTTTG	420
TTCAGACGGG GGAATGCC	439

(2) INFORMATION FOR SEQ ID NO:1256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

CAACAGATGG GTAATGGCAC CAACGAGAGC CTGATGAAAG GGAGGGCGAT CCTCCAGTTC	60
AAATATAAGG TCAGAACCTG CATGGTTTAT ATCAGACATC CCTTCACTCC TTTTAAAGTA	120
AATTTGAATC ATCTGAATTÀ GTAAAATAAA TTCCCACGAA TTTGGGGCGC AGGACGCCTT	180
GAGAACGGCT TATCTCATTT TCGCA	205

(2) INFORMATION FOR SEQ ID NO:1257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GGCAGAGGGA AAATNAAGTA CTCTTTTCAG TTGTGGATCG CAATGATGTC AGCAAAGGGA	60
CATGATGGGA AGGAACCTGT GAAATTGTA GATTTGCTTG GTGACCATGG GAAACATGTN	120
CAGTCCTCTG TGGGAGTTGA TCAAATGGTG CCTGGGTCTG TCAGTGTACA CCATCCCTTC	180
CATTGGACTG GCTTTGTTGG AAGAAAAGCT CAGATATAGC AATGAGAAAT ACCAAAAGTT	240
TAAGGCAGTG GAAGAAAGCC TGCCTAAAAG AGCTGGTGGA TATGCTAGGT GATGATGGTG	300
TGTTCTTATA TNCCCTCACA TCCCACAGTG GGCACCTAAG CATCCATGTN CCTTTAACA	360
CGGGCCTTTC AACTTGGNT TACAACAGGT GTTCTTCAN TGNCCTGGGT TTGCCNGTNA	420
ACCCCATGCC CATNGGACTG AATGCCAAGG ACTCCTTAG GCATCCAGTT GTNGGNGTAC	480
CCTTAAGGTC ATTTGCCCG GTG	503

(2) INFORMATION FOR SEQ ID NO:1258:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

AGNTGAANAN NCCACAAACCC TGACTCCCC GACGTCCACC GTGAATCCAC ATCCGCANCG	60
AGACCTCCGT GCCCGACCAT GTGTCTGGTC CCTGTTAAC ACCCTCTTCA TGNAACCCCT	120
GCTGNCTGGG NTTCATAGCA TTGCGNCTAA	149

(2) INFORMATION FOR SEQ ID NO:1259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

AGCTAAAAAA CGTCGCTGCG GTAATGGTGA CAGNGGCANT GTCTCCGTTT GGNACGNCAT	60
GGGCAAACCA TCGATGTGGT GGTTTCTTCC ATGGGAAATG CCAAAAGCTT NC GTGGAGGT	120
ACGTTGTTGN ATGACACCGC TTTAAGGGNC GTTGGACAGT CCAGGTGTAT GCGCCTNGCG	180
CATGGGCAAT TATTCTGGTT GGCGGNCGCA GGAAGCCTCC GCTNGCGNN ACAGTGTTC	240
AGGTTAACCA ACT	253

(2) INFORMATION FOR SEQ ID NO:1260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

ATATGCCGCA GAAATTGGT CTGTATGAAG ATCTCACGGT GATGGAGAAC CTCAATCTGT	60
ACGGGGATTT GCGCANGTNC ACCGGCGAGG CACGTAAGCA AACTTTTNCT CGCCTGCTGG	120
AGTTTACGTC TCTTGGCCG TTTACCGGAC GCCTGGCGGG CAAGCTCTCC GGTGGGATGA	180
AACAAAAACT CGGTCTGGCC TGTACCCCTGG TGGGCGAAC GAAAGTTTG CTGCTCGATG	240
AACCCGGCGT CGGCGTTGAA CCCTATCTGC ACGGCGCGAA CTGTGGCCAG ATGGTGCATG	300
AGCTGGCGGG CGANGGATGT TANTCCTCTG GAGTACCTNT ATTTTCGACG AAGCCGAGCC	360

ATTGCCTGNA CGTGTAAATT GATGAACGAN GCGNATTGCT GTTTTCAGGG NNGAACCAA	420
AGCCTGNACA CAAACCNGGC CGGACGCAGT TTTTGATGAC CATTACAGG AGGGCAACNC	480
AAANNTTGC	489

(2) INFORMATION FOR SEQ ID NO:1261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GGCANAGGGA GAAGCAGGAG CTGTCGGGNA GATCAGANGC CAGTCATGGC NTGACCAGCG	60
NGACCTTAT	69

(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

GGCANAGGAG ACAGGCCAGTA TACAAATACT ATAAATACAC TGGAGGAAAA CATACTGGGG	60
CTGATTATAG TCGATTTTTG CTCTTTTATT TCCGGTAACA GTAAAACAAC TCTGNATAAG	120
AAAAGGTTTG AACATGAAGG CAGACCTGAA GCGNGTNAGG NNAGTGAGCT ATGCAGCTAA	180
CCAGGGTAAG AGTTCCAGGT AGTGGGGATA GCAAGTGCAA AGGCACATATG GNAAAGGNTC	240
ACATGGNNAG NGGTGTCAGC AAGAAGGGCC ACTGTAGCCA GAG	283

(2) INFORMATION FOR SEQ ID NO:1263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

GGCANAGCAA GAAGGCAGGC GAAACAAACC GCCGTCAACA GATCCCAGAC TACCGTACTC	60
CTCCNANTNT TTNAGAAGGA TCGCTTCAA GACATTGCCA CCAGGGAACA GCTGGCCAGA	120

GAAGACGGGC CTCCGGGAAG TCCAGGGATT CAAATCTGGT TTCAGAATCG AAGGCCAGG	180
CACCCGGGAA CAGGCTGGCA GGGTACTTAC CAGGCAGGCG GGCTTGATTG TTGGGCCCA	240
GGCGGGTTT TAACCCTGNT TNCCCTNGTGG NTCNGTTT	279

(2) INFORMATION FOR SEQ ID NO:1264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

AGCNTGGGNT ACGACGTGGA GAACGACCGG NAGGTGAGGC CGANTTCAAC CGCATCATGA	60
GCCTGGTCGA CCCAACCAT AGCGGCCTTN TAACCTTCCA AGCTTTCATC GACTTCATGT	120
CGCGGGAGAC CACCGACACG GACACGGCTG ACCAGGTCAT CGCTTCCTTC ANGGCCTAG	180
CAGGGGACAA GAACTTCATC ACAGCTGAGG AGCTGCGGAG AGAGCTGCC CCGGNACCAG	240
GCCGAGTNAC TGCATGCCG GNTATGGTGT CCATNACCAG GGGCCCTGAA CGCCGTGGCC	300
CGGTGGCCNT CGAA	314

(2) INFORMATION FOR SEQ ID NO:1265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

GGCACGAGGA GACAGGTCTT AGTCAATTG GTAAGTTAT TTTGCCAAG TTAAGGACGT	60
GCGCCTGCAA CACAGCCTCA GGAAGTTCTG ATGACACGTG CCCAAGGTGG TCTGAGCGCA	120
TTGGNTTTA TACATTAG GGAGATATGA CACATCAATC AATATACGTA NNATGAACAT	180
TGGTTTGGT CTGGGAAAGG TGGGACAAC TGAAACAAAG GCAAGACAAC TGGNAGTAGG	240
NAAGGGAGCT TCCAGGTCA AGGTAGNTTA AGAGACAAAT GGTTGCATTG CTTTGAGTT	300
TCTGNTTGGG CCTNTCT	317

(2) INFORMATION FOR SEQ ID NO:1266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

GTCGTTGNTG TTGTTGTTGT TGNGTATGCN GCAGAATTN ACCAGNTGAT CTTAAAACCA	60
CACAGTGATA ATACAAGTTA CCAGCTATGG TCAAACAGTA TTGAAAAAGA NGATCAAAGT	120
TGGAGGACTC ATATTNCCA ATTTNAAGT TGCTTAANG CTNCTNTAAT CAAGATGCTG	180
TGGTACTGGC ATAAAGAAAG ACATATATGT TGGTGGAATA GAATTGAGAA TCTAGNAANC	240
TTTACATTAA ATNAGTCAAT TGATTTCCA GNNGAATGCT ATTAAGACGG TTA	293

(2) INFORMATION FOR SEQ ID NO:1267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GGCAGAGGGN CCTCTCAAAG TGCTGGGATC ACAGGTATGA GCCACTGCAC CCAGCCAATA	60
CTGTATATAT TTTTTTAAT GGACCAAGGC CACCACAATG TGAGCAGAAA GGTCAAATAG	120
TCTGTTATGT GGGAGAAATG TGTACAGTGN ACTTTGTTT TTAATTCCC CCAGTTTCT	180
AGTTTCTGT TTTAGAAGAC ATGCTGTCAC AATTAACAAAC TCTTACTNAA TAAGNACTTG	240
NTCAATTGAA ATGGTCTAT ACCAATTATG NAAATATGGA GGAAAGTTAG GGCATTAGGA	300
CTTACAAGCA CGTACTTCNN TCTTAAGTGG CTTAGGATTC CCCAAGCTGT NAACANTGCT	360
TTTTTCAGC TGTTTNCCN	379

(2) INFORMATION FOR SEQ ID NO:1268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

GGCANAGCGN ACAGGGGGCG CTGTTTCGT GGAAATCCCC CGGCTGCGAA CCTGGGATCC	60
CTGACCTGGA TCAAGTCTCC GAAGCTGGCA GAGTCATTC TGCATCACCG GTCTGGGCT	120
TTGAAGAAC TAGGAGAAAT TCCGCTTCGG CCATCACGCT ATGGAAAAGT GGATTTTTT	180

TTCTTAAGTC AATTTTTTT TTTGAAAAT ATGAGACTTA GTAGGTTGG GAAGTGGCT	240
AAAAGAACAT TTGATATTGT AAATTGGACC CCCCCTTGA AGGTGACAGT GTTTTCC	300
TACTTNAAAG CGCCAANTTT TTTNTGGCA CTATNAAAG CTATTTACTA N	351

(2) INFORMATION FOR SEQ ID NO:1269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GGCANAGGGA ACTAGTTCTC TCTCTCTCTC TCCATGACCC CGCAGCTTCT CCTGCCCTT	60
GTCCTCTGGG GCNANCAGGC CGCCCTGCAG TGGAAGGAAA GGGGNCCCCA GNAGCTNCTG	120
AACACTG	127

(2) INFORMATION FOR SEQ ID NO:1270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

CAGTTTNAGG CGCAGAATAT CTNNCGAGGC GCTGCGCCC GGTAAAGGTG CCGGAGAAAG	60
TAACGNGGGC GGCGGCAGTT GAACGACGTG ATTCTGCCCN GAATGCCCA TCACGCTGCC	120
AGGCTTCGNT TTCGCGGTAT TGCTGGTACT CTTCCACTAC ATCANCNAAA GGCGTNAAAT	180
GGCGAANAGG NCCTTGTTTC GCCACGCAGC CATGTGCAGT NAAATATTGG CGATCTGGCG	240
GGTAATGGCC GGGAAAACTA AAAGCCATCG NACCAGCAA TGTTGATAAC GCTGNTTACC	300
ANTACCAGCG GTTTATNCGC CCACCTGTTN TCAGCTGATG AAAGACCATG GTTTTACCGT	360
TATCGACGGG CNATTCTTGT TGCAAATCCG CCTGGTATTA ATGCCTGGGC CATTACCN	420
CGGGNTCATG TTTGGTCNT AGGGTCGTTA ATTTTGCGN ATTCAACGT TNAA	474

(2) INFORMATION FOR SEQ ID NO:1271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GGCACGAGAA AGAACGAATT GGCAGCCCTG TCTACACTGG CCCTCTCTCA GGTGCATCAT	60
AACCTATTCC ATTCAAGGCTT TTNACTCTCA GCACTTAGGG GCAGTTATGC TTGGCATAAGT	120
TTCCAAAAAC TTCCATTGCAAAATCTAAA AGTCAGTCTT CTGTTCTCAT CTTGAAAATG	180
AATTATTAAA TTATGTATAT TTGGGCGGAG GCACTTGTTT TCCCTTGAA GTCAGGGACC	240
CCCTGTTTA TACCCATGATTA TGTTCTGTT TCTCTCAGTT TTAAGACAAT	300
TATCTCCTAT ATTGATGAGC AATTGAGAG GTACCTGCAT GACGAGAGCG GCTTGAACAG	360
GCGGCACATC ATTGATAATT AGGGTGCATT GTTGCTTTA CTTTATTCA CCTTTGGAC	420
ATGGGTAAGT AATTGTTAT CGTGGAGAAA TGCTTACTA CATGGGTTG TAAGTTTACC	480
CAAACGGGG ATTTAATAT	500

(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

GGCACGAGAA GAACGACATC AGAGATGAGG ACAGCATTGC TGCTCCTTGC AGCCCTGGNT	60
GTGGCTACAG GGCCAGCCCT TACCCCTGCGC TGCCACGTGT GCACCAGCTC CAGCAACTGC	120
AAGCATTCTN TGGTCTGCCG GCCCAGCTCT CGCTTCTGCA AGACCACGGA ACACAGTGGN	180
AGCCTCTGAA GGGCTTCCCC GAAAGTTNTG GGNACCAGGT CCAGGTGGGC ATGGAATGCT	240
TGATGACTTG GGAGCAGGCC CCCACAGACC CCACAGAGGA TGAAGCCACC CCACAGAGGA	300
TGCAGCCCCC CAGTTNCATG GGAAGGTTGG AGGGACANAA GCCCTTGGA TTCCCCGGGT	360
TTTCAAATTN CTTNNNGTTT TT	382

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

GTTCGCCTTC CGCTTNAGG ATTTGCAACT GTTTTAACC TTCGGCTTA AGGATTCCG	60
CCTGACGGAT CCCTTCCGCT TCAAGAATGT AAGCNCGTT GGNACGTTCC GCTTCATCT	120
GCGCGTCAT TGAAGAGATA AGCTCTGCCG GTGGCGCAC GTCGCGAATT TNAATACGGG	180
TNACTTTAAT CCCCCACGGG TTGGTGGCTT CATCGACAAT ACGCAGCAGG CGTGAAGTTT	240
GATGCTGTCG CGCTTGAGAG AGCATTCTGT CAAGTTCCAT TGAACCCAGC ACGGGTACGG	300
GATGTTAAGT NCATGGTCCA GGTTGATGG TTGCCAACGC TTCCAGATTG CTTGACTTTC	360
ATAAGNCNGC GCGCGGGGGG GGTTNAATT ACCTGGAATT AAAAGGCACA CGGGCGTTCG	420
ATTGGTNACC GTTTGGCGGT TATCCTTTTC GGGGATAACT TTCCCTGGGG AAGGGGNTAT	480
TCGAG	485

(2) INFORMATION FOR SEQ ID NO:1274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

CGGGGGNGAA TCANTTTNTG GAATACTTTG GTGAGGCGCT GTTCCGTGCC GACTTGTGCA	60
CGCCGACGTA GCGATGGCG ATCTGCTGAT TCACGAAGGC GCGCCATGCA TTGCACAGCA	120
ACATGCGGCA AAAGTNTTTA ATGCCGATAA AACCTACTTC GTTTAAATG GNACTTCATC	180
TTCTAACAAA GTGGTTTAA ACCNCTGCT AAACACCGGG TGATCTGGTG CTGTTGATC	240
GCAATAACCA CAAATCTAAC CACCACGGGG CGTTGCTACA GGCTGGTGGC AACACCGGTT	300
TTATCTGGGA AACGGCANTA AACCCGTNTG GCTTTATTG GTGGGCATT GATGCGCACT	360
GTTTTNNAAAG AAAATTACCG CGCNGTGAGT TGATTGGGG AAGTTCCAGG GGGGGGGCCC	420
GTTACCCCAT TTGGNCCNC	439

(2) INFORMATION FOR SEQ ID NO:1275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

CAAGGGGCGC CACAGCNGAG GGAGCTGGCC GAGGTGGATG TGGACTGGCT GATCGTTCT	60
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GGTCGCGGCG CAGTGGTGTT CGATAACACC GAATCCGCG TGGTGAACTC ACGTACTCAG	120
CNGNAAGCGT ATGTTTTGC ACCGGCTACG CTGTCCAACA TTTACTACGG TTTCCTCGCC	180
GTAAACAGCC GTTTCAATGC TTTCGGTGAT GGTGTGGCGC AACTGGGCCG CTCGCTGGAT	240
GTTGATGCCA ATACCAAACGG TCAGGTGGTG ATCCGTGGAT AGCGCCATCA ACGGAAGTTT	300
TNAACACGGC TGAAACCGTG GGGCCGATGC GGTGTTCTC TNAATCGTGC CNTTTNNNGGG	360
GNAATAACCG GCANCGTAGN TGATTAACGN ACGAAATACC AGCGCAATCT GGAATNGNCA	420
CTAANTACAA CCGCATGTGG GGGATTACAN TAAACCCGGG CGTTGGGTAATAAAATGGGT	480
TNNCAAGGGC GAGAAATTAA GGGCAATTN	509

(2) INFORMATION FOR SEQ ID NO:1276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

AAAATTGGTC ATCTGTTGA CTACATCCTG TTTGANTCAG CATGGGTGG CTATGAACAG	60
TTTATTCCGA TGATGGCGGA CTGTTCGCCG CTGTTGCTGG TTCTTAATGA GAACGATCCG	120
GGTATTCTGG TTACGCAATC TGTGCATAAA CAACAGGCTG GTTTTNTCA GACTTCACAA	180
ATTCAAAAAA AAGACAGCCA CATCAAAGGG CAANAGCGTT ATGTACCGCA CAAACGCATG	240
AACAACGCCT TTNTGAATGC ACCCCTCCAC CAGCCCGTTT CTATCCGCTG TTTGCCGCAC	300
TGNANTATCC AACGCCAAAN TGNCATGGAA GGTGTCAGC GGTCGTAAT NATGTGGGAT	360
GG	362

(2) INFORMATION FOR SEQ ID NO:1277:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTCNCCAGA TGGNGTCTCT CTCTNT	56
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(2) INFORMATION FOR SEQ ID NO:1278:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

CGGTTCCANA CTGTAATTGG TTTCCATCGC CACTTGCCA CGCAGCACCTT TGCATTTNCA	60
GGTCGCACAG ACGCCGCCCTT TGCAGGCATA GGGCAGATCC GCCCCCTGGG GCAATGCCGC	120
ATCGAGAAAT GCTTTCATCG TCGGCATTAA GCACGATTTC CCGATCCCAC CCATCCTGAC	180
GTACAGTCAC TTTTNNTCCG TNACTTGCA CGTTAACACGC TACGTTGAA CGCGCGTGCC	240
AGGGGTATTA AACCGCTCCA AATGAATGGT TTTTCTGGG CATTCCCAGT GGCTTTTAA	300
GGCGGTTTTC CGGGTNCATC CATTCAATTG NCGNCGGGNC CACAAATAAA ATGGCCTCNT	360
CCTTAAAGAC	370

(2) INFORMATION FOR SEQ ID NO:1279:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GGTTTCGCCA GTAACGAAC TGCTCACCCA TCAGGCGCAT CGNCATATCC ACACCTTG	60
GGNTCAGCGG TTCACCNTTN TTACCGATAA TGCAGGTTAG CGAAGCGGGGA GAGGCTGGCT	120
TCGTTATGGG TGGAAACCAAG TTTGCCAGTA AACAGCAGCC CCCAGGTGGC GGCATTAACA	180
AACAGTGACG GGCTACGAAC CAATGTNTGA CTGCCAGTTA ACCGTTGCTG ATTTTTTCGC	240
GGAATTAAAC GCGTCGGGGG TGGGCTTGT CGGGGAATAC GCAACAAACGG TTTCCGCCA	300
GACACATTGCG GCGGCCAAGG CTTTCCTGCG NATTGACCAG CGGAAAAATT CCTGGCAATT	360
AANCCCTTGG GACCATAACC TGGGNNGGACC CATTGGGNAT TTTTTGNAT TACGGCGTTT	420
TTTCCGGCC CANTTG	436

(2) INFORMATION FOR SEQ ID NO:1280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

TGGCGCAGGC NCTGTTGCT GATCCGGATN TTCTCCTGCT CGACGAACCG ACCAACAAACC	60
TCGACATCGA CACCATTGCG TGGCTGGAAC AGTGCTGAAC GAGCGTNACA GCACCATGAT	120
CATCATCTCG CACGACCGTN ACTTCCTTGA ACATGGTCTG TACCCACATG GCGGATCTGG	180
ATGACGGCGA GCTGCGNTTT TATCCGGTT NTTGNCGNAT GGAGTACATG ACGGCCGGCGA	240
CCCAGGCGCG TGAAACGTNT GCTGGCCGNT TAACGNCAAG ANGAAAGCGC AGATTGNTGA	300
GTTGCAATCT TTGGTTTAGC CGCTTTAGG GC	332

(2) INFORMATION FOR SEQ ID NO:1281:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GGCCATCCNC TGGGCCTGCA GGTGCATGAN GTCGCTGGTT TTATGCAGGA TGATAGCGGT	60
ACGACCTCGC GGCACCCGGCA AAATATCCGT ACCTGCCCTG CACCCGTNTT CTCCAGCCGG	120
GCATGGTGTAA ACCATCGAA CCGGGTATCT ACTTCATCGA ATCGCTACTG GCACCGTGGC	180
GTGAAGGGCA GTTCAGCAAG CACTTCAACT GGCAGAAAAT TGAAGCACTG AAACCGTTCG	240
GCGGCATTG TATCGAAGAC AACGTGGTGN TCCACGAAAA CAACGTGGGA AAACATGACC	300
CGGGATCTGA AACTGGCGTG ATGGAAAGCT GGTTAATTCC TGCAGCACCG GTCACGTTCG	360
TTGGNGAGNT CAAAAAGAGC CGGTTTCATA ACGATGTTGG GNGCATAACCG TGGCGTTTA	420
GGCGGCGAAA GNTTTTTTT GAATCGGTTG GGGAGAAAA CCCCNNTNN CCGGAACATT	480
TTTTTGGGT TGGTTC	496

(2) INFORMATION FOR SEQ ID NO:1282:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

TAATGAAGAA AACTCCNGGN TGTGGATNTA CCGCAAGCTN GGCGGGGGC TACTCGGAAT	60
TTTAATGGTA CGGGTGCTCG CGGCCTATAC CACCTATNCT NTGGNAGATA AACCGGGCGTT	120

ACGCCAGGCT TTGCGGCTGG ANTTGCNGCC AACATGATCG GCTCCGGGTT TNTCGGCGCG	180
GTCGTTGGCG GNTTGATANC CGGTTACTT	209

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

TACACACAGG CCAAAGAACAT CTGGGAGATG GATACCAAAG AAAAATTGGA GCAGGCTGCC	60
ATTGTCAAAG AGAAGGGAAC CGTATACTTC AAGGGAGGCA AATACATGCA GGCGGTGATT	120
CAGTATGGGA AGATAGTGTC CTGGTTAGAG ATGGAATATG GTTTATNAGA AAAGGAATCG	180
AAAGCTTCTG AATCATTTCT CCTTGCTGCC TTTCTGAACC TGGCCATGTG CTACCTGAAG	240
CTTAGAGAAT ACACCAAAGC TGGTGAATGC TGTGACAAGG CCCTTGGACT GGACAGTGCC	300
AATGAAGAAA NGCTTGATT AGGAGGGGTG AAGCCCAGCT GGTCATGAA ACGAGTTNA	360
GTCAGCCAAG GGTGGACTTT TGAAGGAAAG TGCCTNGNAA GTAAAACCCC CAGANTTAAA	420
GGCTGCAAGA CTGGCAGATC TCCCATGTGG CCAGNAAAAA GGGCCAAGGG NGCACAAACGG	480
AGCGGGGANC CCCAGGATTT T	501

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

GGAGCCGGGG AATCTGCGCC ANTTGATGAT CCCGGAACAG CAGAGNCTG CTGGAGACGT	60
TTACGCTGTT AGTCGCAAT GCCCTTNAGC GGCTGACGCT AACCGCCAGC NANGAACAGG	120
CGCGGATGGC AAGCGAACGT GAACAGATCC GCAACGCCCT GCTGGCGGCG CTTTCGCATG	180
ATTTACGCAC GCCGCTTACG GTGCTGTTTG GTCAGGCAGA AATCTTAACG CTCGATCTGG	240
CAAGCGNANG ATCACCCCCAC GCCCGCCAGG CCAGCGAGAT CCGTCAGCAT GTGCTGAACA	300
CTACCCGACT GGTGAATAAT CTACTGGATA TGGCGCGAAT TNCAGTCCGG CGGCTTNAT	360
TTGAAGAAAG AGTGGTTAAC GCTGGAAGAA TAGTCGGCAN GCGCTGCAAN GCTGGAACCG	420

GTTCNNNTT GCCCNCATG TTTNNTNNN CAGAACCTTG AACCTAATNC CAGTTGAANG	480
GGCCATTNTT NNAACGGGTG CTGATTAATC TG	512

(2) INFORMATION FOR SEQ ID NO:1285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

ATTGTTTAA AAAAGATTAT ATCTTACGT CCGTAACCGG AGATTTCCCG CAAAGCCAAT	60
TTACCGATAA TGAAATATCG TCTTTATAA GGATATCTAA GATGCGTAAA ACAGTGGCTT	120
TTGGCTTGT CGGTACCGTA CTGGATTATG CCGGGCGCGG CAGTNCAGCG CTGGTCAAAA	180
TGGCGTCCGA CACTCTGTT ATGCCAGCAA GAATCGTTGG TCATCGATCG ACTGGAATTG	240
TTGCACGACG CCCGCTCCGC GCTCGCTAAT TTGAAACGCT TAAACGCGAT TATGCCAGC	300
NTTTCGCCAG AAACAGNAAG TGGTGAGCGT TGAGATTGAA CTGCATNAAC CCTGGGATT	360
CGAAGAGGTC TACGCCGTGTC TGCATGATTG CGCCCTGGTT AAGGAGTTT CAGCCAGAAA	420
AGGAAGANCT TTTATTCAC NTCACCACCG TTACCCAGTG GNNGCNATTG GCTGGTTTN	480
GCTGG	485

(2) INFORMATION FOR SEQ ID NO:1286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

TATAAGCAAC GTGATGCCCT TGTGGTCGC GCTTTTAAA GATCCCCTAC TTGNGGANCT	60
CTTCAAACGT TGGCAGTTCA GGAATNGCTT CCCGCGACTG GGCATACAGA TGCCGNATCC	120
ACTCTCCTG GGTACGCCCT TCAGTAAACT GTTGCTCAAC GCCAAGACGT TTTNCCANTT	180
CGCTGGTTCA TTTCATAGAT GGTCTTACAT TCAAAGCGCG GNNTAACAC CTGATCGTTG	240
AAAATCACGT AAGGCNTATN CCCGCAGTAT GCATCCAGCG NAAAGTCCAT CTGTTNCGGA	300
AGCGGTNCAG TCAGGCAGCA GGATGTCCAG CATA	334

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

TGACTCACTG CTTTGCAACA CTCCGTGCTC TCATGCCAA GTTGGAGAC TTACTCTCG	60
AAGTGGAGGT GGAACAGTGT TTCGACCTAT GTCACCAAGT CCTGCANCAC TGCAGCAGCA	120
GCATGGGATG TCACCCGGAG ACAAGCCTGT GCCACCCTTT ANTCCTCAT GAGGTTCANT	180
TTTGGGGCCA NCCAATAATT TTTCAAGNTT AAAGATTCAA GTAACCCAAG GCCCN	235

(2) INFORMATION FOR SEQ ID NO:1288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

GGCACGAGGG AGCCGGGCC CGGNNGGAGCA AGAGGAGGAG GAGGAGGAGA GGTGGAGCC	60
GTCTCCAGGA GCCCTTAGAG ACCGAGTCCC GGCGGCGACG CGGGGGCAGC GCACCGGCAG	120
GCGGNTTCAT TCCACTTAAA ACCTGAAAAC ATTGGACCAC ACAAAAGTCTT ACTGATTCA	180
GGTAAAAACA ATAATTGAAG ATGTCCAGCA AAACAGCAAG CACCAACAAT ATAGCCCAGG	240
CAAGGAGAAC TGTGCAGCAT TNAAGATTAG AAGCCTCCAT TGAAAGAATA AAGGTTTCGA	300
AGGCATCCAG CGGACCTCAT GTCNTACTGT GAGGAACATG CCAGGAGTNA CCNTTGCTGA	360
TAGGATTACC AATTCAGAA AACCNNTTCA GGNTAAAAAA ATTGCTNCTN TTNTATGGAT	420
NGAGAAACAG TTCTTGGCTT TTTCCAACA NGGCAATTAT GAGCAGTCTT GAGGGGTTTA	480
CNTCAGTTAT TTGGTAACCA TGTT	504

(2) INFORMATION FOR SEQ ID NO:1289:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

AGCGAGGCAC GCAGCCTACT AGGTGTGGCG GCGACCCTGG CCCC GGTTTC CCGTGGCTAC	60
CGGGNGCGGC NAACCCGCGC GNGAGCCGAA ACGCCCGGTG GNCNAGACCC CGAGGACCTC	120
	120

(2) INFORMATION FOR SEQ ID NO:1290:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

GGCAGAGCTT CACAATAGAA GTGGAAAGGG CCCTGAGAGT NTTGGATGGT GCAGTCCTTG	60
TTCTCTGTGC CTGTTGGAGG GGTACAGTGC CAGACCATGA CTGTCAATNG TCATTGANGG	120
CGCTACAAACG TTCCGTTTCT AACCTTTATT AACAAATTGG GACCGAATGG GCTCCAACCC	180
AGCCAGGGNC CTGCCAGCAA ATGAAGGTCT TAAACTTAAA TNCATAAAATG CAGCGTTTA	240
TGCAGATACC CATGGGNTTT NGGAGGGTAA ATTTTAAAG GTNTTGTTAG GATCTTTATT	300
NGAGG	305

(2) INFORMATION FOR SEQ ID NO:1291:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

GGCAGAGGNC GCTTCCTGGG CCGCTTTGGT CTGCAGCCCC ACAAAACCAA ACTNTTTGGG	60
GCAACCACCC TGCGCCTTTT TAACATTCCG CAGCGCTGCA GAGAGGGACA AGGCCCTGCG	120
CCGTTTGCA TGGTGCCTCT TGGGAAAGGC CGCCCACCTCA GTGTGCGCCT GGTCCCGGCC	180
CAAGGGCAGC CCCATGGCCA GGAGGAGGGCG ACAGGGAGGGT GAGAGTNAAG CCACCAGTGA	240
ACACGAGTGG CCGACGTGGT GACCCCTCTA TGGACAGTGC CCTATGCTGA GCAGTTGAGC	300
GGNAGCAGCT GGAGTNCGAG CANGTGCTGC AGAAATTGCC AAGAAATCGG GAGCACCAAC	360
CTGCCTTGTGTT GCCTGGTTGT TGAGCAAGGC ACAAGCACAA CAAGGCTGTN NCCGTTGAGG	420
GGGTCAGNCT TANCCCNCAA TT	442

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

AAAAAAATGGG ACCTCGCGA CATCCTCGGC GCGAAAGGTA AGCTGTTCAA AACCAAAACC	60
GGCGAACTGT CTATCCACTG CACCGAGTTG CGTCTGCTGA CCAAAGCACT GNGTCCGCTG	120
CCGGATAAAAT TCCACGGCTT GCAGGATCAG GAAGCGCGCT ATCGTCAGCN TTATCTCGAT	180
CTCATCTCCA ACGATGGAAT CCCGCAACAC CTTTTAAAGT GCGCTCGCAG ATCCCTCTCT	240
GGTATTGCGCC ATTCCATGGT GAACCGCGGC TTTATGGAAG TTGAAACGCC GATGATGCAG	300
GTGAATCCCT GGCGGTGCCG CTGCGGTNCC GTTTANTCAC CCACCNTAAC GGGTTGGATC	360
TTNGACATGT TACCGCGTTA TCGGGCCGGA ACTGTAACTT CAAGGGTTTG GTGGTTGGTG	420
GNTTCGAGCG TGTATTGAA TCAACCGTAA NTTCGTAAAG AGGTNTTTCC GTANGTN	477

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

TTAATGGTAC CGGTGCTCGC GGCTATACC GCCTATTCTN TGGCAGATAA ACCGGCGTTA	60
GCCAGGNTTT GCGGCTGGAC TTGCCGCCAA CATGATCGGN TCCGGGTTTC TCGGCGCGGT	120
CGTTGGCGGN TTGATAGCCG GTTACTTGAA TGCGCTGGGT GAAAAATCAC TTGCGTCTTA	180
GCAGTAAAAT TCAATGGATT CCTGGACTTT TTATCTCTAC CCGGTGCTCG GTANTTGGGA	240
GCGGGCAGTC TGATGCTGTT TGTGGGTGGG GGAACGTTC GCCTGGGATC AATAACTCGT	300
TTAACCGCCT GGCTTGAACG GTCTTTCAAG GAAGTAAACG GGCTGTTGC TTGGGTGNCC	360
ATTCTCGGTT TTAAGGGTT CCCTTTGAAC CTTGGAGGGG CCATGAATAA AAGCCGTTAA	420
GCANTTCTGC CCGGGGNAA TGGGAACGG GGTTAAGGN CCNTATGCCA TTTGGGCTCC	480
GTNAAAA	487

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

AGCTCAATCC CGNCNCCGAC AAGACCCAGC GGNTTGGTGC CGGACTGTNG CGATTTCCG	60
TCCTNTTGCT TCGCGACCAA AGCCAGGCAG TGTTCAGCAC GTCGTGGCG ACCNNNGNCCT	120
CTCAAGTCGT CCGTGGTATT ATCACCCGNA CG	152

(2) INFORMATION FOR SEQ ID NO:1295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

GGCACGAGCC GGCNTCCCCC ATCCCCCGGT TCGGACCGNC GAGCGCCGGC TCTCCCCCTCC	60
CTGAGCACCG ATCCCAAGTT CCAGCTAGAG AAGGTGGCG GCACGCAGCC CGGCGGCCCC	120
TCCCAGCTCC CAGCGATTTG AGAGGGAAGA TCTGATCTCC TAGAATTAGA GTTGGTACAG	180
AAACCATTTC AGCTCCAAAA ATGTTGGAGG AAGATATGGA AGTCGCCATA AAGATGGTGG	240
TTTGTAGGGA ATGGACCACT TGAAAATCA AGTATGATT AGCGATATTG CAAAGGCATT	300
TTTACAAAAG ACTACAAGNA AACCATTTGA GTTGATTTT TGGAGCGGCC AAATTCAAGT	360
TTAATTGATG ANGATGCAGA CTTATGTTAT NGGGCACTNC AGTCAAGGAG GAATTTGNT	420
GCAATTACAA AGGCCTACTT ATCCGGGGAG CCCAGGCTTG TGGTGCTCGG TNTTCCTNTA	480
CCACAGGTAG GGGATT	496

(2) INFORMATION FOR SEQ ID NO:1296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

AGCGGTTCAT CCCCTTCCGG CGTCAGAGGA AAAGGTTAAC TTCTCTCCCA CCACCTGGGT	60
TTCGACGATT TGTCCGTTGT CCATAACCGT TACCCGCTGG CAAAAGCGTT CTACCAGGCG	120

TGAATCGTGG GTGAATGAAC AGGCAGGCGG TGCCAACTG TTNNTGTAGC TTTTCAGCA	180
GGCGAATGAA CACCCGCCCTG TGAACACGAG ATCAAGGTTA GAAACGGCTT CATCCAGAAT	240
CAGTAGTTTC GGTCGACCT TCANCGCGCG ACCAGGCAGA CGCGCTTGTGTA GCTGGCCGCC	300
GTTTAACTGC GGTGGGNCTT TNTNGAGAAC GCTGTTCATC GAGATCGACC GNCTTCAGNA	360
NTTCGTTGG CGGGCGNCAT TTGTTCCGGA TTTTTCCAA TGATTAGCAA GTTGGCGCAT	420
CGGTTCAGGN AGNTTTTCGG GAAGGTTTTT CGGGAATTCA GGGGTTNTGG GNT	473

(2) INFORMATION FOR SEQ ID NO:1297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GGGTAATAAC AGGCCAGACC ATTCTTGCCG TTNATGTTCA GACCGTCGGA ACCGCACACA	60
CCTTCACGGT AGGAGCGGCG GAANGACAGG CTGGGATCTT TCTCTTTAG CTGGATAAGC	120
GCATCCAGCA GCATCATGTC GCGACCTTCA TCCGCTTCCA GGGTGTAAATC CTGCATACGC	180
GGANATNCAT CAACATCCGG GTTATAGCGA TAAATTNANA AACTCGAGTC TCATTTCCCT	240
GTCTCCGCAT TAGTTAAGTA CGGAATCTTN GGTCGGGGAT TGCCNGGGCG GCATTTTCGG	300
GTTCATGTT TTTGAACGTT TTCGGNGGCG TTCANNGGAT TTCCCGAACT T	351

(2) INFORMATION FOR SEQ ID NO:1298:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

TGCATAGTCT GGCAGGATCG CTGGATGTNG CCGATGCCA AATGGTGGAA ATCGTCNGCG	60
GGCTGATGCG CGACTCGGGN ATTCTGAATN CTCGATGAAC CTACCGCCTC GCTTACCCCT	120
GCGGAAACCG AACGCTTGTT TAGTCGCTTG CAAGAGCTGC TTNCTACTGG CGTGGGTATT	180
GTTTTATCT CGCATTAAGC TGCCGGAAAA TTCGCCAGAT TGCCGNATCG AAATTAGCGT	240
GATGCNCGAG CGGGAACCAT CGCCTTNAAG GGGGAAAAC CAGCGGAACG GTTCTNACCG	300
ACGACATTGTTA TTTCAGGCCA TNCAACCCAG CGGGTAGNGG GAAAAATCGG TCTTNTG	357

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

GGCANAGCCT GATCCGACCC CGTCCCGCNG CGCGCCCGNC AGCCATGAGC TCNACGCATT	60
GCAACAAGGG CCCCTCGTAC GGGCTGTCGG CCGAGGTCAA GAACCGGCTC CTGTCCAAAT	120
ATGAACCCCC AGAAGGAGGC AGAGCTCCGC ACCTGGNTCG AGGGACTCAC CGGCCTCTCC	180
ATCGGCCCCG ACTTCCAGAA GGGCCTGAAG GATGGGAACT ATCTTATGCA CACTCATGGA	240
ACAAGCTACA GCCGGGCTCC GTCCCCAAGA TCANCCGCTC CATGCAGAAC TGGCACCAGC	300
TAGAAAACCT GTCCAACCTC ATCAAGGNCA TGGTCAGNTA CGGGCATGAA CCTGTGGACC	360
TGTTCGAGGG CCAGGAACTG TTTTAGAGTT GGGAACATGA NGCAGTTGCA NGTGTAAAAA	420
TTTNGNCCTG GGTTGGGAAG GNCAAGATTA AGGGGTTG	458

(2) INFORMATION FOR SEQ ID NO:1300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

GGCAGAGCAA CAAAGGAGCC AAGGGNGACC GAGGCTTGCC TGGNACCCAG AGGCCCCAG	60
GGNAGCTCTT N	71

(2) INFORMATION FOR SEQ ID NO:1301:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

TTNGCAACCA CGATTTTCGC GTCGGTTGGG TTTTCCAGCA GGTATTCTGC CAGCAGTTCG	60
TTCATCTCCT GTTCAACCGC CGATTTCACCC TCAGAAGAAA CCAGTTGTC TTTGGTCTGG	120

GAGGAGAATT TCGGGTCCGG CACTTCACG GAAACAACCG CAATCAGGCC TTCACGCGCA	180
TCGTCACCGG TGGCGCTGAC TTTGGCTTT TTGCTGTAGC CTTCTTGTC CATGTAGGCG	240
TTNAGGGTTA CGGGTCATCG CCGCACGGTA AGCCTGCCAG GTGAGTACCG CCGTNCACGT	300
TGCGGGATGT TGTTGGTAAA GCAGTNAGAT GTTTGCNTG GGANGCCN	348

(2) INFORMATION FOR SEQ ID NO:1302:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

GGNAGAGCGG GATCAGAAC A AGTACAAGGA GGCTGCCAC CTGCTCAATG ATGCTCTGGC	60
CATCCGGGAG TAAACACTGG GCAAGGACCA CCCAGCCGTG GCTGCGAAC A CTAAAACAAC	120
CTGGNCAGTC CTGTATGGCA NGAGGGCAA GTACAAGGAG GCTGAGCCAT TGTGCAAGCG	180
GGGCACTGGN GGTCGGGAG AAGGTCTGG GCAAGTTTC ACCCANATGT GGGCCANGCA	240
GT TTAGGAAA NNTGG	255

(2) INFORMATION FOR SEQ ID NO:1303:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

GGCAGAGGAG GAAGGGTCT CGTCGGAAGG CGCTGGACGG GGGTGACCGG GAATCGGGNA	60
CAGGGACAGA GATAGGGACA NGGACAGGTC ATCCAAGAAC GNCCGNCCCC CCAAGGAGTT	120
CGGCGNCTTC CTCAGGG	137

(2) INFORMATION FOR SEQ ID NO:1304:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

GGCANAGGTA AACAAAGGGTC AACCTGGTGT GGTTGGTGCT GTGGGCATGA CTGGTNCATC 60
TGGTCCTAGT GGACTNCCAG TAGTGAAGGG GTGCTGCTGG CATAACCTGGT AGGGCAANGG 120
NAGTTAACAGG GTNAACCTGG T 141

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

GCATATTGTT GCGGGTAGTN AGGCAGTCCT GGAACNNCGN CGGCCTTTC TTGAAATCCG	60
CTGGTTAAGN CACCGGCGTC GCTGGCGAAT CTGGTATTAC TCGGTTGGTT ACTCGGCGTG	120
CAATATGCCGTGCGNCATA AATATTNTTA GTGGTCGGCA ATATCCTCAA CATTGTGCTG	180
GATGTCCTGGCTGGTGATGGG GCTGCATATG AACGTGCAGG GCGCGGCGCT GGCGACGTTT	240
ATTGCGGAAT ATGCAACATT GCTGATTGGT CTGCTAANG TGCGTAANAT CCTCAAACATA	300
CGCGGAATTT TCCGGCGNAA TGCTGAAAAC TGCCNTGGCG AGGNAACTTN CNTTGGTTTG	360
NTGGGGGTTT AACCGGGATA TCAAGCTGCG TTCNCTGTTG TTGCAANTNG TTTCGGGGGG	420
ATCANCTACT TGGGGCCNAC TGGGGGGTGC CTTATCNTTT TAACGGGTT	469

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

GGCANAGCGT TTGCGNAGGC TGTTCCACCG CCCTGGGAGG CAGCAGCTTC TTGAGAAGG	60
AATGGAGCCC NNNTTGCCCC CGAGTGCTAC TTTAAGCGCT TCTCGCCAAG ATGTGGCTTC	120
TGCAACCNGC CCATCCGACA CAAGATGGTG ACCGCCTTGG GCACTCACTG GCACCCAGAG	180
CATTTCTGCT GCGTCATTGN GGGGAGCCCT TNGGAGATGA GGGTTCCAC GAGCGCGAGG	240
GCCGCCCTA CTGCCGNCGG GACTTCCTGC AGNTGTTCG CCCCGGGTTG CCAGGTTGCC	300
AGGCCCCATC TTGGTTAACT ACATCTNGGN GTTCAGGGNT TCTGGGACCC GGANNTTTTC	360
GTGTTNCANGG NAATGTTGG GGCCTTTTN GGGGGGNATT TTTTNGAGC AANAAGGGCN	420

CCCTTTTGG AGAAACCATT TCCAGGAAGA AGGGGTTGTT TTGGNCAAGT TTGGGTTCCC	480
TNTAACGCC TTTGTT	496

(2) INFORMATION FOR SEQ ID NO:1307:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

TCCGGTATGT NCAAAGCTGG TTTNCTGGG GACGACGCTC CTGAGNTGTG TTTCTTCCA	60
TCGTCGGGTG CCCNAGNTAC CAGGGCGTCA TGGTGGGGCA TGGGCCAGAA GGACTCCTAC	120
GTGGGNNACG AGGCCAGTG GCAAGCTGG CATCCTGACC CTGNAAGTAN CCCATTGAGC	180
ATGGGNATCG TTAACCAACT	200

(2) INFORMATION FOR SEQ ID NO:1308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

CCGCAGTTTC GCTTCGGCGA GGNGTGTGTG AACCACTTAG CGTCCGTTGG ATCAGCGCAT	60
CCAGCTGCGG GTCATTGAGT TGTTTCCACC ACTGCGCCTG AGNCCAGCCG GAGCTGCANA	120
GAATGAATAT CGTCGGCCAG TTTGAATTG TTCCGGTTTG AGCTGTCAGT GGCATAGGGG	180
CAGCGCGGGT TAAAGCAGGC AGCCGTTCGG GCGGTTCGTA CTTGCCGGGA ACGACACCTG	240
GCAACGACGC CAGACGTTCT TTGTCCTGAG CAAATTCTGG CAGCGCACGC AGCAATGCCT	300
GAGTATAACG GGTTGACGCG GCGCATGGTA AGATGGCGTG CCGCATTAC CGGTTTCCA	360
CCAACTGGGC TTGCATAACA TCACGATGAT TTTANTGTTG CCCGTTCCG NCAACAAGGC	420
CAGTCATGG GTAATTAAAC ANCAGGGCCA GTTNTTTTC TGGTTTNAGT TCCCACA	477

(2) INFORMATION FOR SEQ ID NO:1309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

AGCCACCAGN GCTGGGACGC GGCGGCANGG CGGCGGCGC GGCCCTCCGG CAAAGCGAAG	60
GCTGGNAGNT AGGAGAAAGC GGTCATCAGT ACCTCTCAGA TGGTTTAAAA ACCCCAAGG	120
GTCAAAGGAA GAGNTGCACT ACGNNNGTCC AGATAGTCCA AAAACTCCAA AATCTCCCTC	180
AGAAAAAAACG CGGTATGATN ACGTCTCTTG GTCTGNTCCA CCAAGNAAGT TCATTTCAGC	240
TTCCTGCAGC CAGTTCACCC GATGGGGTAT TGGNATTGN AACAAAGGTCA GNCAGNNGTG	300
CTNAAAAGTG CAAAAGAGGN AGGTTTTTG NTTATNCACC AACGTTTGG TAAGGNCTNC	360
CACCTGNTTT AAGAAGTAGT TNTAAAACA ACGTNCCAAT GGGTGGGGTT GCATTCTGTT	420
CTGAGGTTGG GGGNATGTTT NGCCCATTT CAAGGTCTGT TCAAAGGAGT NACCCGGTTC	480
AGTCAGGAG	489

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

TTTTTTCTGG CGGGCCGCTG CGACACGGGA CTGACTTNGG GATGGGAAGT GGAGTNCCCG	60
GAGCTGCTAC CGTGGCGGCG GCGCTGTGAG GAGCAGCCAG GGGGAGGCAG CTGGGGCTCG	120
CCNNNTGAAGT ATCCGGAAA GCGCCACCAT GGGGCTCCGT GAAGAAGAGC ACCAAGAACCC	180
CCCCCGTTCT CAGCCAGGGA ATTCACTCCTG CAGAACATCATG CGGACATCGT CTCCTGCGTG	240
GGGATGTTCT TCCTGCTGGG GCTTGTNTTC GAGGGAACAG CAGAACATC CATCGTGGTT	300
TCTCACTNTT TCAGCACANT GTTGCTGTA CCCTGCAGCA GAGGGAACAA GCCACGGGGT	360
TCAAAGNCCC CCTNTTTTTT ATGGTGTICA AAGATTTNGG CCACGGTTTT TTTNTTACAA	420
GGTGGTGGGC AATCATTNTT CATGNCACAT TTCAGGAATA NGTGTGTTGGN TAAAATTAAC	480
AAGAGAATGC	490

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

GGCACGAGGT TGGGCTCCCG CTGGAGTNTG CGTTGGGGC GGACCAGGAG CGGTGGTCTC	60
NAGGGAGGTC GAGGCTGGGG CTCCCACCCG GATTTGGAGC AGGGTCGCCG CGGCCAGCT	120
GAACCCGCCG GCNTTTGTAC GTTGTGTGCC CACTCAGGGA GCCATGGACA ACTGTTGGC	180
GGCCGCAGCG CTGAATGGGG TGGACCGACG TTCCCTGCAG CGTCAGCAA GGTTGGCTCT	240
AGAAAGTGCCT GGAGAAGGGC CAAGAGGAGG GCGGTGGACT GGGCATGCCG TGGAAGCNTC	300
CCAAAGGCTG CATGGGGTC CTTGCCCGGG AAGTCCCCCA CCTAGNAGAA ACAGCCGGCA	360
NCCGGCCCGC ANCAGTTTT CCCGGGGNA AAGAGAAGAG AGACCCCCAA CCTTAGTGN	420
TTTCCTTCA GAACAATGGC TGAATTTCAT GGATTNTATT TCAATTCA NTGGGAATA	480
NTANTTCATT GTGGCC	496

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

GGCTGCTGGG TCACGGCGAT TCGCCGCCAA CGTGACCCGC TGTTACTGCCG CGACTGNTTN	60
AACGCTTAAC CGCTGCGCAT GAAATCAGGN ATATCGACCG TTTGCTGGAG GTGCTGCATG	120
GCAACGGTTA ATAAAACAAGC CATTGCAGNG GCATTGGTC GGGCAGCCGC ACACTTATGA	180
GCAACATGCA GATCTACAGC GCCAGANTGC TGACGCCCTA CTGGCAATGC TTNCACAGCG	240
TAAATACACC CACGTTACTG GACGCCGGTT NTGGANCTGG CTGGNTGAGC CGCCATTGGG	300
GNAACGTTCA CGCGCAGTGG GCG	323

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

ATGGCGATAT CGGCGCGAG ATCGNGATCC GCATCATCGA AAACGATCAG CGGTGATTAA	60
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CCGGCCAGTT CCATGGTCAC TTCTTTCAGG GAAGAGGCCG CCGAGTTAGC CATCACTTTT	120
TTGCCGCTGG NGACACCGCC GGTAAAATGA ACACTTGGC AATGCCCGGA TGCTCGGTCA	180
GATAATTGCC CCGGTNTNCG GGGCCAAGN CCNGGCAACA AGGTAAATT ANGG	234

(2) INFORMATION FOR SEQ ID NO:1314:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

CAGGAAAGAC TATGGAACGG AGCGTCANCG TGCCTTATC AATGCCGAGA ATATCCAGCC	60
ACTGCTGCAC CAGTTTTGC TGGCGATCCG AAACGGCCTG ATAAATGCCA ATCGAATCAA	120
AATAGCCAGA AAGAACACA TTACGCACGG TAGTCTGAAC CCGGTAATCC AGATGCAAAC	180
TACTGCTGAC GTAACCGATA TGCTTTTGAT TATCCCAGAT GGTTTCGCCG CTGCCGCGAC	240
GTACGTCCGA AAAAGCGTCA AATCGTTGCT GTTAACCTTG CGGATGATNC GNCAGTTAAC	300
CAGGGTTAAT AACGTGGNT TTTCCNGCA CCATTTGGC CCGACAATTN GN	352

(2) INFORMATION FOR SEQ ID NO:1315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

GGCACGAGCT GCGGCGNCAG NAGCAGCAGC AGCAGCGNGN GGNAGAGGNG GTGGCGGCCG	60
GGTGGACAGC ACGGCCGAGG CTGCCAGAG GCGCCTCCTC CACACCCCCC GCTGCGGCAG	120
CACCGGNGAA CAGATTTTT AAAAATGGA TTTGGCAAC CATGGACTTA TTCTACTGCA	180
ACAGTTAAAN GCTCAGCGAG AGTTTGGTTT CCTGTGTGAC TGCAAGGTTG CAGTCGGGGA	240
TGTATANTTC AAGGGCACAG TAGATNCAGT TACTTANCTT CATTGCTACC AATTAACCTT	300
TANNATGTTG TTTGTA	316

(2) INFORMATION FOR SEQ ID NO:1316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

TGTCACTGGT CCAGTCTCGG AAGGCAGGAA TCACTTCTGC AATGGCTACA CGCACTTCTC	60
TTAAGGACGA NGAGCTGAAA TCCCACGTNT TTAAGGAAAC CCTGCAGGCC TTAATCTACC	120
CCATTTCGTG CACCACTCCT CATAACTTTG AAGGTCTGGN NGGCCACTAC CCCAACCTAC	180
TGCTATGAAG TGTGAAGGNC CTGCTCTGG GCATTGTCCG GCAGGATGNC GCCTGCAGCG	240
AAATGTGGAG TCAAGTGCCA TGNGAAGTGC CAGGTATCTG GTTCAATGNT GGACTGNCTG	300
CCANCAGGGNT GNANATAAGA GCTGTGAAAC ATGGAGCTGA GGGACCGGT A CCCAGAACNT	360
NNNCNTGGGC CNGGAAGGNA CCGCATGGAA GATCCGAGTG GGGAAATTAAN GNCAGAGATN	420
NTTTGNAAAG TTTTCCGGG GANTNTTTTC ACAGTGGAAC AAAGTTGCC NGTGNCAGTA	480
GNTTG	485

(2) INFORMATION FOR SEQ ID NO:1317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

GGCAGAGCTC GGCNAGANAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANAAAGNNG	100

(2) INFORMATION FOR SEQ ID NO:1318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GGCANAGAGA AGGAGAAGGA GGAACCTGGAC AGGGGCTGCC GCGAGTCAA GCGCAAGGTG	60
GCCGAGTGCC AGAGGAAACT NAAGGNGCTG GAGGTGGCCG AGGGCGGCAN GGCAGAGCTG	120
GAGCGCCTGC AGGCCGAGGN CACAGCAGCT GCGCAAGGNG GAGCGGACTG GGAAGCAGAA	180
GCTGGAGGAG ATGCGCAAGA AGGAGAAGAG CATGCCCTGG NAACGTGGGA CACGCTTCAG	240

CAAAGACGGC TTTCAGCAAA GAGCATGGTT AATTACCAAG CCCGAGAAAG TACGGTAGGA	300
GGATTCAAG GAGGTTGAGG GGAGCAGAAA CACAAGACCT TTCTTGGGAA AATTACGGGT	360
AAACAGNTTC AAGCATTGTTG GGCATGTTT CGCCGTTGGG GTTGACAGCC AAAATTACCT	420
TTCAGACAAN TTCCACTTGT TTTCGAGGA GACAGCCCTT TACCTGGTCN TTTGGTGCTT	480
TGACCTAGAG TTGGAGGGAA TT	502

(2) INFORMATION FOR SEQ ID NO:1319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

GGCAGAGTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTNT TNAAAANAAA	50
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(2) INFORMATION FOR SEQ ID NO:1320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

GGCACGAGCC ATGATGACGC CCACGGGNNC TTCCAGTACG ACCATGAGGC TTTCCTGGGA	60
CGGGNAGTGG CCNAGGAATT CGACCAACTC ACCCCAGAGG AAAGCCAGGC CCGTTTGGGG	120
CGGATCGTGG ACCGCATGGN ACCGCGCGGG GGACGGCGAC GGCTGGNTGT CGCTGGCCGA	180
GCTTCGCGCG TGNGTTCGCA ACGACGCAGC AGNGCACATA CGGGNNNTCGG TGAAGCGCGG	240
CCTGGGACAC GTACGA	256

(2) INFORMATION FOR SEQ ID NO:1321:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTCATGTTCA GACCGTCGGA ACCGCACACA	60
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CCTTCACGGC AGGAGCGGCG GAANGACAGG CTGGGAATCT TTCTCTTTA GCTGGATAAG	120
CGCATCCAGC AGCATCATGT CGCGACCTTC ATCCGCTTCC AGGGTGTAAAT CCTGCATACG	180
CGGANATNCA TCCAACATCC GGTTTNATAG CGGATAAAATT GAAAACCTCGA GTCTCATTTC	240
CCTGTCTCCG NATTAGTNAA GTACGAATCT TCCGGNGGA ATGNCCGGC GCATTTNCGG	300
TTCCATGTTT GACGTTCGGN GCGTTCATGG GNTTCCGAAC TCTGGGCAGA TACAGGGNAN	360
TGGGCACANC CATTTCATCA TCATCAAGAT TCAGGGAAAGT CGA	403

(2) INFORMATION FOR SEQ ID NO:1322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTNATGTTCA GACCGTCGGA ACCGCACACA	60
CCTTCACGGC AGGAGCGGCG GAANGACAGG CTGGGATCTT TCTCTTTAG CTGGATAAGC	120
GCATCCAGCA GCATCATGTC GCGACCTTCA TCCGCTTCCA GGTTGTAAATC CTGCATACGC	180
GGANATGCAT CAACATCCGG GTTATAGCGA TAAATTNNNA AACTCGAGTC TCATTTCCCT	240
GTCTCCGCAT TAGTAAGTAC GAATCTTCGG CGGAAATGCC NGGNCGCATT TTCGGTTCCA	300
TGTGACGCT TCGGGCGTC ATGGGTTCCG ACTCTGGNCA GATAACAGGGA GTGGCACAGC	360
AGTTTCATC ATCACGTTCC GGAAGTCGAA GCGGTTNTGG CGCCAAGGTT TTTCGTANGG	420
AATTTGCAG AACAGCNTTG CNTAGGCGTT TCCNTCAGTT ATCCATTCCA G	471

(2) INFORMATION FOR SEQ ID NO:1323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

GGCANANAGA AAGATCCACG ACTTGGCCCT GGAGCTCTAC ACGCAGAGAT CGCTGCTGGT	60
GATGGGGCGG GGCTACAACG ACGCCACCTG CCTGGTAAGN AGCCCTGAAA ATTAAAGAGA	120
TAACCTACAT GCACTCAGAA GGCATCCTGG CTGGGGAGCT GAAGCACGGG CCCCTGGCAC	180
TGAATTGACA AGCAGATGCC CGTTNATCAT GGTCATTATG AAGGATCCTT GCTTCGNCAA	240

ATGCCAGAAC	GCCCTGCAGC	AAGTTNACGG	CCCGCCAGTG	GNCCCCATT	TNTACTGTGG	300
NTCCAAGGGA	CGATNATTGA	AAGTTTCCCA	AGTTTGCAGTA	TTAAGNCAAT	TCGAGGTTGC	360
CCCCCACATTG	TGGGAANTGC	CTTCCNGGGG	ATTCTGAGGC	GTTGATTCC	GTTGCNATTG	420
NTGTTCCCTT						429

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

GGCACGAGCN	CGCGTGGNTC	GCGCACACGC	AGCAGCGGCA	CATAACGGAC	TCGGTGAGCN	60
CGGCCTGGGA	CACGTACGAC	ACGGACCGCG	ACGGCGTNT	GGNTTGGGAG	GAGCTGCGCA	120
ACGCCACCTA	TGGCCACTAC	GCGACCGGTG	AAGANTTTCA	TGACGTGGAG	GATGCAGAGA	180
CCTACAAAAAA	GATGCTGGCT	CGGGACGAGC	GGCGTTCCG	GGTGGCCGAC	CAGGATGGGG	240
ACTCGATGGC	CACTCGAGAG	GAGCTGACAG	CCTTCCTGTA	CCCCGAGGAG	TTCCCTCACA	300
TGCGGGACAT	CGTGATTNCT	GAAACCCTGG	AGGTCTGGGA	CAGAAACAAA	GATGGCTATN	360
TCCAGGTGGA	GGNGTACATC	GCGGATCTGT	ACTCAGCCGA	GCCTGGGGAG	GAGGAGCCGG	420
CGTGGGTTCA	GACGGAGAGG	CAGCANTTNC	GGGACTTNCG	GGATCTGAAC	AAGGGTTNGG	480
CACCTTGATT	GGGA					494

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

GGCANAGCGG	CAGANCANCC	ACACAGAGAT	GGAACATGAA	GTGGCTTGCT	TTGGACATCA	60
CCCCATTAGG	TAGACAGCAA	TGGACTGTG	CCTCTTGTN	CCATTGGCCT	CTGGGACGGT	120
ACATCTCGNN	CTCGTGATCT	TGAAAGTTGC	CCTNTTTTGN			160

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

GGCANAGGCA AGAGTGTGCGT GAACAGGNTC GGCTGCTTGG CTTGCTGATG CCATTAGGG	60
CATTTNGTGG TGTAAAGTTC AAATGGAGCA TTGACCTTCA AAAGNGAGTG ATAGAATCTG	120
GCCCCAGACCA GTTGGAAATGA CAATGAGATA TACCAAGTTT ATTCCCTCCTG AATTATCACA	180
CACCTCCTTA TCTCACTGGC TGAGGCANAG GTAACATTACC ACCGATTGAA GGCCACAGGA	240
TGAAGTTCT GGTGTTGGCT ACTGGATGGG TTGTGGGAGA CTGATGTCAN GGGCCAGGNT	300
GTGGTTAGGA TTNTGGGTGA GTACCTAACT GGGCATGGNA TNC	343

(2) INFORMATION FOR SEQ ID NO:1327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

ACGAGCAGGC TATTCTTGG AGAAGGTATT TGGGCTTCAA TTNAAGGAAA TTGATAAGAA	60
TGNCCANTNT TACANTCTTA TCAGCACCTT AGAGCCCACT TATGTCAGGN CATTCTCGGA	120
ACGNNTCAAG GTACTCACCC AAGCTGGGTC TGCTCATGGT GGCTTGCTTA AGCATCATCT	180
TCATGANNTG GTAAATCGGT CCNGTGGAGN CTGTCATGTG NGGAG	225

(2) INFORMATION FOR SEQ ID NO:1328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

GGCAGAGACT GACCACAGCC CATGAGCAGT TCAAGGCCAC CCTCCCTGAA TGCCGACAAG	60
GAGCGCCTGG CCATCCTGGG CATCCACAAT GAAGGTGTCC AAGAATTGTT TAGACCTACC	120
ACGTGCAATA TGGCGGGCAC CAACCCCTNA CACAACCATC ACGCCTCAGG AGATCAATGG	180
CAAATGGGNA CCACGTGCGG CACTNGTGCC TCGGNAGGGA CCAAGCTCTN ACGGAGGAGC	240

ATGCCGNCA G

251

(2) INFORMATION FOR SEQ ID NO:1329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

GGGNGAATT	CAACAGNCAA	CAAAAGAAC	TTTCAGTGAG	CNGTGCNGCT	GCTTCTNTGG	60
CCAGTTCACG	CTCTTCTGTA	TTGAAAGACT	CGGAATATGG	NTGTTGAAG	TTTCCACCAA	120
GATGTANGTT	TGATCATCCA	GATGCAGATA	AAACACTGAA	TCACCTTATA	TCGGGGTTG	180
AAAANTTGA	AAAGNAAATC	AACTACAGAT	TCAAGANTAA	GGCTTACCN	CTCCAGGCTT	240
TTACACATGC	CTCCTACCAC	TTACAATACT	NTCACTGNAT	TGGTTNACCA	GCGCTTAGT	300
AATTCTGGG	TNGATGCGAT	TT				322

(2) INFORMATION FOR SEQ ID NO:1330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

AGTTGTTCCG	AGGTGACACA	GTGTTGCTGA	ANGGAAAGAA	GAGACGAGAA	GCTGTTGCA	60
TCGTCCTTTC	TGATGATACT	TGTNCTGNAT	GAGAAGATT	GGAATGAATA	GAGTTGTTCG	120
GGAAATAACCT	TCGTGTACGC	NTAGGGGATG	TCATCAGCAT	CCAGCCATGC	CCTGATGTGA	180
AAGTACGGCA	AACGTATCCA	TGTGCTGCC	ATTGATGGAC	ACAGTGGTAA	GGGCATTACT	240
GGTAAATCTT	CTTNCGAGGT	TATTACCTT	AAGCCGTNAC	TTTCCTGGGA	AGCGTTATCC	300
GACCCCATCC	GGNAAAAGGN	GACCATTTT	TCTTNGT			337

(2) INFORMATION FOR SEQ ID NO:1331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

TGCAACAAAT GGTTTATAAC CTGCCGCCAG ACATTACGCT GGTGAAAGCC ANAGTCTTGC	60
TGATATGAAN CCGCAGTGNA TAACTTCTAC ACCGCCGAAA AACGCTGTGC CTGAATGCAC	120
CGCGTAATCC GTTCCGTGGC GTGAAAGCTG TGCAAACCGA NTAAACCGAT AGAACCTGTT	180
TATGCTAATC GCTTCTTTGA ANGTATTAAG CGAAAAGCAT TCAGCCAGAG CACGCTGATG	240
CGTTTACTTT CCAGCATCAG TGGGCAAGGC TGGGGCAAN CAGCCCGANG CGGCGGAAGT	300
TTTANCGGTT AGCGCCAANT TAAAAGGC GT TACGGTAAT GGGATTGTT CGGGACCN	358

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

GGCAGAGCAA CCACGGTGTC GCAGGCCAAG GNAGTNCTGA GCGCCGAGCA GCTGCCAAGC	60
GAGGAGGTGC ACGCCGGCCT GGGCGAANCT GCTGTCTCA CTCAGCAACT TGACGGCNCG	120
CAACGTGAAC CTGGATGCTG GGCAGCCGAC TGTTNCGGGA CCCAGCTCAN TAAGCTTCG	180
CTAATGAACT TCNTGNG	197

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

CNTGGTNAAC CTGCTCCATN AAACAGGTCC GTNAAAATNT TTAATGTGCG CAATGGAAGG	60
GCAGATCCTT ATCGCCGACC TCAGGGGTCA TGAAGGGTCC TGTTTGGCAA GTGGCCTGGG	120
CTCACCCCAT GTTACGGCAA CATCCTGGCA TCGTGCTCCT NTGAACCGGA AATCATTATN	180
TGGAGANAGG AAAACGGCAC TGGGAAGAAG AGCCACGAGC NGGGGGGACA CGANTCCTTC	240
ATTGAAANTC GGTGTGCTTG GG	262

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

CTCTGGAAGC ATTACTTCCA GANTNNCCCA GGGTCTTATT TTTTTGGTAG ATAGAACGA	60
TCGTNAAAAN TTTCAGGAAG TAGCAGATGA CCTGCAGAAA ATGCCTCTG GTAGGTGNAT	120
TTGAGNAGAT GGCAGTCCTG CTGACTTTT NCAAACAAAC AGGNTTGNC CAAATGCTAT	180
GGCCATCAGT GGAAATG	197

(2) INFORMATION FOR SEQ ID NO:1335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

GGCACAGGNA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANNANN	57
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(2) INFORMATION FOR SEQ ID NO:1336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

GGCCCCGTCC CGCCGCCCGC CCGCCAGCCA TGAGCTCGAC GCAGTTCAAC AAGGGCCCCT	60
CGTACGGGCT GTCGGCCGAG GTCAAGAACCC GGCTCCTGTC CAAATATGAC CCCCAGAAGG	120
AGGCAGAGCT CCGCACCTGG NTCGAGGGAC TCACCCGCCT CTCCCATCGGC CCCGACTTCC	180
AGAAGGGCCT GAAGGATGGT AACTATCTTA TGCACACTGC ATGGAACAAG CTACAGCCGG	240
GGTCCGTCCC CAAGATTCAAC CCGGTACCAT GTCAGNAACT GGTCACCAGC TTAGTAAAAC	300
CTGTNCCAAC TTTCATTCAC GGNCCATGGT GCAGGTTGGG GGATGNAACC CTGTGGAACC	360
TGTTTCNAGG NCCAAGAAC	379

(2) INFORMATION FOR SEQ ID NO:1337:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

GGCACGAGGA CCCGAGTTCA CCAGCATCCC TGCCTGCTAC TGGTGGGCTG TNATCACCAT	60
GACGACGGTG GGCTATGGCG ACATGGTCCC CAGGAGCACC CCGGGACAGG TAGTGGCCCT	120
GAAGCAGCAT ACTGAGCGGC ATCCTGCTCA TGGNCTTCCC AGTCACCTCC ATCTTCCACA	180
CCTTCTCCCG CTCCTACCTG GAGCTTCAAG CAGGAGCAAG AGAGGGTGAT GTTCCGGAGG	240
GCGCATTCCCT CATCAAAACC AAGTNCGCAG CTGAGCGTGT CCCAGGGACA GTNAACATCT	300
TGTTACGGAA GTGACCTNCT NCGGNACACC AG	332

(2) INFORMATION FOR SEQ ID NO:1338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

GGCAGAGCCA GTNTCCGCGC CTCCACCCAG CTCAGGAACC CGGGAAACCC TCTNTTGACC	60
ACTATGAAGC CTCCCCTCCA GCCGCGCGTC CCGTGTCCCCG GGTCTTCTGG GCTCCTTGTG	120
CGCGCTGCTC GGCTGNCTGC TCCTGCTGAC GCCGCCGGGG CCCCTCGCCA GCGNCTGGTC	180
CTGTCTCTGC TGTGCTGACA GAGCTGCGTT GCACTTGTTT ACGCGTTACG CTGAGAGTAA	240
AACCCCAAAA CGATTGGTAA AACTGCAGGT GTTTCCCCGC AGNCCCCGCA NTGCTTCAA	300
GGTGGGAAGT GGTTAGCCTT CCCTGAAGAA CGGGGAAGCA AGTTTGTTTT GGACCCGGAA	360
GNCCCTTTTT TTTAAAGGAA AGTGCATNCC AGNAAATT TTGGACAATT GGNAACAAAG	420
AAAAAATTGG GTNAACCAAA AAAGG	445

(2) INFORMATION FOR SEQ ID NO:1339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

GGCAGAGGGN AGCTCTTGGG GAGCCCGGAA AGCAGGGATC TCGGGGAGAC CCNGTGAATN	60
CAGGACCCCN TGGAGACTCT GGTACAGCCA GGCCCCAAGG GNAGACCCCG GNCAGGCCTG	120
GTTTCANCTT ACCCAGGACC CCGAGGNNGCA CCCGGTAGAA AAAGGCGGAG CCCGGTNCCA	180
CGNNGCCCCG AGGGAAAGGCC NAGGCGAACT TTGGTTTGAA AGGAGAACCT GGGTAGGTAA	240
AGGAGAGAAA GGTAGAGCCT NCGGTATTCC TGTTCCCCC TGTTGNAGCC AGTTACCTTC	300
GGGGGGGCCA AGTAGGTAGT TCCCANGGAC CTCGNAGN	338

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

GGCANAGTGA ACGCCCACCT GCCGTTTGCT GTCATTGGCA GCACAGAAGA ACTGNAGATA	60
GGCAACAAGA TGATGAGGGC GCGGCAGTAT CCTTGGGGCA CTGTGCAGGT TGAAAACGAA	120
GGCCCACGN GAACTTNTG AAAGCTGCGG GAGAATGCTG ATTGGGTCA ACATGGGAGG	180
ATCTGCGGGA GCAACTCCAC ACCCGGGCAC TATGNAGCTG TATGCCGCT GTANCTGGNA	240
GGAGATGGGC TTCAAGGACA CCGACCCCTGG ACAGCAAACC CTTCAGTTA CAGGTGGACA	300
TATGNAGGCC AAAAGGAACG AGTTCTAGG GGGAAANTCCC AGNAAAAAAG AAGAGGNGAT	360
GNNGACAGTT GTTCGTTCCA GCGAGTTCAA AGNGGAAAGG AAGCGGGTTT CCAAAGG	417

(2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GGCANAGNAA ACACCCCCAT ATCAAAATGG TGATGGAAAG TGGGGACTGG ACTGGTTGGT	60
GGAGACCTTN AGGTGCTGGA GAAAATAAGA TGGAATGATG GGCTGGACCA ATACCNTCTG	120
AACACCTCTG GAGCTCNAAC AGAAATGTGA AAGGAAATGT AATNCTGATN CGGTGTTGCG	180
ATTCCAGTTG CGCAATCCTG TCCACAATGG CCATGNCCCTT TTTGAATGCA TGACACTCGT	240
CGNAGTTCNC TNAGTAGAGG GGGCTACAAN CACCCGGTT	279

(2) INFORMATION FOR SEQ ID NO:1342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

GGCANGAGGG ACAGCTAGCC CTGCTGCCCG GCTCCACTGT GCTTCTGCC	TTGGCCTGGG 60
CTGCTACGTG GCTGCCGCTG ACATCCAGGA CCTGGTCTCT TGCCCTGCCT	GCTTAGAAAG 120
TGTTTCAGC CGGTTCTATG GCTTGGGGGG CAGCTCCACA AGTCCTGTGG TTCCCTGCCAG	180
CCTGCACGGC CTGCTCTCTG CTGCCCTGCA GGCTGGGNA TTGCTGCTCA CCATCTGCC	240
TAGCACCCAA ATGNAGCCAC ATCCTTGACA GGCAGCTGNC CCGGCTGCC CAGNTNCTTG	300
TGCCAGTGGA AAGTNTGAAC CTGCGGATNG TTGCCGGTGN AAACATTGGC ACTGCTCTTT	360
GAAGCTTGCC CGGAAACCTN GAGGAGGGAT TTGTTTTAG GAGGACATGG AGGNCCTTG	420
CAATGTTCTG GGGAAATTGG GCCATTGANA NTAACAATAC CTTGNCAAGG TTGATTGTT	480
GGGGGCAAGG TTNTA	495

(2) INFORMATION FOR SEQ ID NO:1343:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

GGCAGAGGGC TCTGTCATTG ATTATNAACT GATTGACCAA GATGCTCGGG AATCTCTATG	60
AACGCTGGAG TGAAGAGGAA AGGAACGTGAN TGTTCCAAG TGGATCAGCA TCATGAACCG	120
ANCGGANGGN CCCCACCTCC AGAAAGTATT TGAATAGGTA CAAGAGTTAC AGCCCTTATG	180
AACATGTTGG GAAAGCATCA GGGAAAGAGG TTAAAGGAGA CCTGGGAAA TGCTTCCTG	240
AACCTGGTTC ATGGCATTCC AGAACAAAGCC CCTGTGNTTT GCTGATCGGC TGTATGACTC	300
CATGGAAGGG NCAAGGGGAC GCGAGATTAA GGTCCNTGAT TCAGAATTCA TGGTCTTCCC	360
GCATTGAAGT TGGNCCTGTT TGGAAATTAA GGTCTGGATT TCAAGGGNAA GTANGGGCAA	420
TTCCCTGTAC TTTTATNTTC CNGCAAGGCA	450

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

GGCANAGCCC CTTTNTTGAA GCCAAAGAAG AGTTGCTCA TAAGACCCTG GCAATGGATG	60
TNATGAAACC CGGGAGAAAT GATCCTTGT TGACTGTCCT TACTCAGGAG AGTTATGTAC	120
TGTGGNAAGA TGTAGAGACC ATAATCAGTG GAACCACTTA CAGTGGCTTC CCAGTGGTGG	180
TATCCCGGGN AGTCCCAAAG ACTTGTGGC TTTGT CCTCC GAAGAGATCT CATTGATTTC	240
AATTGGAAAA TGCTCGAAAG AAACAGGGTG GGGTTGTTAG CACTTCCATC ATTTATTTTC	300
ACGGGGCATT CTCCTCCATT GCCACCATAAC AATNCACCCA TTNTAAAGNT TTGGGAANAT	360
NCTCGG	366

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

GGCAGAGTAA AAGCAGACAA CCAGAGGCTA AAGGNTGAAA ATGGGGCCTT GATCAGAGTT	60
ATAAGCAAAC TTTCCAAATA AAAAAAAAAA AAGCAGCANG NAATGGTGT GCACATATTA	120
GTAACCCAGT GGAACCATAN TTNGTN	146

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

GGCAGAGCNA GGNGCCAGTC GTGTGAGTCC AATCCTAACCC TGGGCTATCC CTGCAATCAT	60
GTCATGCTCT CCTGCTGTGA AGGGTGAAGA GCCTCTCATA GTACCTGAAG GTTCGCCGAC	120
CTCCAGAGNC CGCAGNTGCA CCACGGAGAG TTTCAGAGGC AGAGATGGCG GGCCGAGAGC	180

TCGNTTCACT GGGCACAGAG GCCGAGCTGC CGAACAGNCT GCCGGGCGAT GTACCAGGAT	240
GAGTGCCTTC TCCTNCCGGG GNGAGCTGTG CCAGCACCTT TGGCATCAAT AATTGTGGGT	300
TTTTTACCAT GTGGCTGGTT TTTCTGGGT TTTCAATGG CAGNACGNTG GGCGCAATT	360
NTNCGNCCA	369

(2) INFORMATION FOR SEQ ID NO:1347:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

GGCAGAGGNA GGGGAGGCTC CAGCCCTCGG NAGTAAATAT CTTCCCTTCC AACCTGGTGT	60
CAGCAGCCTT TCGCTCATAC TCTACCACCT ATGAAAGAGA GGAATATCAC CGGAACCAGG	120
GTGAAGGTGC CCGTGGGCA GGAAGGTGGA GGGGATGAAC ATCCTGGGCC TTGGTAGTGT	180
TTGCNATCGT CTTTGGTGTG GCGCTGCGGA ACTGGGGGCC TGAAGGGAA GCTGTTNTC	240
CGCTTNTNA ACTCCTTTNA ATGAGGCCAC CATGGTCTG GTCTCCTGGA TCATGTGGTA	300
CGNCCCTGTG GGCATNCATG TTTCTGGTGG CTGGCAAAT TCTGGAGATG GAGGATGTGG	360
GTTNATCTT TGCCCCCCTT GGNAATAACA TTTGTGCTGC CGTTGGTNAA GGCATCCNGG	420
GNATCC	425

(2) INFORMATION FOR SEQ ID NO:1348:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

GGCACGAGTG GAGGCCTTAACTTTAACGA GTACCAGCCA GAAATGCTCG AAAAGTTCCG	60
GAACATGCNC NGCAGCACCC CTACGTCTC ACGGAGGACA CCCTGAAAGG TCTACCTGAA	120
NCAAGTTCAAG ACAGTCCTCG CCGGACAGNG TGAAAGGTGG TCATTNNATT TTNCTGNTGG	180
AGCAGACGGA GAATCTGGCT GATTTACACA GNNGCATCTG AGAAACCTCC GCCAAGAAAG	240
GAGTCCGTGC CCTTGAATCC TGGTGGGCCT TGAAACGANN TGGTTCAACT TGGAAGCGGC	300
TTAATGCATC TGGNGTTGG GNGAGGGTTT ATGTNTGA	338

(2) INFORMATION FOR SEQ ID NO:1349:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAACCCACTN AGGNGACACC AATCTTNGAC TTCCAGATGG AACATGACAT CNATAAAAAG	60
GNAAAGTGAT GGCATCTATA TCATAAATCT CAAAAGGACC GGGAGAAGNT TCTGCTGGNC	120
AGC	123

(2) INFORMATION FOR SEQ ID NO:1350:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GGCANAGCCT GGNTTAAANG GACACAATAG ATTTCAAGGT CTACCTGGTA TCGCTGGTCA	60
CCATGGNGAT TTATGGTGCT NGTGGTTCCG TGGGA	95

(2) INFORMATION FOR SEQ ID NO:1351:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

GATACTCTAA CCGTTTAGT AGTCGCAGCC TCGAAATGAT AGACGAAATG CTCCACCTGT	60
AAGANCAGAA AATCGTCTTA TAGTTGAGAA ATTTATCCTC AAGAGTCAGC TGGGCAGGTT	120
TGTTGAAATA CAGTTTGAA GTTATTTGN ATGTGGCTTT TTAAAAAAAGT TTANTGGGTA	180
GCTCAATGTT GTATTGTTTT ATTAAANGTA GTTTGAANT TAATGGGTTT NATGGG	236

(2) INFORMATION FOR SEQ ID NO:1352:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

GGNACGAGGT CTGGCTCCCG TCCCCGCAAG CAACCACCCC GGAAGCACAC TCGTNCCTGG	60
NCTGTCCTGA AGCTGCTGCT GCTGCTGCTG CNATTGGTG TGGCGGGAGG GCTGGTTGCT	120
TGTGGGTGA NAAAGCTGCA GCAGCACCCC CTCTGCNACC AGCNTGAAAC ACCATCTTAT	180
GAANAATGNG GGTCCAGGGT CTACGCCGCC ATNAGATTCC TCCAGTGGGT CCTCCAAACC	240
GAA	243

(2) INFORMATION FOR SEQ ID NO:1353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

AAGGAACCTC TGAGAAACTT AAGGTTGACA GNTNTNTCCA GCCCTNNACC TGCCTAGTCC	60
TGGGCCCTGG CCCTTTTTTG TGGTGAAGGG TCTGCTGTGC ACCATCCCCC ATNCCTAACG	120
TGGGCCACC TGGCCTACAA ATTCGGGGT GAGNGGTGTT TAAGNCAGGT GGCGGAGGGT	180
TTCCAAGGGA CCGAAANGTG GTTTTTCAA CCNTNTG	217

(2) INFORMATION FOR SEQ ID NO:1354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

GGCACGAGCG GACCTTCATC ACCATTGGAG ACAGAAACTT TGAGGTGGAG GCTGGTGACT	60
TGGTGACCAT CTCAGAACTG GGCGTGGAG CCTATGGGT GGTAGAGAAG GTGCGGCAGG	120
CCAGAGCGGG CACCATCATG GNCGTGAAA GCGGATTCCG GGCCACCGTG NAACTCACAG	180
GAGCAGAAGC GGCTGCTTCA TGGGACCTGG NACATCAACA TGCGCACGGT TCGGACTGTT	240
TTCTAACACT GNTCACCTTC TNACGGGTC ACTTATTCA GAGAAGGGTG GACGTGTGGG	300
ATCTNNCATG GNAGCTTCAT G	321

(2) INFORMATION FOR SEQ ID NO:1355:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

CGGTTGCGCA ATGGGNGAAT ACTTCCGTGA CCGCGGTGGA AGATGCGCTG GATCATTAC	60
GATGACCTGT CTAAACAGGC TGTTGCTTAC CGTCAGATCT CCCTGCTGCT CCGTCGTCCG	120
CCAGNNNGAGA GAGGGATTCC CGGGNCGAAC GTTTCTACC TCCACTCTCG TCTGCTGGAG	180
CGTGCTGCAC GTGTTAANCC GGAATACGTT GAAGCCTTCA CCAAAGGNAG ATGGGAAAGG	240
GGAAAACCGG TTCTNTGNAC CGCACTGCCG ATTATCCGAG ACTCAGGCAG GTGACGTTTC	300
TGCCTTCGTT TCCGACCAAC GTAAATCTTC CATTANCGAT GGTCAGANC TTNCTGGAA	360
ANCAAACGTG TTCAAGGCCG TTATTCGTC CTGNNGTTA ACCCGGTTAT TTTCCGTATN	420
CCGTGTTGG TGGGTGCAAG NAAAGNCCA GGTCATGGA AAAAAATGTT CCGNGGGTAT	480
TCCGTA	486

(2) INFORMATION FOR SEQ ID NO:1356:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

GGCANAGGGA TACACTCCCT TGATGGAAGC TGCCCCGGAA GGACATGAAG AAATGGTGGC	60
ACTACTCTTA GCACAAGGAG CAAATATAAA TCCCCAGACA GAAGAAACTC AAGAAACTCC	120
TCTTACTTTG GCTTGCTGTG GAGGATTTCG TGGAAGTTGC AGACTTTCTT ATTAAGGCAG	180
GGGCTGATAT AGANCTTGGC TGCTCCACAC CTCTGNATGG AGGCATCTCA GGAGGGACAC	240
CTGGGAATTG GTTAAATATT TCCTGGCTTC TGGCGCTAAA TGTGCCATGG TNACAAACAGC	300
AACAGGGGGA CACAGCCTTN AACCTATGCT TGTGAAAAT GGGACATACG GATGTTGCAG	360
ATGTTTTACT TCAAGCAGGG GTTGNTTTA GACAAGCAGG NGGGNCATGA AGACTATTT	420
GGAGGGCNAG ATCCGGCCAG NTCAGTG	447

(2) INFORMATION FOR SEQ ID NO:1357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

GGCACGAGCT CAACTCAGCA GGCAAGATGG ACAAAATGAG GTTATTGAAC ATCCTAATGC	60
AGTTGNGAAA ATGTTGTAAT CATCCATATC TCTTTGAATG GAGCAGAACCC TGGTCCACCT	120
TATACAAACAG ATATGNCATC TAGTAACCAA CAGTGGCAA AATGGTGGTT TTAGACAAGC	180
TGCTCCCTAA GTTAAAAGAA CAAGGTTCAC GAGTACTNAA TCTTNAGTGC AAATGACAAG	240
GGTATTGGGA CATTGGAA GTTATTGGC ATGTGGNGA ATTNTGAGT ACTGCCAGGT	300
TGGGATGGTT CAGACANCCC ATGATGNGGA GNCAAGACTC CTTCAATGCC TTACAATGG	359

(2) INFORMATION FOR SEQ ID NO:1358:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

AAATCCCTGN CCAGAACAC CATTGTAAAC ACGGCAAGTT TGGCAAGTTG GGNTGNGAA	60
CAACACCCCC ATGTGGCGTT TNCCCAGGAC CCCACCANTT G	101

(2) INFORMATION FOR SEQ ID NO:1359:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

ACGTGAAAGC ACCGTAAAGC CGCTGCCNNCC NCGCCGTTGG AATTTCCCTG AGGGGCAGGN	60
TACATCAAGG GCATCGTNAA GNACATCATC CAGAACCCGG GCCG	104

(2) INFORMATION FOR SEQ ID NO:1360:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

AGCGCGGCCG	GCCGGGNCT	TCGTGGCGGG	GCTTGGNAAG	GTGCGGCCCT	ACTCCGTCTA	60
CCTCTTCAGC	TTCTCCATGT	TCTTNAACGG	CCTCGCGGAC	CTGGCGGGCT	CTACGGCGGG	120
CAACTACGGC	GGCCTCGTGG	TCTTCTGCAT	CTTCTTGGC	ATCTCCTACG	GCATGGTGGG	180
GGCCCTGCAG	TTCGAGGTGC	TCATGGCCAT	CGTGGGCACC	CACAAGTTCT	CCAGTGCCAT	240
TGGGCTGGTG	CTGCTGATGG	AGGCGGTGGG	CCGTGNTNCG	TCGGGCCCCC	TTTCGGNAGG	300
TAAAATTCCCT	TGGATGCAAC	CCAAGTTTA	CANGTAAGTN	TTTCAATCTT	GGCGGGGGG	359

(2) INFORMATION FOR SEQ ID NO:1361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

GGCAGAGCCC	NNNGGGCAAG	AAGTGGCAGG	NGGAGCACCT	TATTTGTCCC	AANTGTAAGT	60
AGCCATTC						68

(2) INFORMATION FOR SEQ ID NO:1362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

TGCANAGGTC	CAGGGCCCTA	GCTGTGACCG	CTGTGCCCCC	AACTNCTGGA	ACCTCACCAG	60
TGGCCATGGT	TGCCAGCCTT	GTGCCTGCCA	CCCAAGCCGG	GCCAGAGGCC	ATCCTGCAAC	120
GAAGTTCACCA	GGGCAGTGCC	ACTGCGGTGC	CCGGCTTTG	GAGGGNGGAC	TTGTTCTGAA	180
GTGCCAAGAA	GCTCCACTGG	GGAGACCCCTG	GGTTGCAGTG	CCATGCCTGT	GAATTGTGAA	240
CTCTGGTGGG	AATTAGGATA	ACACCTTCAG	TNTGNAACCG	NTTTCACAGG	TTCAATGN	300
A						301

(2) INFORMATION FOR SEQ ID NO:1363:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GGCACAGCTT GCCTGCCCTG TGTGTAAAAA TGGGGTCCC TTACTAACAT TATCAAGGGN	60
GNAGGCANGA CTGGGACGGC TAGTCANNAG GAAGACCTGG CACCACTGTC G	111

(2) INFORMATION FOR SEQ ID NO:1364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

GGCACGAGGT TTTTTTTTTT TTTTTTTTT TNAAAAAAA NAANCCCTTT TTTNAANG	58
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(2) INFORMATION FOR SEQ ID NO:1365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

NAGCTTGCTG ATGAAACAA CATTGGAAA TACAGATCTG CAGGAGCATG TACAGCTGCA	60
GCATTCCTGA AGAATTTCGT AACTNATCCT AAGTGGGCAC ATTAGACAT AGCAGGCGTG	120
AATGACCAAC AAAGAATGAA AGTCCCTAT CTACGGAAAG GCCATGANTG GGAAGGCCA	180
CAAGGACTCT NATTGAGTTC TTACTTCGTT TCAGTCCAAG ACAATGCTTA GTTCCGATTA	240
CTCCAAAATG TCTTCACTCT GTNTTAAATT GGNCAGTTGA CTTAAAGGTT TTTGATTAAN	300
TGGGTTGGAA ATTTTTTAA CGGGGGCAA GGGTTGGTT TTTAAAATT TGGGGCCCCC	360
ATGAAATTGG TTGCCCGAT TTTTTTTTN CCATTTNCCC CCCGGTTTT TAANGNAAN	420
GTAAATTC	428

(2) INFORMATION FOR SEQ ID NO:1366:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

GGACTTTGC CGTCAGNTGA AAAGTGTGAT TATTACTTTA GTGTGGATGC AGATNTTGTT	60
TTGACAAATC CAAGGACTTT AAAAATTTTN ATTGANAAA ACAGAAAGAT CATTGCTCCT	120
CTTGTAACTC GTCATGGAAA GCTGTGGTCC AATTTCTGGG GAGCATTGAG TCCTGATGGT	180
TACTATGCAC GATCTGAAGA TTATGTGGNT ATTGTTCAAG GGAATAGAGT AGGAGTATGG	240
GAATGTGCCCT ATGTTATGGG CTNAATGTGT ACTTGAATTG ANNGGAAAGA CACTNCNTT	300
CAGAGGTGA	309

(2) INFORMATION FOR SEQ ID NO:1367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

TGACCGANAA NGGACAAGTC GTGTCCCCCG TGTGCCGTCA GACTANGGAC CCGGGTGCAG	60
AATCGGCANA GGTGGGGTT CCTGNTCAAC AGTGCTTGGA CGGACCCGCG TCGTCCCCAC	120
CCCGGCCGCC GCCATAGCAG CTCCGNACCT CTTCACCGAC CCTCGGCTGC CCAAGCCCCG	180
NGCGTCCAGG NCGCGANNAC CGCGCGCGCG CTCTCTTAGT CGCGCATGAC GCCGCGCCAC	240
CTCGCAGTGC GCAGAACTAC CACCAGACTC ANAGGCGCAT CACCGCAGAT CAACCTNGAG	300
TCTACGNTCT ACGTTACTGT CATGTNTACT ACTTAACGGA TGATGTGCTT GAGACTTGCA	360
ATANTTCTCA CATCTATGAG AGAGGACATC TAGAACTGTG AGTNAGACCA CGAGTGNCGA	420
TCTCTTCAGN TACAGAACAG CTGTATGCTG GAGGGGGTGA TGATGAGTTG ATAATTGAAA	480
ATGTATNANC ANTATGACTG AAAC	504

(2) INFORMATION FOR SEQ ID NO:1368:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

CCNAGGTCA TCTGAATTNG ATGCGCTACA NGCAGACGGT TGGNCATCTG GTCCNTGGC	60
TGCATCATGG CGGAGATGTT CACAGGCAAG ACGCTGTTCA AGGGGCAGTG AANCACCTGN	120
AACCAGGTGN AAGGT	135

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

TAAAGCTCNT CACAGTTTA CAGCAGAGAC CAGTNATGAC TTATCATTCA ANAGGGGNGA	60
CCGGATCCAA ATTCTGGAAC GTCTGGATTG TAACTGGTGC AGGGGCAGAC TGCAGGTACA	120
GGGAGGGGAT CTTCCCAGCA GTGTTTGTGA AGGCCCTGCC CAGCTGAGGC AAAAAGTATG	180
TTGCCATAG TTACCGAAGG GNTTGAAAGG CCAAAGCCTT ATATGAATTG CCGAGGGGNG	240
ANTGANGATG GAACTTTCC TTTCAAGGGC TTGGGGGNTG	280

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

AGGGATGANT TGTTTACCTC TAAAATCTT AAACTGGAGC TGCAGAACGT NCCTCGCCAC	60
GCNAGCTTCA GCAACGTCCG GCGCTTCCTG GGCGCTTTG GTCTGCAGCC CCACAAAACC	120
AAACTCTTIG GGGCAACCAC CCTGTGNCCCT TTTTGAACAT TCCGCAGGGC TGCAGAGAAG	180
GGACAAGGCC CTGCGNCGTT TTGCATGGTG CCCTCTGGAA AGGCNGCCA CTCAGTGTGC	240
GCCTGGCCCG GCCCAAGGCG GACCCCATGG CCAGGNGGAG GCGACAGGNG GGTGAAAAGT	300
NAAGCCACCA GTAACACGAG TGNGACGACG TGGGTGAACC CTTCCCTGGG NCA	353

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

AGCGGCGCGT	GCCCAGCAAN	TTNCAGCGCC	CGCGGCTCGT	GAAGCAATAT	GTTCTTCGTT	60
AAGGATGTGC	TCAAGCTGAT	GGCGAATTTC	CTCGANATCC	AGCGCCTTGA	GATGAAATTN	120
CAGACAGCGT	GACAAAATCN	TCACCGGCAA	TTTCTNTGGA	TCGGTCGTG	CCAGCAGAAA	180
CTTAACGTGC	TCCGGCGGCT	CTTCAAGGGT	TTTTAACAGT	GCCGTTAAAG	CTGTGGCGCG	240
GACACATGAT	GCACCTCGTC	GATNCAGATA	AACTTGAAA	CGACCACGCG	CCGGAGCGTA	300
ACTGGGACGT	TTATCCAGCA	GGTCGCGGG	TTTCTTCAA	CTTGGTGCG	CGAGGCGGCG	360
TCGATTTCA	ATCCAGATCG	ACAAAGCGGC	CCCTGCTTCG	TTTCACGAC	ATTATTCGNA	420
CAAGTCGNA	GNNGTCGNNGG	TNAATGCCCG	TTTT			454

(2) INFORMATION FOR SEQ ID NO:1372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

CCCAAGGNGC	TCCAGGTNTG	GTGCAAGGAN	TACCGCCNCG	ATAGTGGAGA	GGAGGCCGTA	60
ACCCTTGAG	AAGACTTGGA	AGCTTAATT	ATCAGGACAA	CAGGTCCCAG	GTCAAGTNCA	120
TGGACCTNAA	ATGCTCGNAA	GGGGGATGGT	GCCTCTGGAT	CCATTCAGG	AGTCCTCNAG	180
CTTAAACCTT	CATCACGAAG	GCCACCCAGT	CCCACTTCAA	ACATTCGTT	CGGAAAACCC	240
CGCCTTTAA	CAGTNACNA	GCTCTTGCCT	GCTTGGCCAC	ATNCCTGCAC	CCCNGCATGA	300
AGGGTANTTC	CCAGAGAAC	AGGCAGATGGG	CATTGCCANT	ATTCACAGC	GGATTCCCCA	360
GGCATGGTGG	AAGATCGAGG	ACNGGCTGTT	NTCCTCANTC	TGGAGGAATG	GGGATTNAAG	420
ANTTGGGTT	GGAGGNATT	TCATAGGGGN	CAACAGGCAG	AGATTA		466

(2) INFORMATION FOR SEQ ID NO:1373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

AAAAAGAAAG ACTCACATTT ACAAGAGGCA GATNTCCAAG TAGAGCAGAA CCGGCAACAC	60
TTCTATNANC TGTCTCTCGA GTATGTNTGT AAGCNGCAGG AAATCCAAGA AAGAAAAGAAG	120
TTTNANTTTG TGGAACCTAT GCNGTCATT TTNNAGGGGA TGTTTACCTT CTATCATCAG	180
GGCCATGAAC TTGCCAAGAA CTTCAATCAC TACAAAATGG AACTACAGAT CAACATTCA	240
AATACACGGA ATCGATTGA AGGAACAAGG TCAGAAAGTGG AAGAGCTCAT GANCAAATC	300
CAGNCAGTTC CCAAGGNCCA CAAACGAGCA AGTCAGTTA CAGCCGAGTT ACCTGTTGT	360
GCCAGGAAAA AGGCCTGCTC CNTTTGGTTC CATTGGGTTTC AANCATTTT GCCNGTTTC	420
GAAAGCAGCA AGGNAGTTCC ANCTGTTCCC CTTTTAGGCA CCGTTTGTT GGGGAATTNG	480
GGGNCGGNGA GGTGTTCTTT	500

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

NTACGTCGCT CCNACCTNCT GGCTGNCTAG GGGGAACCTCT CCCCCAGCGA AAAGGCACATC	60
AAGAAGATCT TGGACAGNTG GGTATCGAGG CGGACGACGA CCGGNTCAAC AAGGTTATCA	120
GTNANTGAAT GGAAAACNTG AAGAGTCNTG CCAGGTTTGG CANCTGNNA TTTACCTCTG	180
GTGGGGTGTGTA GCGTNNGCT GCCCGGTCTG CAGCCTGTGT GGTTNTCCCT GCTGCAGANA	240
GGAGAGNAAG TGAGAGAGGA GGAGTCTGAA GGTCAGTGTG ACNNGGATTG GCNTTGATT	300
ANNTCTGTCC CTGCAATAAA GCTTTACAC TCTCAAAAAA AAAAAAAA T	351

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

GGCAAACGAC GTGGGCAGCG TGGATGGAGA AGTCGTCATC GCACACGGTG CCCCANTGGC	60
CATCATAGTA CACCTCCACC CGGCCCTCGC TGTGCTTCCT CTTCTGCCCA GCCAGGCGCA	120

NTNAATATCT TGGCCACGTT GGCGGGTNTC TNNGAGCTGG TGAATACTNA GGAAGCCGGT	180
TGCTGGAAAT NACTCGGGGT AAATGGGNGC CAGCTGTAAA TACTGTGCCA GGTCAGGGG	240
GGACAGGNGG GCCAGCATTA GCCAGGCANT TGCAGAGGTG GGGAGCACAG AGGCCTTTTC	300
CATCCCTGTT TTTCGGGCTG ATGATTCCCA CGNAANGNC CCTGCGCATT GAAAGGGGGN	360
ACAAGGCAGGG GGTTACAGAA GCANCAGGGG TTTTTTT	397

(2) INFORMATION FOR SEQ ID NO:1376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

CANCAAAAC TAAAATGNN GGTCCAGATC AAACAGAAAT GANCTATTGA GGGCTTGCAGA	60
GCNCACAGTG GAGTATGTGG TTAGTGTCTA TGCCTCAGAA TCCAAGCGGN GAGAAGTNAG	120
NCTCTGGTTC AGAACTGNNG TAAACCAACA TTGAATNGGN CTTAAAAGGN ATTGGNATT	180
CACTGATGTG GGATGTGGGT TTNCATTNAA AATTGCTTG GGAAAGNCCA CAGGGCAAG	240
TTTTCCAGGT TCAGGGTGAC TTATTTGAGC CCTNNGGGTT GGG	283

(2) INFORMATION FOR SEQ ID NO:1377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

GCCANCCCAG NTTCCGGNAA CNTGCCAGGA GCTCAAGGTA AGCCATCAAG AGCCTGCAGT	60
GGNTGGCGGG CGGTCACCTT CACGGGGAG GCCCTGCAGT ACAGGGGGAA CCAGNTGTTG	120
NCGNCCCAGC CCGAACAAACC GTNTCGCCCT GGTCATCATT GACGGGCAGT CAGACANTCA	180
GAGGGG	186

(2) INFORMATION FOR SEQ ID NO:1378:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

CTNCCGGATT CGGCGTGGTC AGCAGCCGAA AAGAATTCC CCGCTTATNC GNACCTTCCA	60
TAATAAGCAA GCNATCTNCT GGCTGAAAAA AGCTGCCCTA CAAGGCCATA CTGGGNCTTC	120
CAACGCCCTT GGCTGGNACA CTGGATCGTG GAGAAGCCCC CATTTATGAA AGANGCGGTT	180
GTTTGGTATC GAATAGCCGC GGAGAGCGGA ATGTNTTATG CGCCAAAATA ATCTTGGGTG	240
GATGTACANA ATGGCAACGG AGTCGCAAAG ACTNTGCGCT GGCTTTNTT GGTNCAAACA	300
GTNGCTTACA GGCCTT	316

(2) INFORMATION FOR SEQ ID NO:1379:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

TGTNNCAGGG AACTTGCTAC TACCAGGCAC CATGNCTAC CAATATCCAG CACTGACCCC	60
GGAAGCAGAA GAAGGAGCTG TNTGGGNATC GGTCACCGGA TCGTGGGACA CCTGGGCAAG	120
GGACATCCTG GCTAGCAGAT NNANTNCCAC TGGGAAGCAT TGCCAAGCGG CTGCAGTCCA	180
TTGGTNACCG AGAACACCGT TGGTGAACCG G	211

(2) INFORMATION FOR SEQ ID NO:1380:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

GGCAGANANA CCTTGGCACC CGNNATCAAC TGGTTGCTTT TNNTCAACAC CATCTTCTAC	60
CCCGTGGAGA TCAGTNAATC CAAGCCTATT GTGGTCTATG ACAAGGNAAT ACCTTGAAGC	120
AGATCTCCAC TCTCATCAAC ACCACCGACA GATGCCTGCN CAACAAC TAC ATNATCTGGA	180
AACCTGGTGC GGAAAACAAG CTCCCTCCTT GAACCAGNGC TTTCAGGACG CCGATGTGAA	240
AGTTCATGGG AAGTTNATGT ACGGGNCCAA GAAGACCTGT TTTCCCTCGCT GGGAAATTNG	300
CNTTGGTGAT CACAGTAAAC ANCCTGGG	328

(2) INFORMATION FOR SEQ ID NO:1381:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

GGCAGAGCCC TGGTCCGCAT CTNCTNTGGC CGCCACCCGA TGCTGTTCA	60
GGCAGAGCCC TGGTCCGCAT CTNCTNTGGC CGCCACCCGA TGCTGTTCA	120
TCCCTGCCAC GCCAGCCCCGT GCCCTCTGTG CAGGACACCG TGCGCAAGTA CCTGGAGTCG	180
GTCCGGCCCA TCCTNTCCAA CGNAGGACTT CGAACTGGGA CCCGGGTCTG GGCGCAGGAA	240
TTCCCTGAGGC TGCAGGCGTC GCTGCTGCAG TGGTACCTGC GGGCTNCAAG TCCTGGGTGG	300
GGCGTCCAAT TATGGTCCAG TAACTGGTTG GNAGGGAATT TTTGTNACCT GNGGATTCCC	314
GGAAATTCCG NTTG	

(2) INFORMATION FOR SEQ ID NO:1382:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

GGCACGAGCN AGCCTCAGCC TTCCCTGGCC AAGAGCTCAT GCTTTCCCTTG CTCTCCCCAG	60
GGTCCTGCTG GTCCCGCCGG TCCTGTCGGC CCTGTTGGCG CCCGTGGCCC CGCCGTAAAG	120
TACCCCTGCTG TNTCCCCCAT GCCTTCANAA CTCTACAGAT GCAGACAGTG CCCCACTCGA	180
TGCCAATGGA AACTTCCGCC TGAAAGTTG TCCCTTNTC TCTTCTAGGG GACCCAAGG	240
NCCCCGTGGT GACAAGGGTG AGACAGGCAG ACAGGGCGGA CAAAGGCATA AAGGGTCACC	300
TTGGGTTCTT TGGGCCTCCA GGGTNCCCCCT TGNNCCTCCT GTAAGTTATG GTTCAGNCCT	360
TNCCCAAGTCC CCTGNTGTTG TGTGGGTTAG NAAGGGGGAG TTTGGNCTNA ATTTTCCCTT	420
TGGGTNGTTN ATTNTTTCCCC TTCTNATGG GGATTGGGGG TNTNAAGATT TNTGGGNAT	480
TTCCAAGT	488

(2) INFORMATION FOR SEQ ID NO:1383:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

GGCACAGCAG GGTCACACC GGTGAAAGCC CTNACGTGTG TGGTGA	60
TGTGTACTGT GGGAAATTCT TCAGCCGAAG CTCCAACCTT ATTCA	120
GCCATA AGAGGGTTCA CACTGGTGA AAGCCATATG AGTGCCAGCN ACTGTGGAA GTTCTTNAGC CAGCGTTCCA ACCTCATTCA TCATAAGAGG	180
GTTCATACGG GCAGAAAGTGC CCATGAGTGC AGTGAATGTG GGAAATCTT CAACTGCAAC	240
TNNAGCCTA ATTAACAT TGGAGAGTTC ACACTGGAGA AAGACCTTAC AAGTGTAANA	300
NATGTGGGA AATTTTTAG NCCACATTGT NCAGNCTTCA TTCAA	347

(2) INFORMATION FOR SEQ ID NO:1384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

AGCAACGGCG ATCATTGTA CTTCAATTCT GGTGCCAATT CTNACCTCTA TCTGGNCAG	60
TAAAGTCAAA GCCAGAGCAG CGAAAAATCG AAATTTAGG TACGGTAAA TAAACCTGCT	120
TCCTTAATCC CCACNGTCGG ATGANCTAAC GTTCGTCCGG TTTGCTATTG AGTCCTGCC	180
TGGAATACTT ACCGAGAAAA ACAGCACGNC TGAACATTAA AATAAAATNT GGGTACTAAA	240
TGGGGAAAT TTTCTGCGTG GGAGAGGGAA ACAGATGNCG ATTATTCCGN TTGATTGTNT	300
NACACAGGAC AAGGTTCCG GGATTTTCC CGGANGG	337

(2) INFORMATION FOR SEQ ID NO:1385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

GAGGATAAAA AGTACATATA CAGTTCATAC AATAATCTTA TGTATGTANA ACCCCGTTAC	60
GATGTCGGCG ACGGGGCCCA TCAGTAACCA TTACGTGGAC TCGCTCATCT CTNACGACAA	120
TGAAGACCTC CTAGCGTCCA GGTTTCCGGC CACCGGGCT CATCCCGCCG CCGNCAGACC	180

CAGCGGTTTG GTGCCGNCT NTAGCGATT TCCGTTCTG TGAGCTTCGG GNCCAAGCCG	240
GN	242

(2) INFORMATION FOR SEQ ID NO:1386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

GGGGACCCCC AGGAGGTGAC CCTGCAGCTC TTCACAGATG GAATCACAAA TAAACTTATT	60
GGCTGTTACG TGGGAAACAC CATGGAGGAT GTAGTCCTGG TGAGAATTAA TGGCAATAAG	120
ACTGANTTAT TAGTCGATCG AGAATGAGGA AGTAAAAGAG TTTTCGAGTG TTGCAGGCTC	180
ATGGGTGTGC CACCACAAC NTACTGTTAC CTTCAATAAT GGACTATGNC TNATGGATT	240
TATACAGGGA GGAAGCACTG GGATCCAAAG CCATGTTCTG GCAACCCCAG CCATTTTCA	300
GGGCTAANTA GCTTCGTTCA GTTGNTTAA AAATCCCATG NCTTATTTCG ATGGCACCAC	360
CAATTGGGCT GGGTTCCCC CAAATTNTAA TTCTTTGGG NTTAAAGATT GGGGGNAAGG	420
TTATTTNTT TT	432

(2) INFORMATION FOR SEQ ID NO:1387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

TCCTCCTGGC CATNATCTTC CTGCTGGGA AGATCTGGAA GGTNCAAGTG CTGCAGGGCA	60
TCTTGGAAGCCAGNTC CTGTTGCNC TCGTTTCAG CAC	103

(2) INFORMATION FOR SEQ ID NO:1388:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

ATGGCTGTGC CACCCACGTN TGCCGATTG NGCAAATTG CCAGGAAATN TTTTCACCAA	60
GGGCTATGGT TTTNGTTAA TAAAGCTTNA TTTGGAAAAC AAAA	104

(2) INFORMATION FOR SEQ ID NO:1389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

TGAGGGACTT NACCCAATNA ACTACCTGGG CATTANNACC AACATTCAAG GCCAGGTGCC	60
TNACGTCCCA GCAAATTAA CAGTCCACAT CTCTCCCTAC AAGGAGCTGT ACCACTACTC	120
CAACTCCACT GTAACCTCTA CAAGTNCCNG TAGACTACTC TNTAACTTTT GGTGCAATCA	180
ACCAAACATG GTGCTACCGC ATCCACCAGA ACATCACTTA CCAGGTGTGC AGGTACGNCC	240
CCAGACACCC GTCCTCCNC ACCACCCAGN AGNTTGAACG TGGACCGGGT TTTTGCCCTT	300
TGTNAT	306

(2) INFORMATION FOR SEQ ID NO:1390:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GGCAGAGNCT TGGAAGAATT TATTTAGATA TGCTTAATGT ATACAAGTNC CTCAGTGAAA	60
ATATTCTNC AGCTATCCAA GCTAATGGTG AAATGGTTAC AAAGCAACCA TTGATTAGAA	120
GTATGCNAAC TGTAAAAGG GAAACTTAA AGTTAATATC TGGTTGGGTG AGCCGNTCCA	180
ATGAATCCAC AGATGGTCGC TGAAAATTGTT GTTCCCCCTC TGTTGGATGC AGTTCTCATT	240
GNTTATCAGA GAAATGTCCC AGCTGCTAGA GAACCAGAAG TGCTTAGTAC TATGCCATA	300
ATTGTGCAAC AAGTTAGGG GGACATATTA CCAGCTGAAA TACCTCAAAT ATTTGATGCT	360
GTTTTGAAA TGGCACCTTG GATTATGGTA AATAAGGACT TGNAGGATTT TCCCGNACCT	420
GGACGGACTT TTCCTTACTA CTPCNGGTGT TCAATTNNCC TTGTTT	466

(2) INFORMATION FOR SEQ ID NO:1391:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

GGCAGAGAGA NGCTGCGTCC CGGAGTAATC TGAAGCGGGT NACGCTGNAG CTNGGGGGGG	60
ANGAACCCCTT GC	72

(2) INFORMATION FOR SEQ ID NO:1392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

AANAAACCAT CTGGTTCANG TTCTTAATTG GGCCAGCAAG TAAGGATGGC CAGGCCTCTG	60
GAGCAGGCCG TACTGCNATC NTTTGCACCT TCCAGGTAAT ACGCAGGTGC TGTGGGACA	120
AATACAAGCN CTGCCAGGCG GACTCAAGGA GCTGCTGCAG AAGGAGCTGG CCACCTGGNA	180
CCCCGANNAA TTTTCGGAA ATNTAACTAC AACAAATTCC ATGANTNTTC CTGGGACACC	240
ANCAAGGACT GCAAGGTGGG ACTTTTTGG GAGTATGTGC GCTCACTTGC TCTGNTCGCN	300
TTTTCTACTG CC	312

(2) INFORMATION FOR SEQ ID NO:1393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

AAACNTTNTN TTNTCCCTGTA AACAGTGGCC AGCCCCCAA CTATGAAAAT GCTCAAGGAG	60
GAGCACGAGG TGGCTGTGCC TGGGGCGCC CCANAACCCT GCTCCCCGA NGTCCACNGT	120
NAATCCANAT CCGCAACGAA GACCTCCNTG CNCCGACCAT NTGGTNTGGT CCCTNTTCAA	180
CANCCTCTTC ATGNAANCCC TGCTGCCTGG GNNTCATAGC ATTGCCTTA NTCCGTGAAA	240
GTTTTAGGGA CAGGGAAGAT GGTTGGGGGA CGTNAACCGG GGGNCCCAAG NCTTATGGTC	300
TTCCAACCG	309

(2) INFORMATION FOR SEQ ID NO:1394:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

TTTATGCTGA AGTATTATCG ACGAATGCAA TTATCATTGA	AAAAAAACAT AATATATAAG	60
TNATTATCTC TAAAATCATT GATGATTCA GAGTGTAGG	TTTCAATGAA TGANGTTAA	120
AGGATGTTAG CATGTTTAC CTTTATAATG ATGATAACTT	TTCCAAAACT GCTTGACTGT	180
NGAGGTTAAC TAAATTNCT CTTGGAGCCC TACATACCAT	CTGGATTCTT CCCATACCCA	240
CCAATTAANT CCCGGATCGG TTGGTCCATA AAACCGTGGA	TATTGGGTCT NTCCAGTGGC	300
CGCCGTTAAA ATGGGNTTAA CCCCGTATNN CACCGGACAC	T	341

(2) INFORMATION FOR SEQ ID NO:1395:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

AGCCACATGC NCTACGNNTA NNANGCCTAC GCATACCTNC	AATATATTGA NTCTGCAGGA	60
CTTTGTAGNC CGGNTAAGGN GTTAACGCCG ATACAGGCAT	TAACAAAGCG NATTTGTCAG	120
CAATCTAAGT AACGTCGCAA TCANTTTCT TNAATCCCAC	ATCATTGCA NTTCCATTAN	180
TTCTCAAACA TCCATGCCCA ACG		203

(2) INFORMATION FOR SEQ ID NO:1396:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

TAGTNAGGGT CAGGTGCAGA TGGCGATGAN CGGCAGCATC	TANAATGAAA GCAATGCC	60
GCTCGGTTTG TACATNGAAA ACGGTCAGCA GAAGGTGGCG	TTAAATCTCG CTTCAGGTGA	120

AGGGAAATTN NTTTATCCGT CCTGGCGGCG TGTGTTAATG TCGCGGGAGA ATAAAGTCGG	180
CATCGTTCGT CTGGTATGCC TTCAAAACCA GTNAAGNGA TTCATTTGC GGTGCAGTCC	240
AGGGCCAATN TTGATGGAAA ACGGTGTAAT TAATCCGCGT NTTCATCCCA ACgtCGCCTN	300
AAGCAAATT CGTGAAACGGT GTTGGGGTTA ATAAAACCTG GGGAACGCCN TGTTTTTTT	360
TGNGCCCGCA GGCANCAAAT TTTAATGGA TTTTGCCCN GTTATGNCCC AGGGAAACT	420
TAACCTTTG	429

(2) INFORMATION FOR SEQ ID NO:1397:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

NAGCTTTNG TATTTAAAT ATNAGGTACA TAAGAGTTTN AATTGTTCC TTTTTTAAAA	60
TAACTTNAA AATTATTATA TG GTAACCTT CTTTATTATG AATACTTGNA AAATGTAGGC	120
ACACAAATAA CCTTTTGAA TTTATATCCT GTAATGTATA TTTCCCCAGT CTTTNACTT	180
TACTCCAGTC CACTAGGAAA TCAGTGGTTG GTTGTACCC TCTCTGAAA TGTCTTTTG	240
TATTGTGGTC TCCACCGTGC CATTTCNATA ATGGCATATT TNTNTTGNG CCTAGCCATG	300
TTTAGNGGTG TTTG	314

(2) INFORMATION FOR SEQ ID NO:1398:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

TCCATCATAG TCAACTGCTT GGGANGAGAA AGCCAAANGA NTGCAATGTT GTGAAAGATT	60
CCANTTNATG CCAGTAAACC TAATCCAAAT GAATGTGGAG TTTGAATAAA TCTGTATTTG	120
GATATGATTG GAATCATCCA TCCCTGTACT CATCCTGAGG ACAAAACCAGC ACCAAAAANT	180
GNGGNTGNNA ATGAATGGTT GCAATT	208

(2) INFORMATION FOR SEQ ID NO:1399:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

TGANTATTCA	NCGTGNAAA	GAAGANTGG	AACAAAGGA	AGCTGAAC	T CAGAAAGTCC	60
GGAAGGCTGA	GGAAGAGAAG	GCTGCCAG	GNAAGCAAAG	GNGAGAGAGA	AGGAGCGTAT	120
CTTACAGGAA	CATGANCAAT	TCAAAAGAA	AACTNTCCGA	GAANCNTTG	GN	180
AGAAAACAGA	ACTGGGTGCC	AAANCTTC	AAGGTATTGA	ATATTGAAGA	CCTTNAGGNA	240
TTGGTTCCA	GT	TTTCCT	GGGTTAANCA	GGTGANCAC	TGGGAAAG	289

(2) INFORMATION FOR SEQ ID NO:1400:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

GGCACGAGCA	TGGCTTTAA	TGAAGAAGGA	CAGGCAACAG	AAACAGACAC	AAAANTCAGA	60
GTGTGCACCC	GGGCCTACCA	TCTGCTTGTN	AAAAAACTGG	GCTTTAATNC	AAATGACATN	120
ATTTTNACC	CTAATATCCT	AACCATTGGG	ACTGGAATGG	AGGAACACAA	CTTGTATGCC	180
ATTAATTTA	TCCATGCAAC	AAAAGTCATT	AAAGAACAT	TACCTGGGNG	CCAGANTAAG	240
GTGGAGGGTN	TTTCCAAC	TT	GTCTCTCC	TTTNCCGGGG	ATTGGAAGGC	300
GGCATTGCTT	GGGGTTTCC	CTTTACCCTT	GCATTCAAGT	NTTGGCTTGG	CCTTGGGGGT	360
TNTTNATTNC	TGGGAAACCC	CCCCGTGGNA	TTGGGG			396

(2) INFORMATION FOR SEQ ID NO:1401:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

GGCACAGGNT	TTTTTTTTT	TTTTTTTTT	TTTTTTTNG	GGNTTTTTT	TTTTTN	56
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(2) INFORMATION FOR SEQ ID NO:1402:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

CAAAGGCGGA GGACCCGTGG CCCACGAAGC TCATCTTNA ACTNTCCCCG CNTTCTCCG	60
CCTTGAANTT GTGAACCCTA GGCCCTTTGG GGCGACCTNT NAACCCAGCT AGCCAGATCC	120
CGGACCCAAA CCATGTTCCC TGTGAAAGGT GAAAAGTGG AAAAAATCAGA GCTGGAGATG	180
GCCAAAGCCC GGTAACCAAC TGGTTGCTGT TTTGCAGTNT CTGCTTGGAG GANGAGTCAC	240
ATGGNACAGG GAGCGTNTGG TTGAGGGAAAG CTGGGGAAAA CACCCCTCAGG ACACCCACAA	300
TAAGGNACTG TTTCCATCGC AGGCCACTGG GNAAAAAGGG CCATCTTNCC CGTTTTCCC	360
CCACCAAGGG GAGGGAAAGAA GAAGGNGGGG NGATTGGTTG	400

(2) INFORMATION FOR SEQ ID NO:1403:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

TATATTGTAG CTCATCANGG GNAATNGGNA CTGTTCAAAA NGGATTGCC CACAAGTGTT	60
ACCATGGGCA AAACTGGAAG AGTCTACAAT GTTACCCAGC ATGCTGTTGG NCNNNGTTGT	120
TATNCAAACA NGTTTANGGG GCAAGATTCT TTCCAAGAGT NTTTAATGTG CGTATTTAG	180
CACATTGGC ACTCNAAGTG TCCCGGATAG CTTTCNGAAA AGTGTNAAG GGNAATGAA	240
TTCAG	245

(2) INFORMATION FOR SEQ ID NO:1404:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

GGCAGAGTGG TCATCGAGTT CTCCAGCCGC CCCGGCCAGC ACGAGCTGAT GGAGCCCGAG	60
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GTGAAGCTCN TCGGCAACAT TCATGGCAAC GAGGTGGCGG GCCGGGAGAT GCTCATCTAC	120
CTAGCCCAGT ACCTGTGCCT CTNAGTACCT GCTTGGTAAC CCCCACATCC AGGCCCTGCT	180
CCAACACCAC CCGCATCCAC CTGNTGCCCT CCATGAACCC TGACGGCTAT GAAGGTGGNC	240
AGCTGCCGAG GGTTGCCGGC TTACAACGGG TGGGACGGAG CGGGAAAGGTN AGTAACGTGN	300
CAAAACCTGG GTNTCTNGAA CCGAAATTTC CCCGGGACNT	340

(2) INFORMATION FOR SEQ ID NO:1405:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

AATCGCAGAG CTTGTNACAT TTTGGAATGC TGTAATGGGC TGGCCCAGGA ATGTNATCGG	60
CTCCATCGGA CAAGCCTTTA AGCTCCGGTT TAAGCAATAT TTACAGTGTC CTACCAAGAT	120
TCCCGCTCTC CATGAATCGA NTGCAGAGTC TGGATGAGCC ATGGNACGGT AAGAGGAGGG	180
AGATGGCTCA GAACCACCCA TTACTTACAA CAGCATCCCA AGCAAGATGC CTCCTCCCAG	240
GGGGCTTTTC TTGGATACTT AGGACTGAAA CCCAGACCCC ATGGTTCCCTG AACACAGCCC	300
AGTTTGCAAG GAAAAGAGG CAGATTTTT ACCAGGGAAG ACATTTGGGG GACATTTGG	360
CGANANTGGG CAGCAAACAN CTTTAAGGGC AAGGTNCCCG GANAT	405

(2) INFORMATION FOR SEQ ID NO:1406:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

GGCAGAGCCC AATTCTTCGA AGGTCTGGAA TGTATACTGT AGCCATTGCT TNTTGTGGCT	60
CTNGTAACAA CAAAGCAATT CGAGGACTGN TAGATGTTGC TGTAAGTAAT GTTAATGATG	120
ATGTCAGGAG GGCAGCAGTA GAATCACTTG GGTCATTCT ATTCAAGAAC CCTGAACAGT	180
GCCCAAGTGT TGTCTCTTG TTGTCAGAGA GTTACAACCC TCATNTGCGC TATGGAGCTG	240
CAATGGCCTT NGGGATATGC TGTGCTGGTA CAGNAACAA GGAAGCCATT AATTGCTAG	300
AACCANTGNA CAAACGACCC CGTGGAACTA CGTGAAGGTC AAGGGGCACT TCTTAGGCTT	360

NCAGTNCTTC ATCCATGTTT CCAGGCAGAC TNGNAATCCA CTTGTTCCAA AGGTNGAT

418

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

GGCAGAGGAA GATTGACGTG GGGGAAGCTG AACCACGGAC TGTGTGATNC GGCCTGGTAC	60
ATTCGTGCCA AAGGAGGAAC TGCAGGACAG GCTGGTAGTG GTGCTGTGCA ACCTGAAACC	120
CCAGAAGATG AGAGGAGTCG AGTCCCAGG CATGCTTCTG TGTGCTTCTA TAGAAGGGNT	180
AAACCGCCAG TGANACCTCT GGACCCCTCCG GCAGGCTTCT GCTTCCTGGT GGAGCACGTG	240
TTTNTGAAAG GGCTATGNAA AAGGGCCAAC CAGATGGAGG GAGCTCAAGC CCAAGAAGAA	300
AGTCTTCGA GGAAGTTGC CAGGCTGGAC TTTCAAATTT TCTGAAGGGA GTTGCATCGC	360
CCAGTTGGGN AGGCAAACCA ATTTCATGGA CCAGTTGGGT TNCCNTTNCC GTAAATCGTT	420
GAAAGGGGGG NACATTAGTT TGCCAGCCCG CNTTTCCCC TTTTTTCCAC CTNGGGTCAT	480
NTGTGTNTTT TCNTTGTTC	500

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

TACTATCCGG AACTGGCTGC GCTGAATGTN GNAANCTTA AAACCGACAA ACCACAGCCG	60
GTAAACGCGC TGCTGAAGAN CCGAAAAACG CAACCTGTGCG CTGTTACAGG CACGCTTGAG	120
CCCAGGNCT GNCGCGCGAG NAAN	144

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

GGCACGAGGC GGGGCTACAA CTACGCCACC TGCCTGGAAG GAGCCCTGAA AATTAAAGAG	60
ATAACCTACA TGCACTCAGA AGGCATCCTG GCTGGGGAGC TGAAGCACCG GNCCCTGGCA	120
CTGATTGACA AGCAGATGCC CGTCATCATG GTCATTATGA AGGATCCTTG CTTGCCAAA	180
TGCCAGAACG CCCTGCAGCA AGTCACGGCC CGCCAGGNTC GCCCCATTAT ACTGTGCTCC	240
AAGGACGATA CTGAAAGTTC CAAGTTTGC GTATAAAGGN CAATCGGAGC TGCCCCACAC	300
TGTGGGACTT GCCTTCAGG GGNATTCCCTT GAGGCGTGGA TTCCGTTGGC AGTTGCTGTT	360
CCTTNCACCT GGGCTGTTCT TCCGAGGGAT ATGACGTTGA CTTTCCCCAG AAATTTGGCC	420
AATTTTAAA ANTNTGGGAT TAGGNTNAGA CCGTNAAAAG GCCATTAACC ACTTT	475

(2) INFORMATION FOR SEQ ID NO:1410:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

ATGGGAGTGG ACATCCGCCA TAACAAGGAC CGAAAGTTCG GCCGCAAGGN GCCCAAGAGC	60
CAGGNTATCT ACCTGAAGGC TGTGGTCAA GTTATACAGG TTTNTGGCCA GAAGTAACCA	120
ACTCCACATT CAACCAGGTT GTNTTGAAGA GGTTGTTTAT GAAGTGGCAC CAACCGGCCG	180
CCTCTTCCC TTTCCCGGAT GAATACGGNA AGNATGGAAG CTTTCCTGGG CCGGGGAAAA	240
CAAAGACGGG CCGTGGGTTN TGGGGGGACC ATAAACTGAA TGATTTGCGG GGTTCAGGA	300
AGGGTTACCC AAACTTAAG TTATGTGNCA CTGNGCGTNA ACCCAACGGG GNCCC	355

(2) INFORMATION FOR SEQ ID NO:1411:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

ATGATAATAG TGTTGATACA GCCACGCAAA ACCGCGACCA GACAGATAAT TTTAAATGCA	60
GCCATGCTGA CCACAGCCGC AGCGNCGTGA ACGGGAAAAT CCAACCCCAT CATGGTTAAC	120
GCATCAACCG GCAGACGCAT ATGGNAAAC TCGCCGGTAA ATGTAGCTT TACCGGTAAT	180

CGGTTGCCG TTGAAAATC AGCCCGCCGC CAACACCGGT GCCGAGANTC AACCCCATCA	240
CCAGTGGAT ATTGGAGTAA AATTTCATCA TCCCAGGNTT CTGNAAGGGG CAAAACAGTT	300
GGCATCGTTT ATTCAAGGCG TACATCGGGG TTCAAGAACG TGCGTTCACT TCAGCAGGNN	360
GCGGTTTAC NTTGTCNAGG GGGGAACCA TGGGNNGCTT ACAGGGTTAC CCTCTTTGG	420
TTT	423

(2) INFORMATION FOR SEQ ID NO:1412:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

GGCAGAGCNA GNCCGGAGTG TCAGGNATG ATGCGTTNA TGCTATTATT CAGCCGGCAG	60
GGGAAAACTG CGGCTGCAA AATGGTACCT GGCCACTTCG GACAAGGGAA CGGAAGAAGA	120
TGGTNCGCGG NCTCCATGCA GGTGTCCTG GCTCGAAAGC CCAAGAATGT GCAGCTTCCT	180
GGAGTGGAGG GNACCTCAAA GTTGTCTATT AAGAGATATG CCAGCCTCTA ACTTNTGCTG	240
CGCCATTGCA GGGCCAAGAC AATGNAGCTT CATCACACTG GAGCTGTATT CCACCGATAC	300
GTGGAGCTCT TTAGGACAAA TACTTGGGC AGTNTGTGCC GAAGCTGGAC ATCATCTTTC	360
AACTTTNNAG GAAGGNCTNA TTTCATCCCG GGATGAGTTT TTTGATTGGG GGGGGNNTT	420
CCAGGACAAC TTCCAGAAGA GTGTGCTGAA GCCATTGAG CAAGGTGANC NACTGNANA	480
GGG	483

(2) INFORMATION FOR SEQ ID NO:1413:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

AGCCCCCTAG ACAGGTTAAA ANGTTATCTN TGGCAATCAA NGGCAGTTG GATGAAGCCA	60
AGGNTCTTN CAAACCTCCA AAGGACTCCC AAGAATGACG AGAGTNAACT CAAATGCCGN	120
GGAGGAGCAG ACTACGANGC GCCCGGAGAA CCCACACTGG GGGTTCATTT GGNCGNCAA	180
CG	182

(2) INFORMATION FOR SEQ ID NO:1414:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GGCANAGGGN TCAACTACCT CACTGTAATT GGCTACCCAA ATGCTGAGTT CAAATCTTGG	60
TGGCCGGCCA CTGCTCATAT CATAGGTAAG GACATTCTCA AATTCCATGC CATCTATTGG	120
CCTGGCCTTC CTGTTAGGGG NCCGGTCATN AGCCCGNGCA CAGCNCATCT NTNGGCCATT	180
ACCCACTGGA CAGTCTGTGG CCAAAAGTTG TTCCAAGAGC TTGGAGCAAC GTGGTNGNNNT	240
GCCGAGGACT TNGCCTTAA CCGCTATACC GTGGTATGGG NTT	283

(2) INFORMATION FOR SEQ ID NO:1415:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

GGCAGAGTNT CGATGCCACT NTCAACAAGG CCCTGGCAGA AAGATTCCAC ATCTCAAAGT	60
TTCCTACGTT GAAGTATTTT AAGAATGGAG AGAAATACGC ATGCCTGTGC CTCAGGTACA	120
AAGAAGAAGT TTCTCGAGTG GATGCAAAAC CCTGAGGCC CCCCCCCCCC AGAGCCCACG	180
TGGGTAAGAG CAGCAGNACA AGCGTGTGAC ACCTGGTGGG GGACAACCTC CGGGGGGACC	240
CTNGAAGAACAG AAGGAAACAC ACTTGGTTCA TGTTCTTACG NCCTTGGTGC CCACACTGTA	300
AGAAGGTTCA TTNCCGGATT TTACTGTTAN NGTTGATGCC TTTCAAAGAT GGACCGAAAG	360
NTTGNCTGTT GCCGTTGTTT GATTTTTAA AGG	393

(2) INFORMATION FOR SEQ ID NO:1416:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

TCCCNTTGGG ACAAAACTGT TGGTTCAATT AAGGGTTGTT TTTTCANGAG GNTCCTTGGT	60
TCTTTAAAAG GCAAGGTCCC GNNGGGGAAG GGTCCAAGGT TCAAGTTTG NAAGGGG	117

(2) INFORMATION FOR SEQ ID NO:1417:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

GGCANAGGGA AGAAGGAAAC CCAAGGTTGT GGTATGCTGC TTTACTGTCT TTCACAAGCG	60
CCTTTNATAT CCTGTCAATC ATCTGTGTCG GGCTGCTCTA TACATATTAC ACCAAACCAG	120
ATGGCTGCAC AGGAAAACAA GTTCTTCATC AGTATTGAAC CTGATCCTTT GCGTTGTGGC	180
TTCTATTATG ATCGATCCAC CCAAAAATTC CAGGGAACAC CAGCCTTCGN TTCCGGCCTC	240
TTGNCAGTTC CTTCCCTNCA ATNCAACCCC TNCTGAC	277

(2) INFORMATION FOR SEQ ID NO:1418:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

GGNACGAGCT GGTGGCTGGC AAGATCGTGG AGATGGAGGA TGTGGGTTA CTCTTTGCNC	60
GCCTTGGAAA GTACATTCTG TGCTGCCTGC TGGGTACGC CATCCATGGG CTCCTGGTAC	120
TGCNNGTCAT CTACTTCCTC TTCACCCGCA NAAACCCCTA CCGCTTCCTG TGGGGCATCG	180
TGGACGCCGC TGGCCACTGC CTTTGGGAAC CTCTTCCAGT TCCGCCACGC TGCCGCTGAT	240
GATGAAGTGC GTGGAGGAGA ATTAATGGCG TTGGCCAAGG CACATTACAGC CGTTTTCATC	300
CTGGCNCATC GGNGGCCACC GTNCAACATG GGACGGTGGC CGACGGTTCT TTCCAGTGCG	360
TGGGCCGCAA TGTTTCATTG CACAGTTCAAG CCAGCATTCC TTGGANTTCG TNAAAGATCA	420
TCACCCANCTG GTCAGGGCAC AGGTCCANGT TGGGGCAAN GGGCATCCTG CTGGAGG	477

(2) INFORMATION FOR SEQ ID NO:1419:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

TCAGCAATCA GACTGTCGAC ATTCCAGAAA ATGTCGCATT GACTCTGAAG GGACGCACAG	60
TTATCGTCAA AGGGCCCCAG AGGAACCCCTG CGGAGGGNAC TTCAATCACA TCAATGTAGN	120
AACTCAGCCT TCTTGGNAAA GGAAAAAAA GAGGCTCCGG GTTGACAAAT GGTGGGGTTA	180
ACAGNAAAGG GAACTGGNCT ACCGTTCCGG GACTTATTTG TGAGTNCATG TTACAGGAAC	240
ATGGATTCAA AGGGGGTGT TNACCACTTG GGGGGCTTT CCGGTTAAC CAAAGGNNTT	300
GNAGGGGTNC TTGGTGGTTA TTGGGCTCCC AAATTTTCC CCCCCAAAAA	349

(2) INFORMATION FOR SEQ ID NO:1420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

CAAGNTCNNC GGCAAGGNCT TTTCCANACC CTGGTTGCTT CAAGGACACA TTAGAACTCA	60
CACGGGGGAG AAGCCTTTT TTTGCCCTCA CTGCAACAGC NGCATTGAC AGACAGGTGA	120
ANTCTGAAGG NGTCATCTGA CAGACCCATT NTATTGTGAA NGAAATACCA	170

(2) INFORMATION FOR SEQ ID NO:1421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

GGCAGAGCGA GAGCATGCC TTNTGGCTTA CACACTGGGT GTNAAACAAC TGAATTGTCG	60
GTGTTAACAA AATGGATTCC ACTGAGCCAC CCTTTTTTT TTNTTNGTNT GTT	113

(2) INFORMATION FOR SEQ ID NO:1422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

GGCANAGCAG CCACGGATCT NCGGGTGGAG GCATNAATGC TAACATGAGG GGTGTATTTC	60
TACATGTTTT NGCAGATACA CTTGGCAGCA TTGGGN	96

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

GGCACGAGCC CAATTNTTCG AAGGTCTGGA ATGTATACTG TAGCCATTGC TTATTGTGGC	60
TCTGGTAACA ACAAAAGCAAT TCGACGNCTG ATNANATGTT GCTGTANGTG AATGTTAATG	120
AATGATGTCA GGAGGGCAGC AGTAGNAATC ACTTGGGTTTC ATTCTATTCA GAAACCCCTG	180
AACAGTGCCC AAGTGTGTC TCTTGTTGT CAGAGAGTTA CAACCCTCAT GTGGCGCTTA	240
GGGNGCTTGC AATGGCCTTT GGGGATATGC TGTGCTTGGT ACNGTAAACA AGGGAAGNCC	300
ATTGAATTTT GNTAAGAACCC CCANT	325

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

AACAAGACGG AATTGGAACG GGGTTNTGNG CTACTATGGT NCCACTCCGN AGTGTGTGGG	60
GATGCTAGGA AACCCACCC	79

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

CNCATGAANC GCTTCGAGGG GNTCACGGTG CTTAAAGGNT GCGCCGTGGA NCCGGGACTG	60
GGAACGTGGG CAGTCAGGGT GCTAGCTGCT TCTGGAGGTG AGCGAGCGGG TGCGAAACCT	120
TGACCCGGCC TACTTNNTNCC CGGAACGNCC CTGCTTCTTT CCTTNACCCA NCT	173

(2) INFORMATION FOR SEQ ID NO:1426:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

GGCANAGCAA GANCTCACCT CAAAGAGAAG CCCTTGACT GCAGTCAGTG TGGAAATGCA	60
TTCCGGACCC TCTCGGCCCT GAAAATCCAC ATGCGAGTNC ACACTGGCGA GAGGCCTTAC	120
AAGTNTGATC AGTGCAGGAA GGCTTACGGC CGNNNGCTGCC ACCTCATCGC ACACAAGAGA	180
ACGCACACCG GAGAGAGGCC CTACGAGTGT CACGACTGTG GGGAAAGCTT TCCAGCACCC	240
CTCCCACCTC AAAGAGCACG TNAGGAATCA CACGNGGGA GAAGNCCTTA CGNNNT	295

(2) INFORMATION FOR SEQ ID NO:1427:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

CCGATCGATC AGCTGGCGAC CGATTCTAAC TACCTGGAAG TTTGTNACAT CCTGCTGAAT	60
GGTGAAAAAC CGACTCAGGA ACAGTATGAC GAATTAAAAA CTACGGTGAC CCGTCATAACC	120
ATGATCCACG AGCAGATTAC CCGTGTGTTCC CATGCTTTC CGTCGCGAAC TCGCATCCAA	180
TGGCAGTCAT GTGTGGTATT ACCGGCGCGC TGGCGCGTT CTATCACGAC TCGCTGGATG	240
TTAACAAATCC TCGTCACCGT GNAAATTGCC GCGTTCCGCC TGCTGTCGAA AATGCCGACC	300
ATGGCCGCGA TGTGTTTACA AGTTATTNCC ATGGTTTCAGC CATTGGTTT NACCCGGGN	360
AACGATCTTT TCNTANG	377

(2) INFORMATION FOR SEQ ID NO:1428:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

GACCAGCCCC TNCCGGGNGT CCTCTTATCC NTGAATTGGT GGCCTGTTTC NTTCCAACCT	60
NTTGACCCAG GACAACGGCA TTTTACCATT TTCAAACCTG AGGCCCTGGA CCANTNTTA	120
CTTCAAACCC ATGAATGCAA GGAGTTCCGG TTTGAAGCCA TCCTACACAG AATGAATNGA	180
GN TGCAN	187

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

GGCAGAGCTC GTCCANGANA GNATTNTNCC CCATGGGAA GAACTNACAC TGCGTCCGGT	60
TTGTNCCCCA GGAGATGGC GTGCACAGGT NCAGCGTCAA GTACCGTGGG CAGCANTTCA	120
CCGGNCAGCC CCTTCCAGTT CACCGTGGGG CCACTGGTG AAAGGAGGCG CCCACAAGGT	180
GCGGGCAGGA GGCCTGGCCT GGNAGAGAGG AGAACGGGA GTCCCCAGCT GANTTCAGCA	240
TTTGGGACCC GGGGAAGCAG GCGCTGGAGG CCTCTCCATC GCTGTTGAGG GCCCCATTAA	300
GGCCGAGATT TACATTGAT GACCNTAAAA ATGGGTTCGT GCGGTGTTAT CTTATATTGC	360
CCAAGAGNCT GGTAATTAGG AGTGTCCNC AATTCAATG TTGNGCACNT CCGGAAGCCT	420
ACNGGTGCNG TTNTGAAC	438

(2) INFORMATION FOR SEQ ID NO:1430:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

GGTACAGTAA TCATGGACTC CCGTCACCCG GATACCCCTGC TGGCGGCACG TTCTGGTAGT	60
CCGCTGGTGA TTGGCNTGGG GATGGGCGAA AACTTTATCG CTTCTAACCA GCTGGCGCTG	120
TTGCCGGTGA ACCCGTCGCT TTATCTTCCT TGNAAGAGGG TCGATATTGC GGAAATNACT	180

CGCCGTTCGG TAAACATCTT CGATAAAA ACT GGCGCGGAAG TAAAACGTNC AGGATATTG	240
AATCCAATTC TGCAATTATG ACGCGGGGGA ATAANGGGCA TTTTACCGTC ACTACATGGC	300
AGGAAAGGGA TCTTACGAAA CANACCGAAC GGGANTCANA AAACNACCTT TACNCGGAN	359

(2) INFORMATION FOR SEQ ID NO:1431:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

CCCCCGCCCCG TGAATGCCGA AATGGTTGCC GATGTGCGCG TACTGGGGGC CATTNGCGTG	60
GTCGAAACCA CTNCATCCGG TGAATATGGC GGCGCTGCAA AAATTCTTTG TCGAACAGGG	120
TGTCTGGATC CGGCCTTTG GCAAACGTGAT TTACCTGAAT GCCGCCCTAT ATTATTCTCC	180
CGAACACAGTT GCAGCGTCTN ACCGCAGCGG TTAAACCGGC GTTACCAGGA TGAAACATTT	240
TTTGCCAAT AAACGAGAAG TCCGCGTGAG GGTTTCTGGC TACACTTTCT GCAAACAAGA	300
AAGGAGGGTT CATGGAAANT CATCAGTAAA CGGTCTGCGC GTTGGGGNTT AAATTGCCCG	360
CANTCGTCAT GTCTTTAAC GGGCATGGGG TTACNGATGG GGGTTAATAT TTTCANCNGA	420
TTTGGGGTGG GGNTGATGTT CNCNGGGGA CGCAAAAGTT TTTTGTACAC CTGTTACGN	480
CC	482

(2) INFORMATION FOR SEQ ID NO:1432:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

CAACGGATGA AACCAAACCT GGTGTGCGGT CCGGTACAAA TNTGCTGGCA TAAATTGCC	60
CGCNACTGGG AATGTGGAGC TGCCTGAAAT CCCTATGNGC CCCCCTGTCAG TTGTTTATGG	120
ACCCGAAACG CATGATTGAA AGCCTGTGAA CGAAAACACC ATCGGCGTGG TGCCGACTTT	180
NGGCGTGACC TACACCGGTA AACTTATGAA GTTCCACAA CCGCTGCACG GATGCGCTGG	240
GATAAAATTCC AGGCCGACAC CGGTATCGAC ATCGACATGC ACATCGACGN TGCCAGGTGG	300
GCTTCCCTGG GCACCGTTNG TTCGCCCGG ATTATCGTC TGGGAATTNC GNCTGCCNG	360

TGTGAAATCG NTCATGTTTC AGGCCTNAAT TCGGTTGGT TCCTTGGGTT NGGTTGGGTT	420
ATTGGGGTAA GANAAGCGTT NCCAGAATNG TTGTTNACGT	460

(2) INFORMATION FOR SEQ ID NO:1433:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

AGCAGGGAGC AGCACTTAT CGGGNTCGGT GNTTCACCG TCAATGAACA ATTTTTNCG	60
GATTAAATAA GTTGATAGCA ATGGCGATGG TTTTACCCAG ATGACGACCG ACATACTCAA	120
TTACTTCCGA CGCCAAACTA TCGCCTTNT TCGCGGCTTT GCAGATTAGT TTTGAATGGT	180
GCAGTCGTCC AGCGGCAGGA NCTGCTGGTA GCCCTGCTTT TAACAGGTTAACACCCGTT	240
GTTCCAATGG CAGCGTTGGC AGCGATATTT TTCCAGGCAG CCAAGTTGCC GCAATGGCAG	300
CGTTTCACCC AGCGGTTTCG ACCTGAATTA TGGGCCATTT TCACCGACGT TGCCCTTGNG	360
GGCCAATAAA AATGCGCCCN TTTAGGGGNT NATNCCGGGG CCCGGTNNC CCATT	415

(2) INFORMATION FOR SEQ ID NO:1434:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

TTCTGGCAA AACCATGACC CGGAACAGAT TGATTGATT GATTTACTAG TGCAAGTTGTG	60
GCCTGGCNAG ATGACAATCA TCATTTCCGT CATTGTGGCT ATTGGCCTGG CTATTGGGAT	120
ATTGGCAGT GGCGGAGGNG AAATGGGACG TCAACAGCAA TTATCACTCA GCCCGACGTG	180
GGCAAATTG CTGGGCTATA ACAATGCCAT GAATGTTAAT CTATGGTCAG GCTGCACCGA	240
NAAGTTATCG GNTTTCCAG GANGTCGTTN AATTGGTCGG TTTTCAGTTC TGCCNNCTC	300
TGGCATTNAG CAGAAAACGC TTGGGATAAT TCAGGGNAGG GANCGNGGAA AANNTTTACC	360
CNTGGAAAC CTTGCTGTT TAGGAANCCA GGCAATTGTA CCCTTGGATC TTGTTTCTT	420
AATGNTNNNGG GGCAAAACTN TCAGAGGGGG GGGCACAAATT TGATAGTTT	469

(2) INFORMATION FOR SEQ ID NO:1435:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

GTGAAGGGCT GAAAAATCGC TACGGCGCGC TGATGGNNGC CATTNCGGC GTGCACTACA	60
NTTTCTCTTT GCCAATGGCA TNACTGGCAA GCAAGTGCAG TGNTATCTCG GNCGCTGATG	120
CCAAANAGAA AATTCTGCG GGCTATTCCG GCGTTATCCG CAATNACTAT CGTTTCGGTT	180
GGGN	184

(2) INFORMATION FOR SEQ ID NO:1436:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

TAACCCGTCT NACCTTGAGA TTGTAAGCCC GGTAGTTATC GGTTCTNTTC GTGCCCGTT	60
GGACAGACTT GAATGAGCCG AGCAGCAACA AAGTGCTGCC CAATCACCAT CCACGGTGAC	120
GCCGCAGTGA ACCGGGCAGG GCGTGGTTCA GGAAACCCCTG AACATGTCGA AAGCGCGTGG	180
TTATGAAAGT TGGCGGTANG TAGTATTCTGT NNATCAACAA CCAGGTTGGT TTTCACCACC	240
TCTAAATCCG CTGGATGCC GTTCTACGCC GTACTGTACT GATNTTCGGT AAAGATGGTT	300
TCAGGCCCCG ATTTTCCAC GTTTAACGCG GACGATNCGG AAGCCGTTNG CCTTTNTGAA	360
CCCGTTGGG GGTTCGTTTT NCFTAACAAAC TTTTAAAGGN GA	402

(2) INFORMATION FOR SEQ ID NO:1437:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

GGCGGGCGTA TTAAGACAC GNTCAAGGCC AGCTGTNAAG GCATCGGCAG AGTTTCCTG	60
CGGCGGAAA CCTGNGNCAT TCAATGAGTG ATTAAACAGT AAATAATGTA ATTACCCGGT	120

CATCACGGTG CGNAAAATCG TTGAATTGC TGGCTNTCGG NCTGCACCCA TTTGCAATGG	180
GTTCCGGGCA TGNCATAAAG AGAGGAAGGA GCCAGNGCTC GCGCGCCGNT TCAATTGTGT	240
TTCTTCCGNC GGGNGTTCAC ATTGTGGTTT ATCGTCATGA GAGACACATT AATCCGGGA	300
TTAATCCCAG ATTATTGTNC GCCAANTNGA CGNTTAATT GTTTCGGCCA TTAGGACGGG	360
NAAAACAGGG CCAGG	375

(2) INFORMATION FOR SEQ ID NO:1438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

TCAGAGGCAA GTTCAGACCG TGGTGTTC TTTTCACGGA TCCNGCCCTN NCTTCCCGNA	60
AAGAACAGACAG CCTTGGGTCG CGATTGTGGG GCTTNGAAGA GTCCAGCAGT GGGCAATTTC	120
TAGGAATTG GGAATCGAGT GCATTTNCTG ACATTGAGT ACAGTACCCA GGGGTTCTTG	180
GAGAAGAACCCAG AGGAGCTTGA CTGACCATAA AAATGAGTAC TGCAAGATGCA	240
CTTGATGATG GNAAACACAT TTAAAATATT AGTTGGCAAC CAGGTNATTN CATCTTGGNT	300
TTTATGGGG GAAAGGTTGC AGTCAGNGGG	330

(2) INFORMATION FOR SEQ ID NO:1439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GCATGANGAA TGTNCAGCTC GTCGATTTCN TGGGGTTCCG CGCGGCCAG ACTCCAGCTC	60
AACGCTTCT CTTTNATCTC TTCATAGAGC GCCANACGGC GTTTTCGCT CAGCTTTTG	120
GGAATCATTC AGCCCGCAA TCGGGCGCGC CCGGGTCAAG GATCACCGCA GCGGTGACGA	180
ACCGGCCAA CTGAACGGAC CCGCNTCCGA TTTCATCCAC ACCCGGCAAC CAGCTGNGTG	240
TGCGGGATNA AACAAATTG GTGCATTGTG NTNAATNCCA GNAACGGTT GTGCCACCTG	300
GTNCATCGGA CATTGACAGC GGNTTGCTA GATGGNAGTT NCACGGNAAG GTTTCGTNN	360
CANCGCGTGG TTGGTTTNC CNGTTAGGNC AACAGTGGTT AACAGTGACC GCAGCCAGTT	420

TTTTAGGGTT CACATTTTN CTGGCANTAA TTATTTGGGA TAA 464

(2) INFORMATION FOR SEQ ID NO:1440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

ATACGTCCGG TGGAGAAGGA GATATGGCAC AGCACTAAAG AGGCCACCAT CACCACCATT	60
TCTGGCGCAC CAAGTGCAAA CTGCAATTG TTACCCGTCA TAAAGGCAAT TAGCGTGACG	120
ACAGGTONACG GTGAAGCGAA AATGGTTGCT AACACTGGAA CCAAAGAACAA GATTCATCGC	180
GCGCTGAAAC CTGGTTGTT AACACTGCTT TTNAATGCAC CTGAAACCTT CCGGCGACAG	240
ATTCAACAGT GCCACCAGGN AAGCCAGTTA AAGGCGACCA GGGGTCAATT CATGCTGTTC	300
GAGGCAATGT CTTCCCAGCG AGCTTGGCGT TNCAATTG GTTCACCGNA ATTAACGGGN	360
AATTCAAGNTG GGNTAATTCA AACC	384

(2) INFORMATION FOR SEQ ID NO:1441:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GANTACCAAT GGTACCGACC AGCATAGAAG CCATAAAGGT TGACCACTCA ATATTCAACC	60
CGCTGGTCAT CAAGATCATT CGGGAACCAT GACCTATCGA GCCAAGCAGC GCACACCAGC	120
NTTAATTTC GCTCTGTAAA ACGTTCATCA TGCCTTGAA TTTGCCCGCT ACAACGCGCT	180
NAAGGCTNCA TACTGGTATT GCAGGCTGTT ATCGGAAAC TGGGTGCGTT CGCGAATACC	240
ATAATAACGGA CGGTATTNAC CGTCCAAGNC GAAAGGCTGG TNCCGGGAAT NACGGTNTTT	300
GNCAGTTCCCT GCGGGTAGG NAGGGCGTTC ANGCCCTGAC GCCCGGGNAA TGTTGTTGA	360
CGTTGGAGG GTNCATCGTN CAGTGNCAAC CCACCATTGG TTTGNATACC CCGTTCCCAC	420
GTTTGNATG NACNTTTT TNAAGTTCA CTGGGGCAAATCGGTTATT CGNGGGGCCT	480
GN	482

(2) INFORMATION FOR SEQ ID NO:1442:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

AACTCCGTGC NTGGCGACCG CAGCCCGGTT GTAGATATCA NCTTCCCGGA AATCGAGAAG	60
TTTGACCGTN TACCGGAACC GCGCGCCGAA GGCCGGACCG CTTTTTTTTC CATCATGGAA	120
GGCTGCAATA AATATTGCAC CTACTGCNTG GTGCCTTACA CCCGTGGTGA AGAGGTAAGC	180
CGTCCGTCCG ACGGATATTC TGTTTGAGAA TTGCCAGCT TGCGGCTNCA GGGCGTGCNT	240
GAAAGTCAA CCTGCTCGGT CAGAACGTGA AACNCCTGGN GTGGGTGGAA AATAACGACG	300
GGCACCAACCG GTTNCGTTT G	321

(2) INFORMATION FOR SEQ ID NO:1443:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

TTTCTGCATC CCCTGCGGGA AGCCTGCTGC CATGACAGCC TGAGCGTGAA TGCGCGGNTA	60
TCAATGCCGA CAATTACGN CCGTATCACC CCAACAAGCG CAGATGTTA AATATCATCA	120
GCTCGCGGTG GACAACAATT GCCACTCCCC TAGACTGNCC CTCATTGCCA TCAATCCGGC	180
TATCAGGGGC GCATGGCGAT CCACGNAAAT GGATGGTGGT GACGCCGGNA ATTAACGGGN	240
CCGCTAATTG CATGAAAAT GTGGATGNAA CAAGCACTGG GAGGCGAACT TAGTACCGGN	300
CAACAACACA AGGNCTTCA ATCAAAATG GGCCTGCAA AAGTGATNAG CGGTGTACAC	360
N	361

(2) INFORMATION FOR SEQ ID NO:1444:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

TTATAACGGC GCGCTGGTAC AGAAGGCCGC TGATGGTAGC ACCGTGGCGC AAACTGCTCT	60
CAGCTATGAC GACTATCGTT TCCTGGAAAA ACTCTCTCGC GAGTCGGTTC TCATTCNAC	120
GCCCTGGACC GCACCACGCT GTACACCGCC AACCGTGAAT ATCAGCTACT ACACGGTGCA	180
TGAATCCTTC GTTGCCACCA TTCCGCTGGT GTTCTGCGAG GGAGNAAAAT GGACCCAAT	240
ACCCAGTTCC TGAAAGTGAA TGATGATTGA TGAACCCGCC ATCCTCGGAC CAGGCTTATT	300
CGCGCGTTAT TTCCCGAGAA GTTGNAAGA GGAAATATTA CCGTGCTTGN AAAAGTGGCG	360
NCNGTAATTT CCTCGGAATT CCTCGGTTAA ACGGGGTTAA ACAAAGGTTA CGGGGGGTNG	420
AAAATCATTG GGCCNACGTN TTAAGTTTT NAAACCGGAG GGAATTCATG GGGGNTTTGG	480
	480

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

GGCACGAGTA ACTCTNTCTT TTCCCTGATAA CATGGCCAGC AAGAAAGTAA TTACAGTGTT	60
TGGAGCAACA GGGGAAGCTG GTGGCAGACT CCGCCAAGCA CCTGGGTCTG AAGCACGTGG	120
TGTACAGCGG CCTGGAGAAC GTCAAGCGAA CTGACGGATG GCAAGCTGGA GGTGCCGCAC	180
TTTGAACAGC AAGGGCGAGG TGGAGGAGTA CTTCTGGTCC ATTGGCATCC CCATGAACCA	240
GTGTCCGCNT GGCGGCCTNA CTTTGAAAAA CTTTCTCGN GGNGTGGCGG CCCGTGAAAA	300
GCCTCTGAAT GGNG	314

(2) INFORMATION FOR SEQ ID NO:1446:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

TAATGCNCAC GGAACCTGGAA GGGAAATTAA AATGATTCCA CCCTGCTGGC GGATCTCAAT	60
AGCCCATTGC CAGAAGGCTC CGTGCCTAAC TGGAATCCTG CCGGTCGTCG CGGNNTAGTG	120
AATTCTGGTC ACTAAAGAAG CGCATTGCCT TGGCGATTTG TTGATGAAAG CCAATTAACG	180

GCAGCCTGGA TGTCGAAATC GCGGCAGTTA ATTGGTTAAC CACGATAATT TACGTTCTCT	240
GGTTGAGCGT TTTGAATAAT TCCGTTGAG CCTGGTAAGC NCATGNAAGG GTTTAACCG	300
NAAAGGNGCA CGNTTCAAAA GATGGGGGG	329

(2) INFORMATION FOR SEQ ID NO:1447:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

ACTAATGGCA CCTGCAGATG ACCGTGGCT GGATTTTAG TAAGTCTCTG GGGGTTGATG	60
AATCCACCGT GGCAATCGTT GTTATGGCAA CCATGCTGCT GCTGGGTATC GTTACCTGGG	120
AAGACGTGGT TAGAAATAAA GCGGGCTGGG AATACCTTAA TCTGGTACGG CGGTATTATC	180
GGCTTAAGCT CCTTATTATC GAAAGTTAAA ATTNCTTCGA ATGGGTTAGC TGAAGTCTTT	240
AAAAATAAAC CTGGGCATTT TGTGGGTCCA CGGGTAACGT TGNGTGTCTT CGTTAATTAT	300
TTTNCCTCAG GATTGTTCGT GGCGTTAATT TCCTNNNGNT TTCCCGTTAG GTG	353

(2) INFORMATION FOR SEQ ID NO:1448:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

GGCANGAGGG NAGACAGAAA ACAGGTCTTG NTTCCCAAN TGGCATTGGA CTTTTCTGAT	60
ATTACTGCCA ACTCTTTAC TGTGCACTGN GATTGCTNCT CGAGCCACCA TCANT	115

(2) INFORMATION FOR SEQ ID NO:1449:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

GGCAGAGGGN AGAATGGAGA GGGGGCTGCC GCTCCTCTCC CCCGTGCTCG CCCTCGTCCT	60
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CGCCCCGGCC GGCNCTTTC GCAACGATAA ATGTGGCGAT ACTATAAAA TTGAAAGCCC	120
CGGGTACTTN ACATCTCCTG GTTATCCTCA TTCTTATCAC CCAAGTGAAA AATGCGGATG	180
GGCTGATTTC AGGGTTCCGG ACCCCATACC AGNGNATTAT GATCAAANTT NAAACCTTCA	240
ATTTGGATTT TGGAGGGACA AANGAC	266

(2) INFORMATION FOR SEQ ID NO:1450:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

GGCANAGGCA AAGATCCCTG AGGATGTGTC TGGTCTCGTT TCTCTTGAGG TTCTTATCTT	60
ATCAAACAAT CTTCTAAAGA AGCTTCCCCA TGGTCTTGGA AACCTTAGGA AGTTAAGAGN	120
AGTTGGGATC TAGAAGAGAA CAAATTGGGA ATCCTTGNC AAATGNAAT TGNCATATCT	180
TAAGGNTTA CAGAAATTAG TCTTGACAAA CAACCAGTTG ACCACTCTTC CCAGAGGCAT	240
TGGTCACCTT ACTAATCTGC ACACATCTGG GGCCTTGGAG AGAACCTGAC TTGACTGCAC	300
CTTCCCTGNA GGAAATTGGT ACACTGGGAG GAACCTTGGA GGNACTGTAT TTGNANTGAC	360
AAACCCCAAC CGGCATAGGC NTTCCCTTTT	390

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

GCGAAGCTGC CTGCAACCTG GAACCGGGNA GCGGCACAGG AGACGGTGCG GCTGCTGGGC	60
GGGCCAGNGA AGCAAGGNGG GGCGCCCCG AGGGAAACCA TGCTGCCTTC CAGGCTGACG	120
TNTCTAAGGC CAGGGCCGCC CAGTGCCTGC TGGAAACAAG TNCCAGGCCT GCTTTTTCG	180
CCCACCATCT GTGCGTTGTN TCCTGTGCGG GGCATCACCC AGGATGAGTT TTCTGCTGCA	240
ATTGTTGGA GGATGACTGG GANCAANTCA TNAGCTGTNN AACCTCAAGG GGCACCTTTC	300
CTAGTCACTC AGG	313

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

GTCGTCGCCT TTAATCAGAC GGGTATTAAA ATCATCGGCA AAGCAGCTAT TAAAAATTTC	60
AATCAACTGC TCGTANTGGT GTGTACTGTT CATTAGTTCA TCCCCAACCA NTGGGGNTC	120
TCCTGTCCGT GGTTGTCGTA ANTTAATTG GCACTGCATC ACCGTNCGAG ACGNNTAACAA	180
	180

(2) INFORMATION FOR SEQ ID NO:1453:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

AACCTGGCCT CANTTGATT CACCCGCTTC AGGTGTTCGA GGTTGAACAG CAGGATAATG	60
AAATGNTGGT CTATGCTGCC CCCCGTGAAT GTGCGTAAA CGTACCTGGG CAGCTTGATA	120
CGCCTTTATT TACGTTGCGC TTTTCTCCC CACAGGTAAAG GTATTGTCGG TGTGCGGATT	180
GAGCATTTC AGGGGGCGCT GAATAACGGT CCTCATTATC CGCTCAATAT TTTGCAGGAC	240
GTGTAAGGTC ACAATCGAAA ACACAGAACG TTATGCTGAG TTTAAAAGT GGGCAACTTA	300
AAGCGNCGCG TNTTCAGCAA AAGGTGGAGT TTCTGGTCA CTGGGATTTC TCTGAGGCAA	360
CGGNNGNCG TTATTAACCG GTTAGTTCAAG TGGAAAATTA ATTGGGTTAC GTGCAGGACA	420
NGANTAATTAC ACGCAATTAT ATGTTNAGG CGGTTGATCT TGGGTTGGG GAACAGTTA	480
GGGTCNNNGG	489

(2) INFORMATION FOR SEQ ID NO:1454:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

TATCAATGCC GAGAATATCC AGCCACTGCT GCACCANTTT TTGCTGGCGA ATCCGAAACG	60
GCCTGATAAA TGGCCAATCG GAATCAAAT GAGNCCAGTA AAGGAATGCA CATTNACGGN	120
ACGGTAAGNT NGNAGCCCGG TNAATGCCAG ATGGCAAACG AACTTGCTGN ACGTGAACCG	180
NATNATGNCT TTTTGAATAT CCCAGAATGG GTTTNCGCC GCTGCCGNGA ACGTTCGTTC	240
CGAAAAGGC GGTGCAAATC GTTTGCTGTT AACCTTGCGG GATGGATNGT CATTAACCAG	300
GGTTTNATTA AGTGNGTTT NCCGG	325

(2) INFORMATION FOR SEQ ID NO:1455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

AACCATTCG ATATCTCTCT GGCGATGTTT ACCCATGTGG GCGCGGCGGC ACCGGGTAAT	60
CCTACCGCTA TCGATACCCA CTGGATTGG CAGGAGGGTG ATTGTGCCT GACCCAAAAT	120
CCGCTGGAGA TTAAAAACGG AAAAATTGCC GTTCCTGATG CGCCCGGTNC TGGGGTGGNA	180
GCTGGNACTG GGGAACAGGT NNCAAAAGGC ACATGAGGCC TATAAAACGT CTGCCTGG	238

(2) INFORMATION FOR SEQ ID NO:1456:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

GGCACGAGCC TTCATTGCCT CATGTAAGAC AACCTCACCA AATACAAGAA AACAGTGTCC	60
AGCCCACCTT TGACACAGTT TTTNCTTGAT TGTGGAGGAC TAGCTCGAAC AGATAAGAAA	120
CCTGCCATTT GTAAAAGTTA TCTCAAACTA ATGACAGANC TGTGGCATAA AAGCAGGCCA	180
GGATCTGTTG TGCCTACTAC TCTGTTCAA GGAATTAAAA CTGTAAATCC AACATTTCGG	240
GGGTATTCTC AGCAGGATGC TCAAGAATTG CTTCGGTGTT TAATGGATTG GCTTCATGAA	300
GGATTTGAAA GAGCAAGTCA TGGAAGTAGG AGGAAGGTCC GGNAAACCAT AACCCTTNT	360
GGGGGGCCAT TGGGAGGGNG GGNCAAGGGC NATCCGGTTT TTGGGTTTTC CAGG	414

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

GGCACGAGGA CATATTGATC CCTCTCTNAG ACTCATCTGG GATTTGGCTT TCCTTGGAAAG	60
CTCTTACGTG ATGTGGAAA TNACAACACA GGTGTCACAC TACTACTTGG CACAGCTCAC	120
TAGTGTGAGG CAGTGGAAAA CTAATGATGA TACAATTGAT TTTAATTATA CTGTTCTACT	180
TCATGAATTA TCAACACAGG AAATAATTCC CTGTCGCATT CACTTGGTCT GGTACCCTGG	240
CAAACCTCTT AAAGTGAAGT ACCACTGTCA AGAGCTACAG ACACCAGAAG AAGCCTNCGG	300
GAAACTTGAA GGAAGGATCT NCNTGTAGTT ACCCAACAGA GCTTTAGTAA TTTTTTAAAAA	360
AGGAAAAANT GATNCTTTT TCCG	384

(2) INFORMATION FOR SEQ ID NO:1458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

CTGCTGCCCT TNAGGGGCCA AGCCAACANA GGCTGCTACG GGATCCCAGG GATGNCCGGC	60
CTGCCCCGGG CACCAGGGAA GGATGGGTAC GACGGACTGC CGGGGCCCCAA GGGGGAGCCA	120
GGAATCCCAG CCATTCCCGG GATCCGAGGA CCCAAAGGGC AGAAGGGAGA ACCCGGCTTA	180
CCCGGCCATC CTGGGAAAAA TGGCCCCATG GGNACCCCCT GGNTNTTAA GGGGTGCCCG	240
GCCCCATGGG CATCCTTGGA GAGCCAGGTN AGGAGGGCAG NTACAAAGCN GAANTTCCA	300
GTAAAGTTT TCACGGGTCA NTNGGCAGAC CCCAACCAAGC CCCTTGNAAC CNAAAAGCTT	360
NTTANNTTAA AAGGGGGTT CTTAACAAAC CCGAAGGGGT TTTTTNNACA AGGGCAATTG	420
GNAATTAA CTTGAAAANT NCCCCGTTTT AATATTTTT TTTTACCA	468

(2) INFORMATION FOR SEQ ID NO:1459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

GGCANAGCCA GCATCAGGCT TCCAGAGTTT GCAATTCCGA CTATTAGAAA ACAAGATAGG	60
TGTTCTTCAG AACATGAGAG TCCCTTATAA CAGAAGACAT TATCGTGAAT AACTTCAAAG	120
GAGAAGAAAA TGAACTGCTA CTTAAATCTG AGCCAGGAAA AGACACTTCT GGAAATTAGT	180
GGAGGCATGG CTGGAAAGAA CTCCAGGTTT AGAGCCACAT GGATTTAATC TCTGGGGAAA	240
GCTTGAAAAA AATATCACCA GAGGCCTGGA AAGAGGAATT CCNTAAGGTT TCAGGCTAAA	300
GAAGAGTCTG ANGAAAAGGG GGAACAGTGG CTGAATTCC GANGCAAAG AGGTGCTATG	360
TCCNTATTTG TTGAGAACG TCCTGAACCA TTCCCTTNGT NAAGGTTAAA NACGG	415

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

GGCACGAGCT CGGCTACATT CACCTGCTAT GCTTGTNACT CCACCCTGCT CTAATGCCGC	60
TTTCTCTGCA GGCTCTTCTT GGTTCCCCAA GCTAAGTGGC TCTTGCCCTT GTGTACCTGC	120
ATTGCAGTTT TATGATACTT CTCATGTCGT GTCTGTGCTT TCCTACCATG CATTATTATT	180
CACGTGCTTG TCTCATCTCT TCTGCCAAAT TCTAAGCATC TGGATGGCTG GGTTAAGTT	240
GCATCTCTGT GTCCTTCAGA CCATATGCCA TAGTGCCTTG TGCCTCACGG TGACTTGTAT	300
TTTGCAGAAG CTTAACAGAT ATTAACAGGG ATATCCAATT ATAAAAGAGT CATNAAATAG	360
ATGGTATTTT ATGGTTAACCA ATATTTAAAT GTAGGAAGTT TATTCAGTTC CTGCGNAAA	420
TCAACTCTCA AATTCCAGTT TTGTTTTCT TTGAAAGTGT CTGAAAACACT NG	472

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

GGCACGAGGT TTCTTATATG CACACAGCAT GCCTCTGCAA TGCCATCATT GCTTGCTGA	60
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AAGTTCCCCT TTCTTCCAG AGATATTTT TCCAGAACT ACAGTCTACC AGCATCAAGC	120
TTGCTCTGTC ACCATCGCCC CGGAATCCTG CAGAGCCAT TGCTGTCCAG AATAACCAGC	180
AGCTGGCGCT AAAGGTAGAG GGAGTGGTC AGCACGGAT CTAAACCAGG ACTCTTCCGC	240
AAAATTCACT CTGTCTGTCT TGAATGTTTT CTTCCACACT GCAGAGTAAA ATCTGGGACA	300
AGACTTACAA GGTTACCCA TTTGACAAAC ATGGACCAA TGNGGTTGGA GCAAAGGGTT	360
TGAACCNCCN AATGGTTATT TTCAGTACTC NATTCTGTT GGAACCTTG GTTATCCTTG	420
GGACCACACA CCTTTCAGTG GGATNTTTT TTGAAAGATG NCCATGGTT GGTTTGGAG	480
GCTTGAG	487

(2) INFORMATION FOR SEQ ID NO:1462:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

GTTCGGCGTT TTGCGTCGCT GTGNCCCTCC ACCATCGNAA TCATCCGATC CAGAAATNTC	60
TCGCCGGGGT TAACGCTACA CTCAAATCACC AGCCAGTNAG AAAGNAATAC GCGTGCCTTC	120
GGTGAACGGA GGCAAANATN CGCCGCCGGG ATTACCGGAT CACCGGTGAC CNATNTCCCC	180
GGTGATGGTC GNNTTGCATA CGACCGANGC ACCCCCTTCA ATAAACTTNA CCATCGCAGG	240
GGG	243

(2) INFORMATION FOR SEQ ID NO:1463:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

GGCANAGCCG CAGGACCCA TCCTGTTCTC GGGGACCTG CGGATGAAAC CTGGACCCCT	60
TCGGCAGCTA CTCAAAGGAG GACATTTGGT GGGCTTGGA AGCTGTCCA CCTGGCACAC	120
GTGGTGTGGG TCCCAGCCGG CAGCCTGGG CTTCCAGTGC TCAAAGGGCG GGGAGAATCT	180
NAGCGTGGGN CANAGGCAGC TCGTNTGCCT GGGCCCGAGC CCTGCTCCGC AAGACCCGCA	240
TCCTGGTTTT AAAACGAGGC CACAGCTGCC ATCGAACCTG GGNGACTGAN AACCTTCATT	300

CCAGGGTTAC CATCCGNAC CCAATTGAA TACCTGNANT GTTCCTGACC NTGGAAAACG	360
GNTTTAACAT TTTCNGGATT ACANCAGGTN CTGGTTCCTG GACAAGGAGT AGTAGTTGAT	420
TTAATTNTCC AGCCAACHTTC NTGCAGTAGN GGCATTTTT AGGGATGGCC AAAATNTTGG	480
ATTTGTC	487

(2) INFORMATION FOR SEQ ID NO:1464:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

CCTGTGTACA NAGGATTGCT NCCNCTACGC TATGTGGAC ATTGNCCATC CCATGCAACA	60
ACAAGGGAAG CTCNATCAGT GGGTTGAAT GTGGTGGCAT GCTGGGCTCG GGAAAGTTCT	120
GCGCATGCGG TGGGCACCAT TTTTCCCCGT TGAGACACCN CATGGGAAGG GTTNATGTCC	180
TNGTCCTCGT NACTTCNGAC AAGAG.	205

(2) INFORMATION FOR SEQ ID NO:1465:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

GGCAGAGGAT TTGAGTGGCA TATAACCAAA GGCGGAAATA TTGGGGCTAA GTGGACTATT	60
GACCTGAAAA GTGGTTCTGG AAAAGTGTAC CAAGGCCCTG CAAAAGGTGC TGCTGATACA	120
ACAATCATAAC TTTCAGATGG AAGATTCAT GGAGGTGGTC CTGGGGCAAG CTTGACCCTC	180
AGAAGGCATT CTTTAGTGGC AGGCTGAAGG CAGTAGGGGA ACATCATGCT GAGCCGGAAA	240
CTTCAGATGA TTCTTTAAAG ACTTACGGNC AAGCTTCTGG AAGGGGCACA CTNACACTTT	300
TTANTGAAAA ATGGGANTCC TTTAAATAAC TCTCTTCAC CCCAANTANG GTTGNNNTA	360
TTCTGGAAA AGTGATTTAG GANCTTAGGT TGCAGGGAA ATTGGTTTA ACTTTTNCA	420
GTTC	426

(2) INFORMATION FOR SEQ ID NO:1466:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

GGCAGAGCTT TTTCCANAAT TTAAAATTGT AATAGAAACA GAAGATGAGA TTATGCCTGA	60
GGTTGTGGAA AAGGAAGATT ACTCAAAGAT TATAGGGAGC ATGGGGATAT AATGGGAAAG	120
CAACACTCCA GTGGTGCAGA TGCTCACAGT CTTATGGAGG AGCCCAAATG AATATCTGGG	180
GAAGTTAAAG TCCATATGAA TGNACTGATA AAGAGTACAA TACAGGTGCC ATGGGGANCA	240
CGTGNGCATT CACTGGAAGA CTGCCTGGNA GGGGGCCGCG CGTGTTCCTTCC ATGGCCTATT	300
ACGGTTAACN CTGGTNACAT AATGGAAAAT GCTTATNCTT TAGGTGGAAA GGNGAGCCTN	360
GAGTTTAGCC GGTTTCAGGG T	381

(2) INFORMATION FOR SEQ ID NO:1467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

GGAACGACCT TAATNAAAGC NATTNAGGCT TATGGAATGA NGCCACATNA AATATTCAAG	60
GCAAATAACC TTTTTANGAA TTGGAAAACA TGNCCCAGGT TCAAACACTACT CTGGTGGCTC	120
TGGACAGGTC TGGCTNAAAN CAAAAGGTTT CCATACANCC ATTGACATTG GGGTTAAGTT	180
TGCGGANAAC CAANCAAGAG GTTTTGATG	209

(2) INFORMATION FOR SEQ ID NO:1468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

GGCANAGCTC GAGTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTAN NCCCCCN	57
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(2) INFORMATION FOR SEQ ID NO:1469:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

AGATGCAACT ACCATCACAG AATGTNTTCA TACCTNNNGT AAAAGCTGCA TCGTAAGACA	60
TTTTTACTAC AGAACAGAT GTCCAAAATG CAATATAGTA GTACATCAGA CACAACCTCT	120
TTATAACATA AGGTTGGACC GACAGTTACA AGACATAGTG TACAAATTAG TGATCAATCT	180
AGAGGAAAGA GAAAAAAAGC AAATGGCATG GATTCTATA AAGGNAAGAG GTCTAGNNGT	240
ACCTNAAACC TGCTGTTCCA CACNC	265

(2) INFORMATION FOR SEQ ID NO:1470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

AAAGGNTTGA ACCGTGCCTC ANAGGCAGTA NAAGCCCCAT GGTGGTGGTG CTGNGTGGNA	60
GTATGGAGCC GGCTTTGAA AAGAGGTGAA CCTCCTGTT CCTAAAAAAAT TTCCGGGAAA	120
GNCCCAATNA AAGATGGTGA AATAGTTGTT TTTAAAAGTT GANGGGNCAG GN	172

(2) INFORMATION FOR SEQ ID NO:1471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

NATGTTAAG ANCCTCGTN AACTGCNTT CAGGCCATCA AGGGTATGCA TATAGAGAAA	60
GCCACGAGTA TTCTGANAGA TGTGCACTTT ACGGAAACAG TGTGTACCN TCCGACGTTA	120
CATGGTGGNG TTGGCNGTGT GCGNGGTCAG G	151

(2) INFORMATION FOR SEQ ID NO:1472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

GGCANAGGNC AAAANATACT AGAATTNATA GTGGAGAGAA ACCTTACAAG TGTAATGN	60
GCAGCAAGNC CTTCCGTCTA AGGTCATACC TTGCAAGCNA TCGCAGNGTT CATAGTGGT	120
AGAAAACCTT ACAAGNGTAA TGAGTGCAGC AAGGNCCTT	159

(2) INFORMATION FOR SEQ ID NO:1473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

GGCANAGGGG ANGCCAACTT CANTNTATCC TCAATNCATG GAGACATNCC CANAAAGNGC	60
GGGNGTCCAT CATGAAGGAG NTCCGGTTCG GGCGCCACCN GGTGCCTTAT TTCTGACAGA	120
TNNTCTGGGC CAGGGGGTTG GATGNCCCTC AGGTGTCCCT CATCATTA	168

(2) INFORMATION FOR SEQ ID NO:1474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GGCAGAGACG GNCACGAGAA GACTTAAAGG TAAAGCGTAT TACCCCTCGT AACTTGGCAA	60
CTTGCTATTC GTGGAGATGA AGAATTGGAT TCTCTCATCA AGGGCTACAA TTGCCTGGTG	120
GTTGGTGTAT TCCACACATC CACAAATCTC TGAATTGGGA AAGGAAAGGA CAACAGGAAG	180
ACTGTCTGAA AGGGTGCCTG GNATTCCCTT GTTAATCTCN AGGNACTGTT AAATNACTCT	240
GAGCAGNTGG TCCCAGTGTGTT GGTGATTCCC AGTGGACTGT GATGNTCTGT GAAAAAAACC	300
ACAATTTTG CCCTTTTTG GGTAAATTGC TGTTTNAGG CCAAGTTGG GGAAGNTTTA	360
AATTAGNNNTT TTCC	374

(2) INFORMATION FOR SEQ ID NO:1475:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

TGCCAGTATT TGANCATTAC CATGAAGGAA CTAGCAGTTA TGAAC TGACT GGTTTAGCCA	60
GAGGTGGGAA ACAGTTGGCT AAATTAAGA GGAATTATGC CAAAGCAGTG GAACTNACTG	120
GTGGNAACTN AGCTTCTCTG CCAGACTTCT TTTGTTACTT TGGATGAAGC TATTAAGATG	180
AACCAACAGG CGTGTGAAAT GCCATTGNAN CATGTGCATC ATTCCCCGGG ATTGANCFTA	240
CTCTTGCTTA TATCATCCAC AGTAGCTGGG ATGGAGGAGA GAGNN	285

(2) INFORMATION FOR SEQ ID NO:1476:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

GGCAGAGATG GGCAC TGGGTG CTGGATTTAA NGTTGATGCC ACTAAAGATC CTTGGAAAAA	60
CCAAC TACAG AATGTNCTCT TAATGTNACA AAGGAGCTTC CCCAACTNAT AAATGCCAA	120
TTTNCAGTG GGATCCCCAA AGGAATGTCT ATTTTGCC ACTCCATGGG AGGTCATGGA	180
GCTCTNAATC TGTGCCTTG AAAAATCCT GGGAAAATTA CAAATCTGTG TNAGCATTN	240
NTCCAATTG GNNAACCCTG GTAATTCTGT CCCTGGGCA AAAAAGNCTT TGGTGGAT	298

(2) INFORMATION FOR SEQ ID NO:1477:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

GGCAGAGNCA CCAGCCTCTN ACGGAGGCAT CTTAATGTNA ACCTACCTAC CATTGCCCTG	60
TGTACACAGA TTCTCCTCTG CGCCTATGTG GACATTGCCA TCCCAGTCAA CAACAAGGGA	120
AGCTCACTCA GTGGGTTGA ATGTGGTGGA TGCTGGCTCG GGAAAGTTCT GCGCATGNTT	180
GGGCACCATT TCCC GTGAAA CACCCATGGG AAGGTCATGC CTGGATCCTG TACTTCTACA	240

GAGNATCCTG AAGAGGATTG AAAAAGGAAG AGGCAGGCTG CTGCTGNAGG AAGGCAGTGA	300
CCCAAGGAGG GAATTTTCAGGGTGAATG GACTGCTTCC CGTTTCCTGA GTTCAATGG	360
TTAATTAGG CTTGNGTTNN CANATTTGGT TTN	393

(2) INFORMATION FOR SEQ ID NO:1478:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

GGCANAGCTA TGGGTCGTGG AACAAAAGTT AATCCTACAC CTAAAANANG ACCAAACTAA	60
GTACTTGGAG GAACGAGNNA TAAAGGTG	88

(2) INFORMATION FOR SEQ ID NO:1479:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GGAAGAGTNT CTACTGTGGG CAAGTNNTTA AGANGCCCC CATGCGGTAA AAGANCTTNG	60
GAATCTGGCT GC	72

(2) INFORMATION FOR SEQ ID NO:1480:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

CTCCGTGNCA CTTTATGAGC GCATGAATCA GTCTCTCTCC CTGCTCTACA ACGTGCCTNN	60
CAGTGGCCGA GGAGATTCAG GATGAAGTTG AATGAGGTNC TTCAAAAGA GGCAAAACTG	120
ATTNCAAATG ACGTCTTGGC CAACATGATT AGTGAACCAA GGAATCAGTT ACGGAAACGA	180
TGCTCTGCAT GCCATTCTTT NAACCGAAC GAAAACCACC GTGGGNGGNT TCCTTCCCG	240
TNGNAATGG	249

(2) INFORMATION FOR SEQ ID NO:1481:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

GGCAGAGGNT GAATCTCCTA TAATGATGGA AGAAGAGGTT CTCTTGTCTT AGATAGATNA	60
GAGCCTTCTC CAAGAGCAAT GTCAAAACTT GGGCTGTCAT CTTTGAGCTG TTTACCAAAA	120
TACAGACCAT TATTGAAGAA AAACAAATTA TCTATTTGT TTTCCCCAT CTAATATGAT	180
AGTGCCCCCA ACCAGGTTGT AGCATTGCCT TTTAAAAGAG ACTCACTCAC TCTTAGTTT	240
TAAGGAACTG GGAAATTCC CATCCTCAGA TCCCTTAAAG GATGAAGAGT TGGCTGTACA	300
CTTAGCGGAC TTGCCTCNTG GTATGCAAGG GANTACTGGT TTGAAGGTCN GTTTGNNCG	360
TGTC	364

(2) INFORMATION FOR SEQ ID NO:1482:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

GGCANAGGGA CAGACCAAAG TATCCTGGAA TCAAATTGGA AGAACTCTT CCAGATTGGA	60
TATTGGCATC ANAATCTAAG CGAGACAAAA TAAAAACAAG TCAAGCCAGA GAATCTGTTA	120
TCAAAAATGT TAGTGAATTG NATCCTGNAC AAGCGGATCT CTGTAGACGA ANGCTCTGCG	180
TGCACCCATA CATCACTGTT TGGTATGACC CCGCCGAAGC AGAAGCCCCA CCACCTTCAA	240
ATTTATGAAT GCCCAGTTGG GAAGAAAGAG AACATGGCAA TTGAAGATTG GGAAAGAGCT	300
AATTTTACAA NGAAGTCCTG GGTTGGGAA GGAAAGGAAG CAAGGANTGG TGTTGTAAA	360
AGGATCNAGC CTTCCGATTG CCAGCAGTNA GTTGNCAA	398

(2) INFORMATION FOR SEQ ID NO:1483:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

GGCANAGTNA GGAATGGAGA AGCCAGAGAT TATTGATGAG CTGCTGAATA TAGAGAAAAAA	60
TCCCCAAAAG CCTCAATATA GTATGGCTGT AGAATTCCT CTAGTCTTAT ATGAACGTG	120
ANTTTGAAAA TGTGCAAGTG GATCTATGAA CCAGGAGGCT CAGGAGTTCA ATATTACCCA	180
CCTACAACAA CTGTGGTCT TAATCATGCT GTNCAAAACT GCACATGGTT TGTTATTAGG	240
TATNNGTAAC NTGAGTTNT	259

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

GGCAGAGGAG TTTTTTTTT TTTTTTTTT TTTTTTNNAT TNTNAAANTT TT	52
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(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

ATCCTAACTC CAACCCACCA TGTNACAAGA CAATGGATGA GGATATTGTG AATTCAAGCAG	60
GACGATGAGA TCCGCTAAA GATTGTGGGG ACCCGTGTGG ACAAGAATGA NNATTTTG	120
TAATTGGCTC CCTGAATGGA CGATTACTTG GGGCTTGTAA GCTGAGCCTG GTGGCCTCCT	180
ACCNTGGTC CTACTCTAGG AAGTGTGATT GTAACNCTTA TCATGTTGTC CAGAGGTCCA	240
GTGTTGGCTGC TGTTGTGGAG GCAAGGNAGG CAACTCATNC CAGAAGGCAT CTGGGTGCTT	300
CTTGTAGCTT AAACTAATTG CCTCCTCATN TTTCAAGTAT GTGGTTCTTA AGTATTAAAA	360
AGTNCCNGG TTTCTCCAAA AAAAAANAAA AN	392

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

GGCANAGGGA GACCCAGGTT GCTAGGACTC TNTTCTTGGC TTGATGAAGC AAGAGGCCAT	60
GTCAGGGATC CATGAGGCCA GGAAGGAGGG CAGCCCACAG GAACTTCTGC AATAACCTAG	120
GTGAGCTTGG NAAGCAGCTC CTTCCCCAGC CTCACGTTCA GATGAGCTCT CCTCCCTGAG	180
TGATACCTCG ATCAGATCAC AATTCTCAGC AGACTCAGCA AAGCCATGTC CAGCCTCCTG	240
GCCCACAGAA ACCACAAGAT AATAACTGTA TGTTGTTAG GACCTTAAAG CTCNTAGTCA	300
TCCATTCCAC AGCAATAGAT ANTACTGGAT AAAAGGAGGT TAGGAAAGAA ATTNTNTTAG	360
GTTAGGTTAG AGTGAAAGAG TCCCTCAGCC AGAGTTCCC TTTTTAACAC AAAGCAGNCC	420
CNGGNAAAAC ATTTCTNGTT TTAACAAGGG GC	452

(2) INFORMATION FOR SEQ ID NO:1487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

GGCACGAGAG ATCAATGACT TTTGCCGTT TCAGTGCCCT CCAATTAAGT TTATCAGTGC	60
AGATGTACAT GGAATTGGT CAAGGTTATT TTGTGATTT GGTGATGAAT TTGAAGTTT	120
AGATACAACA GGAGAAGAAC CAAAAGAAAT TTTCATTCA AACATAACGC AAGCAAATCC	180
TGGCATTGTT ACTTGCNTTG AAAATCATCC TCACAAACTG GAGACAGGAC AATTCTAAC	240
ATTTCGAGAA TTAATGGAT GACAGGTTA AATGGATCTT TGACAACAAT TAACGGTGAT	300
NTCGCCATTN TNCTTTAGT ATTGGTGGAC ACCACAGAAN TGGNAACCTN TTTGACNGGN	360
GGCCTAGGNG TGCCAGTTNA GGANTCCTAA AACANTTTT TTGGATTCAAN GGNGGGNCG	420
TTTAAAACNT CCAAGTGCCC TNTTGTGGGT TTTNGNCAAC NGGGCGGGCA CCTTGGGGGT	480
TTCACACAGT TTGTTGNCC TG	502

(2) INFORMATION FOR SEQ ID NO:1488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

GGCANAGGAA AGATGGTGT ACTGCAAGNA TGTCACTCGT GAGGTGNAAT TCGTGAACTG	60
ATACCAAGTTC TGTCATTGAT GCACAATGTT CAATCCTTGT GGGTATTGCA TGAATGGATG	120
AAATCGGATG GAACTTATTG GACTATTCAA CATCACTNCA GACCAGANTT TCTTATGTTA	180
GNTTGGACAA CTTAGTCAGC CTCTATGATG NCNGTCAGAA GT	222

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

GGCACGAGGT NTCCCTGTTG CCCTTGGTCT CGGGGNCGCT GTGGCGCTG AGGCTGCAGC	60
TATCATGGTG AACTTACTTC ANATTNTGCG GGACCACTGG GTTCANGTTC TTGTCCTAT	120
GGGNTTGTC ATTGGATGTT ATTTAGACAG AAAGAGTGTAA TGAACGGGCT AACTGCCTTC	180
CGGAACAAGT AGTATGTTCA TNTAAAAGGG AATTGCAACC CAGTGAAGAA GTTGATCTGG	240
TAAGTTAAAG ACTAGCTNAG NATTATCGAA TGTTCACATT TNNAAGTTCA TGTGGAGAAN	300
AAAAAACATG AAG	313

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

GTTGTANGNA ANGTAATCA AAAANTGGA AGCTGTACAC AGCAAGACGT TAAGTTACAT	60
GTTCCAAAAG ATTTATGTNA TCAGTTGGC TGACCCCCGT CTCCCCCTGC GNCTGGNTGA	120
TGCTGTNCGG CCTGAGGCAG AGGGAGANG	149

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

AGTAACATGA TAGANAGTTG GTCGATTACA TTGCNATACT GCTTAGTTN AACTGGTTA	60
TTTTAATTGT AGCAGAAATG ANCNGAAAAA AAATATGGGT TTAANANTCA CACACATGAA	120
AGTNCCATT TGTAACTCAN CNAAAGNTAA ANCATTCTTN ATCAAAAGGC TTCTNGCTTG	180
GTGTCAGGTT GTCACATGTG ACCNCTGTGN CAATGCGAAG CATNACTTCT TCAGTGCCAC	240
AANGTCATGT TTAACCTTGG GAAAGGNGGN TGCTACAGTG GTTTCCAAAG TTCCGTGTTG	300
TGGGCCNNNGG AATTTCCCT TAGTCTTGCT TG	332

(2) INFORMATION FOR SEQ ID NO:1492:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

AACAGTGCCT CCNAATNAAA TCTAACGANA GCTTCCAAA TCGTTAAC GTGGATATCG	60
GCANANGGTT TTCCTAGACT GTGGAGCCAT GGCTGAGCCA AACCTGAAA ATTNACTGGG	120
TCACTCCCAT TGGAAATAA GNTAACTNTG GAAACCCTTT NAAATAATTN CAAGCTAAGT	180
NGCGAGGGTA CCTTGGAAA TATCTAAGCA TACAATTGTA NGACTCAGGA AGGTACACAT	240
GTNTTGCCTA GANTGTCCAG GGGCAGNCAT CGGGTGGCC ACCATTNAGG TTTACGGG	298

(2) INFORMATION FOR SEQ ID NO:1493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

TNATTATCCA AATGTNAACC ATGCCAAGGT GAAATTCAA GGNAAGGAA GTTGGTGT	60
ATAANGCTCT GAAGATGACA GCTGGCTCAA GGGANGATTT TTTNACGACT GACCAGCGCG	120
TGGCGCTCNT	130

(2) INFORMATION FOR SEQ ID NO:1494:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

CTTCAAAAAA TAACTGATTT NCAGAACCAA CTCAGAAC AGGAGGAAGA CTTTAGAAAA	60
CAGCTGGTAA GATGAAGAAG GAAGAAAAGC TGAAAAAGAA AATACAAACAG CAGAATTAAC	120
TGNNAGAAAT TTAACAAGTG GCGTCTCCTC TATGAAAGAN CTATATAATA AANAAAACC	180
TTTCAGCTA CAACTAGATG CTTTGNAAG TAGNAAANCA GGGCATTGTT GGAATG	236

(2) INFORMATION FOR SEQ ID NO:1495:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

GGCANAGCGG CACGAGGTTG GACCGACAGT TACAAGACAT AGTGTACAAA TTAGTGATCA	60
ATCTAGAGGA AAGAGAAAAA AAGCAAATGC ATGATTCTA TAAAGAAAGA GGTCTAGAAG	120
TACCTAAACC TGCTGTTCCA CAGNCAGTGC CCTTCAAGCA AAGGNAAGAT CTAAAAAAAGT	180
CCTAGAAATC AGTGTTCGT ATTCCACCTG AACTTGGATA TGTCTTTATT ACTGGGAGTT	240
CCATTGGTGC TAAATGAAAG GCACGGGNAC ATTTAAAGC CATTGGGAAA AGAAAGTTG	300
TTCCGAGTTT TCAGGAGGAA GCAACTATTG GGACCATGTT GGAAAATTTC CTCAGANGAA	360
AATGGGGTCT TGATCCCNCT TGTNCCAGTA GGTTAACATCC GTGGTGATCA CTGTTGGGGC	420
CGTNTCAACT CTTAGGGNAT TC	442

(2) INFORMATION FOR SEQ ID NO:1496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

GGCANGAGAA GGTACTGCAA CATTNAATG GGACGGCAAT AGCAAATGCA GTGNTAAAG	60
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ANCTTGCTGA GACTATAAAA TGTCGTACAT TATTTCNAAC TCACTACCAT TCATTAGTAG	120
AAGATTATTC TCAAAATGTT GNTGTGCGCC TAGGAACATA TGGCATGCAT GGTAGAAAAT	180
GAAATGTGAA AGACCCCAGC CAGGAGACTA TTACGTCCT CTATGAAATT CATTAAGGGA	240
GCTTGTCCCTA AAAGCTATGG CTTTAATGCA GCAAGGCTTG CTAATCTCCC AGAGGAAGTT	300
ATTCCAAAAG GGNCATAGAA AGCAAGGNAT TTGNGGNAGT TGANTCCGTC CCTC	354

(2) INFORMATION FOR SEQ ID NO:1497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

TNATGTNCTT TCTGCATGGT TATATACTAC TAGTNNTTT ATCAAAACTN CTAAAATTAA	60
AATTACGTGG TAAAAGATCT GTAAAAGGCT GCATAAATGT TAAGTTGGCA CATAAAGACA	120
ATTGTAGAACG TTGAAAAAAAT GATTGCAATA TTTCAATGNT TATNCCCACG CAACATACTG	180
NCTTCTAAAG CTTCCCTTTT TTTGTTCCAA AGGCATGNT CTTGAAAGGT NATGTTAAG	240
TTAATGGNTG TAATGCCAGG GTTCCCTACA CTGTGATTTN GGGCGCATGT GCNGTGGGCC	300
CTCTGTGCCCTAGANTATA TGCCACACAG GGGGNCAAGT TNAAAAGCT	349

(2) INFORMATION FOR SEQ ID NO:1498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

GGCACGAGCT GTCTGGAATT TAGCCAAGTN ACAATCCCC TCATATCCAG GCTTTATNAT	60
CTATATAGCT TCCAGGTCAT CCCTGNCTG GGAGAGGTCA TCGCTGGAGA CTGNAAGTCC	120
TATCAGTACC TTGTAGAGAG TATCCGAAGG TTTCCGTCTC AGGAAGNAGT TCAAGGACAT	180
GATAGAAGAT GCAGGCTTCA ACAAGGTGAC TTACGAAAGT NTAACATCAG GCATTGTGGC	240
CATTCATTCT GGCTTCAAAC TTTAATTCCCT TTCCTATCAT GGAGCATGAN CCAGTCATAT	300
CCTGTTGAA AGCCTGGAAC TTNAAGGNTA ATCTGGCAA TGAAGACAGC AGCAGAGCAT	360
CTCCCTCTTT AAGGATACGT GGCCTTGGNA CTCATGTTG AATCGGACAG TCTCAAAGTG	420

GGGAGGACAA TTCTTGTAC CTTTTTACAG GTTTTCTTT GGGGTTGTTT CAGTCCCATT	480
TCCCCAAG	487

(2) INFORMATION FOR SEQ ID NO:1499:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

TCNNCAANNT NGAACGATGC AGGGTCCAGC TGGGCGGATC TGATCAACTA GGCAACATCA	60
TGTTCCGGAT ATGAGTTCAT CAACAAGTTG ACTGGAGAAG ATGTATTTGN GAATCACCGT	120
TCCTCTAATT ACAAGTACAA CTGGNGCAA GNTGGGGAAA GTCTGCTGGC AACGCTGTTT	180
GGCTAAACAG AGATAAGACCA TCTCCATTG AATTGTATCA ATTCTTGTC ANGCAACCAG	240
ACGTTTCANT GGNAAGGTAC CTGANGNTGT TCATTT	276

(2) INFORMATION FOR SEQ ID NO:1500:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GGNGGCGTTC AGCTGCTTCA AGATGANGGT GAACATNTCT TTCCCAGCCA CTGGTTGCCA	60
GAAACTCNNTT GA	72

(2) INFORMATION FOR SEQ ID NO:1501:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

AAAAATNTCCC AACTNATGAT ATCCACATGA NGCAAGTTGA TCTGGAGANT GTATGGCTTC	60
ATTTTATCCG GGAGTTCATT GCACCANTTA CACTGAAGGT NTTTGAGGC TATTATACGA	120
NGGGNTTTGC ACTACTGAAT TTTGTAGTAA AATACTCCCC TNANGACAG CNTTCTCTTN	180

GTCCTCATCA TGATGCTTCT ACATTTTACC ATAAACATTG GCACTTAATA ACGTGGGGAN	240
AAGACTTTCC AGGGGAGNTG GTTGCAAATT TNNAAGGGNT CCAATTGCC C	291

(2) INFORMATION FOR SEQ ID NO:1502:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

TGGAAATACT TGGTTATTGC ATGATCCAAT GGCTTACTGG CCATCTTCCT TGGGAGGATA	60
ATTTGAAAGA TCCTAAATAT GTTAGAGATT CCAAAATTAG ATACAGAGAA AATATTGCAA	120
GTTTGATGGA CAAATGTTT CCTGAGAAAA ACAAAACCAGG TGAAATTGCC AAATACATGG	180
AAACAGTGAA ATTACTAGAC TACACTGAAA AACCTCTTA TGAAAATTAA CGTGACATTC	240
TTTGCAAGG ACTAAAAGCT ATAGGAAGTA AGGATGATGG CCANTGGAC CTCAGTGTG	300
TGGAGAATGG AGGTTGAAA GCAAAACAT TANCAAGGAN GCGNAAGTAA GNATTGNTGA	360
AAGCAAGGAN CNCGTGTTG AAGTTACGGN TTGTCCAACN CACCGTCCGN GGTGGGCCTT	420
CCGACCCNTT TCAGGACCCG AAGGGGTCCC GAGTATTCGG TGCTGTGACC CGTTTCC	477

(2) INFORMATION FOR SEQ ID NO:1503:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

GGCACGAGCA AAGGCGAGGA GTCCAACAGC TCAGCCANCA AGTGTCTGCT GAAGGTGGCT	60
GGTTACGCTG NGCTNCTNGA GCAGTATCAG AAGGCCATTG ACATNTACGA NCAGGTGGGG	120
NCCANTGCCA TGGNACAGCC CCCTTCCTCA AGTACAGCGC CAAAGACTAC TTTCTTCAA	180
GGCGGCCCTC TGCCACTTCT GGCATCGNCA TGGCTCAGCG TGCAAGNTGG CTGGTCCAAA	240
AGNATNNAGG	250

(2) INFORMATION FOR SEQ ID NO:1504:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

GGCACAGAGA AGATTCCCTTC ATGAGTGTAG AAGTTGGACT GATTTCTAAA GTNCCTTTCT	60
ATTTTAAGAN TCTNTTCTGC ACAGTTATGA GCTACACATA ATGCACTGAA TCTGTTCCCT	120
TGNATAGTT CTGCATAGGC TTTGGTTGTG CCACAAGTGT GCCTGGCAGT GAAATGAACC	180
TGGTCTAACAC TCTGGCATTG GTCCCTAGGGN CTGNAACTGT TNCAGGAATN TNGNCTAATC	240
CTNGNGGG	248

(2) INFORMATION FOR SEQ ID NO:1505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

ANACAGCCAC ACCCGTNACG GTGCATTAGG GACAATGGCA GTCGGTGAGG CGGGCGGTGA	60
GTTGGTAAAA CAGCTGCTTA ATGACACCTG GGATATCGAC TATCCGGGCG TGGTTGCGGT	120
GCATCTAACCC GGAAAACCTG CGCCGTATGT GGGGCCACAG GATGTNGCGC TGGCTATCAT	180
TGGCGCGGTG TTCAAAAACG GTTACGTCAA AAACAAAGTC ATGGAGTTCG TTGGACCGGG	240
CGTTAGGGCG CTTCTCTTAC CGATTTCCGT AACAGCNTTG ACGTGATGAC CACTTGAAAC	300
GGACCTGTTT AAGTTCTGTT TGGCAAACCG TTGAAGNAGT NCCATAACTG GTTGGGGGTT	360
TNAACGTTNG GGG	373

(2) INFORMATION FOR SEQ ID NO:1506:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

GGCANAGTCC AGAAGCTACG CTTGGAAAT CTATGACATA GACAACAAGA CGCCAGACCT	60
GAGGGATGAT GACTTCCTAG GGGGTGCTGA GTGTTCCCTA GGACAGATTG TTTCCAGCCA	120
GGTACTGACT CTCCCCTTGA ATGCTGAAGC CTGGGAAAAC CTGCTGGCG GGGGACCATC	180

ACGGTCTAG CTCAGGGAAT TAAAGGACAA TCGTAGTA ACCATGGAGG TAGAGGCCAG	240
AAACCTAGAT AAGAAAGGAC TTCCTGGGNA AAATCAGATC CATTNTNTGG AGTTCTTCC	300
GCCATGGTGA TGGGNAATG GGCACNGGGT GTTACAGTTC TAAGGGTNCA NTCAAGGACC	360
AACCTGGAAC CCTTACATGG GAAGTTTTT TTNAA	395

(2) INFORMATION FOR SEQ ID NO:1507:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

CAAACAGCCC AACAAATTCA CCACTGCGAA CCGCCAGACT TATTGGCGTA CGCACGTCTG	60
TGTGCTTCA CAGCATCAAG ACGTAGGGCN TGCCCTGCCA TGAAC TACGC GGTTGCCAGC	120
CGTAGTATNA TCGTCCAATG ATCGTCGACC CGTACCNATN CGNCTCTTGG TGTGGGTGT	180
GT	182

(2) INFORMATION FOR SEQ ID NO:1508:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

GGCAGAGTNT TGGGGCATTG CCGGCGGGCC CACCCGGACT CACGCAGCCC ACTCTGTGTC	60
CCCCGGCAGT ACCCTGGCTA AAGCCGGGNC CGGAGCCTNC TGCCCTCTC ATGCCCGCAG	120
CCAGCCTGGG CTGTGCAACA TGTTACAAGG ACTCACACCA CCCGGNCAAG AACTGCTCAC	180
TACGGCTCCC TGCCCCAGAA GTTCACACGG NCCGGACCCA AGATGAAAAC CCCGTAGTCC	240
CACTTTCTTT CAAGAACATT GTGAACGCCT NGCACACCAC CCCCGTTCGC AGGGGAAAGG	300
GNGAGAGGGA CTGTTCCNTG AGCAGATTT AGCTNNGGG GCCGAGCAGA GNAACCCAGG	360
NTTTTGGTTT ACGGAGGCAG AGCGTTCCGA TTTAAATCG GTTCACAAGG GGTTTCAAGG	420
GATTCTGTTGC CCAGGGAAGT TTTCAAATT TTTAAAGTTG GGAGNAGAGN TAGTTGGTTT	480
TGGT	484

(2) INFORMATION FOR SEQ ID NO:1509:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

GGCANAGNCT GCATCCTACA GAGCCATGGA TGGNGGCAAG TGTTTGCAAT GGGAAAGTGTG	60
TGTGTTGGA NTCATGAAAC ACAGACACTG GTGGAAGACA TTTGAAGTGT GTGATCTTCC	120
TGTTTCGTAG CTNCAAAGTT TGGTTGNCAA AGGGAAGNAT TNTTTNGTGT TG	172

(2) INFORMATION FOR SEQ ID NO:1510:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

GGCANAGGCA TCAATGTTAT AGCGTGTGTC AGTCCTTCAT GACTTCTGT GGATGAATAA	60
TATTCCATTG CATGGATATA CAGCAGTTCG TTTANCCATT CAGCAATTGA TGGATATTTG	120
GGCCTGTTT CACATTTGG CTATTATGAA ATCCANTTTT TTAAAGAGAA GATAGNAAAC	180
CTGGATTTTT GAAATCTAGT GTTAAATGT TGGCTGTGNA ATTTTAAAAAA TTNAAGAATA	240
TGGTTTGAGC TAATTAaaaa GCTATCTGGG GATGGGCACA GGNNGCTTGG TTGACTGCC	300
ATTGGTCCAT CTCTTGCCA CTTGGGNCA GCCTGGGAC CCTTTNTNGG TT	352

(2) INFORMATION FOR SEQ ID NO:1511:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

GGCANAGNCA AGACTGGTCA CCCTCGGTTC TTCAACCAGC TCTTNTCTGG GTTGGATCCC	60
CATGCTCTGG NCAGGNGCAT TATCACTGAG AAGCCTAAC ACCAGCCAGT ACACATATGN	120
AAATCGCCCC CGTGTGTTGTG CTCATGGAAG AGGAGGTGCT GAGGAAACTG CGGGCCCTGG	180
TGGGCTGGNA GCTCTNGGGA CGGAATCTTC TGCCCTGGTG GCTCCATCTC CAACATGTAT	240

GCTGTNAAAT CTGGCCCGCT ATCAGGCTTA CCNGGGATTG CAAGCAGAGG GGNCTCCGNA	300
CAATGCCGCC CCTGGCCCTT ATTCACATC GAAGGAGGTT GGGAAAGAGGC ACAGGNCCAA	360
CCCTGGGTTC NTGATTTAA TTTCCAGCCN GTTAAGTAGA GACCTTCCAG TTTTGTTCCT	420
GGCCTNNNTA ACATTC	436

(2) INFORMATION FOR SEQ ID NO:1512:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

GGCANATNGG GACTTCCCGT GCNCTCTGGC TGAGGGGTGT TGCTGCCTTT GGTAGCTGGC	60
CCTGGTGTTC CAAGTACAC CCTTAGGGTG GAAGTGGTAG CNTTTTTAAA GANTGTNNCC	120
CAAAACTACA GTTNCTGTGC ACTCACTTAC ACAGTATT	158

(2) INFORMATION FOR SEQ ID NO:1513:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

GGCAGCAGCT TCACTAAGGT GGGATGGATA GCAGGGTCTN AGGCACAACC AGTAATGGAG	60
AGACAAANCC AGTGTATCCA GTCATGGAAA AGAAGGAGGA AGATGGCACC CTGGAAGCGG	120
GGGCACTGGT ANCANAAGN TGGAGTTNT CCTGTNAGTG GCTGGGGAGA TCATTGGCTT	180
AGGCAACGTC TGGNGGTTTC CCNATCTTG CTAACAAAAN TGGGGGAGGT GAGTTGAGAG	240
CCCTTTGCC CACCNACCC ACTCCTGGAA GGGGNTTACT TCCATCTCCC TGCATTTACG	300
NNCCCTTT	308

(2) INFORMATION FOR SEQ ID NO:1514:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

GGNAGAGGGG ACACAAAGGT CGGNAGGCAG CACACAGAGG GACCTACGGG CCAGCTGTNC	60
CTTCCCCCAA NTCAAGAAC CCCGGAAGNC CCGGNGGCTG NCAGCAGGAG AGANCCATGA	120
AAGTAAGCTG AATGGTGGTG CCTGNGTCTG AATTGCCTGC AGCCTGGGCC AGAGGAGCAG	180
AATGAANTTG GTGCATGGCG GACCCTGNGA NCAAGACATC TTNACCCCTN ACCAAGCTGC	240
CCTCTNACAC CTGGGGCCAC TTGCTCTGTG GTGGGGTCCT TATTCCATCC ACTGTGGGTC	300
CTNANAGNTG CCCACTGCAA AAAACCGTTT TTCCAGGTCT TCCTGGGGGA GGGNTTAACC	360
TTGGNGCAAA GG	372

(2) INFORMATION FOR SEQ ID NO:1515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

TGCTGAAATT AAAGAAATNT NGCAATGATT TTAAAAACGG AGNTGTGACA GTAAGGAGGC	60
CTGACCCCCAT TAACTGGTCA TTGAAGTATA AAACTCCTGN ATTTTANGNC TNCGGGTTTT	120
ATGACAGTGG CAATG	135

(2) INFORMATION FOR SEQ ID NO:1516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

AATTCGGCAN AGGNNAAGCCA TGNCTGGCGA TGGTGGCAGC GGCTGTNACC TTGGAGGTTG	60
CTGCAGGCCCT GTGGCTTCC ACAAAATTTT GCACCCAGCC TGGGCCTANG AGCGAGGACT	120
TGTTCCCAGG GCGACTGCTC GTNATTNCNG CANGNCTGT	159

(2) INFORMATION FOR SEQ ID NO:1517:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

AGCCCCGCAT CTTCCACCCCT CGNCGCCGCC GNAGCTCCCC GCGCTCGTGC CACCGNCGCC	60
GGT	63

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

TATTATGGAA AACTGTTGCG GGGCATATGG AAAACTGTTG CGGGGCATGT GGTAGAGACC	60
ACCCAGATGA GGCCCTCCAA GACCTTGTG TCTAGGGTGA TTTATTCCCT TTATTTAGAG	120
ACCCAGGCAA TTGAATTCAAT TTCTTTTG GTGNATGATAGG CTTTTGGCTG TTAGACCAGA	180
CCAGACGCTG TGTTACTCTA TGAGATGAAT AATAGTGGAG AACTATATAA CTTAACTATT	240
TTGACTTTTT ACCTTGGCTT CCAGGAAGCA TAGAGTGCAA TCTCGNTTAC TGCAATTNC	300
AATGAATTGA CACATAGCCT AGGTTTTGG TACAACCACC TTTG	344

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

GGCACGAGCA TGTTTCCTGT TTTGTGTGTG TAGTCTGTGG AATGNCCATT CGGATGAATG	60
TTTTTCACCTT GGAGGATGGT GAACCCTACT GTGAGACTGA TTATTATGCC CTCTTTGGTA	120
CTATATGCCA TGGNTGTGNA ATTTCCCATA GAAGCTGGTG ACATGTTCCCT GGAAGCTCTG	180
GGCTACACCT GGGCATGTGA CTTGCTTTGT ATGCTCCAGT GTGTTGTGAA AGTTGGNAA	240
GGTCAGACCT TTTTCTCCAA GAAGGACAAG CCCCTGTGTT ANGAAACATG CT	292

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

GGCACGAGGG NGCACCCNGG TAGGGGNCG GCTGAGCCGG CAGTGC GGTA CCCTCGCGGG	60
GAAC TGCGCC GCCGACACCA TGTCTCAGGA AGGTGTGGAG CTGGAGAAGA GCGTCCGGCG	120
CCTCCGGGAG AAGTTTCATG GGAAGGTATC CTCCAAGAAG GCGGGGGCTC TGATGNGGAA	180
ATT CNGCT	188

(2) INFORMATION FOR SEQ ID NO:1521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

GGCAGAGCTC ATGATGACGT TTGCTTTCC TCCCGACTCA AAATTTACCT TTTGGGGTCT	60
TACCCTGGTT GTAGGGNGCTG GNTTTTCCTG GGGATTAAGG CCTAANTCTT CCTACNCNTC	120
GCACTGCCTT GCACTGCCCC CCATATGTTCC CCAAGGGTAGC TCTCCAGCTG GANCCTTGCT	180
GATGCCATGT CCCAGAAACA CCTCCAGATC AACCA GACGT TTGAGGGAGCT GCGAACTGGT	240
CACCGAGACA CAGAGNAATG AGTTTAAAAAA AGCTGCAGCA GACTTCAGGA GTTACTTTCA	300
TGCATCCAGT TACCAGGNAG AGCCTNGAGG GATTCCAAGC TCAGTTTGG GCCC GTTGG	359

(2) INFORMATION FOR SEQ ID NO:1522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

GGNANAGGCA ACCCCTTGTN TCGTGTGGAT GGGGCCTNG CCGGCCTGT GAACCTNAAC	60
CTGCAGNCCG ACTGCAAGNN TGCCCTGGAA GTCCTGGCAC GACATCCGCC GAGACA ACTG	120
CTCTGGCCAG AAGCCTCTGC TTCTGCTGGG AGCACANCCA GCTCCNAGCA CAACCTGTNT	180
GNCCTTCCTN GAGGTTCA	198

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

TTGCCATCGC GAATGGGCC CAGTGGCTA ACGCCCCGC GGCCTTNGG TAAAACCGAC	60
ACCACGGCAC TCTGTCGGCC AGGTTGCAGG TTCCCATTTC TCCGTGGAAG CAGTGGCGAG	120
AATTGCCGTT TTTNAGGTTG GTCATCAGCT TGTCGAAGAA ATACACACCA GAGAAAAAGC	180
GTAAATTCTG TTCCGACCGT GCAGTTNACC GTAGAGCGAA AATTTTGCG CCATATAAGC	240
CGAGAATGCT GGCGCGCTT ACCGGNAACT TNTCTTCCA GATCCATCCC CAGCACCAAGC	300
GCCTGGTCCG GAAAGTCGG CACCAGAAA CCGTACATNC ANTTTAAAGG TGGTCGATTT	360
TNACCCGGGC CTTTGGGCC CCAGNAAACC AAAAATTTC CCCAAGTTN AAGGGCAAAT	420
TTGACGTGAT CCGTTGGNG GCAAAATNCC CCAATTTC TGGTCAATT TTNGGTTGG	480
GTT	483

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

AAAACAATCC CTTCTATCAA TTATATCGGC TATCTTGAAG CCAATGAGTT GTTAACGGC	60
AAGACAGATG TGCTGGTTG TNACGGCTT ACAGGAAATN TCACATTAAA GACGATGGAA	120
GGTGTGTC GGTATGTTCC TTTCTCTGCC TGAAATCTCA GNGTGAAGGG AAAAACGGT	180
CGTGGTGGCT ACTGTTATTA AAGCGTTGGC TACAAAAGAG CCTGACGAGG CGATTNCAGT	240
CACCTCAACC CCGACCAGTT ATAACGGCGC CTGTNTGTT AGGGTTNCGC GGCACGGTGA	300
TTAAAAAGTT CATGGGTGTC AGCCAATTCA GCGAGNTTT TGCGGTTCGC GATTNGAAC	360
GGCATGNCAG GCGGTGCAGC GACCAAGTTN CNTCAGCGG	399

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

CACCNCTAA AAAACTCGCT GGATCTNNAT CTGGAAATGT NCCCAGGCCA GGTGNCAGCT	60
TCCTCCNCT CCAAGCNAGG NTTNANTTCC ACCTGGGAAA TCTGGCCANA GAAAGGTGCT	120
TGAAAATCCT TCCNGCACAT GCCAAACCCT AGAACCCGGG GANAGCACGG GGGNGGTGGG	180
ATTACCTGGT GCAGCANACT	200

(2) INFORMATION FOR SEQ ID NO:1526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

GGCAGAGTGA ACAGCCCCCG NCAGCGCANA CGAGCCCGGA CCACACCCGG TNCCGGAGGT	60
TCCCCACAGCA AAGACAGGCA CCGGAAGGAG ACGGACCCGGG AAGCGTAGGG GCAGCGNCAG	120
CAGGTAAGGN ACAGCCGNCA CCGNCG	146

(2) INFORMATION FOR SEQ ID NO:1527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

GGCAGAGNCA ACGCCACTCC TTCTAAGTCT TCATCGATCA ATGACATTN ATCCATGTCC	60
ACTGAGCAGA CGCTGGCCTC AAACACAGAC AGCAGTCTTA ATGCCTCGAA CGGGNACCCC	120
TTGAAAGGCT GTCGAATGGA TAGGTTAGGA AATAGCAAAC CTGTNNAGCA TTGAAGGGAA	180
CTCTGNACCT GCCGTGGGGC CTGAAATGCT TGGGAGTTGA TGGGAACCAA ATAGAAAAAC	240
TCCATGTTCC TGGCATGTAA AGAAACACAA TGNCTGGNC CTNTTCAAA CCGGTGGGGT	300
TTGCNCTGCT TTAGATGGTT AAAAATGGGG GGCAGGANTA TGTTTG	347

(2) INFORMATION FOR SEQ ID NO:1528:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

GGCAGNGCAG CTATGCTAAT TTGCAAACAG GTTCTGGAGT NCTTAAAGAT AGTTTNTCTG	60
GTGGAATGCA GTTGCTTCCA GATCCTNTAT ATTCTCTTCC TACNNATAAT ACTTACCTTT	120
TAACAATAAC TTNCACTGAT AATGGGCAGA ATTTTCTTGG CTGGNAAAGG ATGGCTGTTT	180
ATATGAAAGT AGCCTACCAG GCTGTAAGCA GGGTGGTTA GCCAAAGATG TAGGGAAAAT	240
AAACCACTCA AAGAGCTTCA CTTCTTTNC CTTGGTNCCT TCCTTGGCTA CCAATTTCAC	300
GTTCCTTCAG AAGGATGNAT NCCNTATTC TT	332

(2) INFORMATION FOR SEQ ID NO:1529:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

GGCACGAGGG AAAATCGCAA TACTATATTA TGTTTGGNCC CGATATTTGT GGATTTNATA	60
TCAAGAAAGT NCATGTTATT TTACATTCA AGAATAAGTA TCACGAAAAC AAGAAACTGN	120
ATCAGGTGTA AGGTTGGATG GCTTCACACA CCTGTTACAC TCTAATTTN AAGACCAGAT	180
CTTTCTTATG ATGTGNAAAA TTGATGGTCA GTGCAATTGG AATCCGGCAG CATAGAGTTA	240
CGGACTGGGA ACTTAAACAT CACTCCAAGA GGGAAACGTC CCCCGGNCAG ATTCAAGGA	300
TTGGGCAACA GGACTTAAGG GNICAACAAA GCCCCAGGGGA CTTGGGGC	348

(2) INFORMATION FOR SEQ ID NO:1530:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

GGCACGAGCT CGTNCCNTGC AAAACCACTC CCACCAAGTG AACGCTTGG ACGAGAACTC	60
TTTTCTGGAG GCAACACTGG GATTAATTTC NAGAAATACG ATGACATTCC AGTTGAGGCA	120

ACAGGCAACA ACTGTNCCTC CACATATTGA AAGTTTCAGT GATGTTGAGA TGGGAGAAAT	180
TATCATGGGA AACATTGAGC TTACTCGTTA TACTCGCCCA ACTCCAGTGC CAAAAGCATG	240
CTNATTGCCCT ATTATNCAAAGAGAAAGAG ACTTGATGGC TTGTGCCCA AACAGGGTTC	300
TGGTAAAAAC TGCCAGGNAT TTTTNTGCC CNTCTTGAGT NCAGATTTAT NCAGATGGTC	360
CAGGCG	366

(2) INFORMATION FOR SEQ ID NO:1531:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

GGCACGAGGC TTGGCGGGGT GGATAATATC CTGGTCAAAA TNACTGACCC ACATCANTAA	60
TGTCGTTCCCT CCAAAGATGC CGTGGTCAA ATATCTGTNC ATGTGGACAT CACTGCCACC	120
CCAGGAACGG GAGATCATAA AAGTCACTGT AAAAAGTGAA TTGCTATTAA TGACCTAAC	180
TGGCAGACCA CAGCAATGTT CCGCCCCTTT NTGGAAGTTT GTATACTGGG ACCAACCTT	240
GGAGACAAGA AGAGAAAACA AGGCACAAAA ACAAAAAGCA ACACATGGTC ACCAAAGTTA	300
CAATGNAACT TTGCAGTTCC TTTTGCAGAA AGGAAATTGCG GCCAGGGTTT ATGAAATTGC	360
TCTGTCCGTT AAGGGTTATG TTTTGCANG NAGTTCCNTT NTNGGATG	408

(2) INFORMATION FOR SEQ ID NO:1532:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

GGCACGAGGT TTTTTTTTTT TTTTTTTTNG GAAAAAANAA NCTTTNAAAAA NT	52
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(2) INFORMATION FOR SEQ ID NO:1533:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

GGCACGAGCC CGACCGTNAA TGTGTGTNTN CTCTTCCCCA GTNCTGGCCA TTCAGGCCCG	60
AAAGCGGAGG CCGAAAAGAG AGAAACATCC GAAAAAGCCG GAGCCTCAAC AGAAAGCTCC	120
TTTAGTCCT CCTCCTCCAC CGCCACCACC ACCACCACCG CCACCTTG CAGACCCCAC	180
ACCCCCGGNG CCAGAGGNNG AGATCCTGGG GTCAGATGNT GAGGAGCAAG AGGACCTG	240
GGACTACTNG CAAGGNATT ACAAGTTTG TNACTATT TAAGGAGNAAT TATTTTTAGC	300
T	301

(2) INFORMATION FOR SEQ ID NO:1534:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

GGCACGAGGT TGGATGGTGC AGTGGCTGTA TTTNATGCCT CTCCTGGTGT AGAGGCCAG	60
ANTCTCACAG TATGGAGGCA AGCTGATAAA CACAATATAC CTCGAATCTG TTTTTTAAAC	120
AAGATGGACA AAACCTGGAGC AAGCTTTAAG TATGCAGTTG AAAGCATCAG AGAGAAGTTA	180
AAGGCAAAGC CTTTGCTTT ACAGTTACCA ATTGGTGAAG CCAAAACTTT CAAAGGAGTG	240
GTGGATGTAG TAATTGAAAG AAAAACTTCT TTTGGGAATT TGCCAATTCC AAATGGATGG	300
AAAAGACTTT GAGGAGAAGN CCCCTTTG GGAATGNATN GTTCCNGGAT TTGCTGAAGG	360
GGAACCACCT NAGGCAAGGG	380

(2) INFORMATION FOR SEQ ID NO:1535:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

GGCACGAGGT GAAGTTCAAA GATGTGGCTG GCTGTNAGGA GGCCAAGCTA GAGATCATGG	60
AATTTNTGAA TTTCTTGAAA AACCCAAAGC AGTATCAAGA CCTAGGAGCA AAAATCCCAA	120
AGGGTGCCAT TCTCACTGGT CCTCCAGGCA CTGGGNAAGA CGCTGCTAGC TAAGGCCACA	180
GCCGGAGAAG CCAATGTCCC CTTCATCACC GTTAGTGGAT CTNAGTTTT GGAGATGTTG	240

GTTGGTGTGG	GCCCTGCTTA	GAGTCCGAGA	CTTATTTGCC	CTTGCTCGGA	AGGAATGCC	300
CTTTGCATCC	TCTTCATCG	GTGGAATTG	TGCGGTGGNG	AAGGAAAGAG	AGGAAGAGGC	360
AANTTTTGG	AGGGGCAAGA	NTTNNGNCAG	GGGGG			395

(2) INFORMATION FOR SEQ ID NO:1536:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

TGTTTTNAGT	TTCTTTTTT	NCGTTTNATT	TTTNNAAT	TGCATTTAC	AGTAGAAATG	60	
CAGACCAC	TT	TGGATAGCTA	TGGCTCGATA	CTTCTGGGTG	CCCTCCTCCT	AAGANATCCT	120
CTTCTTACAT	TCCACTGANC	AGAAAACCAT	CCCTTCTACT	GGCATGA	ACT TCTGCCAAT	180	
GAGGCATTG	CTGCAGCAAG	AGCACAGAAA	GCACTCTGTG	GNATGCATGC	CAGCTGAAAT	240	
TGTTATAGGT	CACCCGNTGC	ACTTNCTGGG	TCGATGGCA	TTGTGGGCNT	CCTTGACACA	300	
CCACAGGGTG	ATTNTTNCA	AATAGC				326	

(2) INFORMATION FOR SEQ ID NO:1537:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

GGCACGAGAA	GCTTTCCCAC	ACACATCACA	CTCATAGGGC	TTCTCTCTAC	CGTGGATTG	60
CTGGTGTCCA	ACAAGAGCTG	AACTGTATCT	GAAGGCCTTT	CCACGCTTGT	CACATTATA	120
TAGTTTCTTT	CCACTGTGGA	TTTCTGGTG	ACAGAAGAGG	CCCAAGCACT	AGCTAAAGCT	180
TTTCCCTCAC	TCACTACACT	GCTATGGCTT	CTNTTCAGTA	TGAAC	TCTGA TGTTGTCTCA	240
GATATGA	ACT CAGAGAGGAT	TTCCCACAAT	CATTACACTG	GTATGGTTTC	TTTCCGTGT	300
GGAGTTTCTC	TGGTGTCCAA	ATAACATCTG	AGGTNGTGG	TGGAAAGGAC	TTTCCCACAC	360
TCAC	TTACAT TGGGAAAGGG	TTTCTTCCTG	TNGTGGGTG	CTTCAAATGN	TGNNTAAGGT	420
TATGNACTGT	AATAAAAGG					439

(2) INFORMATION FOR SEQ ID NO:1538:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

GGCAGAGCAA AGAGGCATTT GGGCAGTCCT TCTCCATCCA CCGGAAGGTT GCTGAAGATG	60
GAGAGACTCG GGAGGAAACG CTTCTCCAGG AGTCAGCATC GAAGGAGGCT TACTATCTGG	120
GGAAGATCTT GGAGATGCAG AACGAGCTGA AACAGAGCCG GGCTGTGGTC ACTAATGTAC	180
AGGCAGAAAA CGAGAGGCTC ACCGCAGTCG TGCAAGGATCT GAAGGAGAAC AATGAGATGG	240
TGGAGCTACA GAGAATACGG ATGAAGGATG AAATNCGCGG ANTATAAGTT CCGGGAGGCA	300
CGGCTCCTTT CAGGACTATT ACTTGAATTG GGGAGGANGA AATTTTCACC TTGCAGAAC	360
TAGTGTCCN CGTTTGAGG CAGANCCAGT TGATTACGNG GGTTTAAAGC CTGGGTTTAG	420
CGCTTTT	427

(2) INFORMATION FOR SEQ ID NO:1539:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

TTTCNAGTT TCTTTTTTN CGNTTAATT TTTCNAAATT GCATTTNACA GTAGAAATGC	60
AGACCACTTT GGATAGCTAT GGCTCGATAC TTCTGGTGC CTCCTCCTAA GACATCCTCT	120
TCTTACATTC CACTGAACAG AAAACCATCC CTTCTACTGG CATGAACCTC TGCCAATGA	180
GGATTTNNTG CAGAAAGAGC ACAGAAAGCA CTCTGTGGAT GCATGCCAGN TGAAATTGTT	240
ATAGGTCAACC CGCTGCACCTT CTGGGTCGAT GCCATTGTGG CATCCTTGAC ACACCACAGC	300
GTGATTCTTC ACATAGCAGG GCTTGCACAC GGGCTGTNA TTGACCATCA CGTATATTCT	360
CCCCAGNTAG ANTGNNTCA CAGTCAAAGC AGCAGAAAGTG TTTCAGGTGC CATTCTGGTT	420
TTCTGCCTGG GTATACTCAT TGTNGATATC AGTCGTCAC AGCCAGCACN CGGGGTTTTT	480
GGTGTCA	489

(2) INFORMATION FOR SEQ ID NO:1540:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

GGCANAGGNT TTCTTGCCC GATTCTTCA TGCTATATCT CATGAACCTC TGTAAATCTTG	60
GGGGAGAGAC TATATTTAAT GATGACAAAC CTGTCACCAG TGTAGCAACA ACAGTGTGAG	120
GACAAAAGCA AATAAAAATT AAGNAAGCGT TCAAATTAT ATTCAACAAG GAAGTCATTT	180
CAATCAACAA CTTCTGCTGC ATTATTTTC CAAGATGAAC CGATACACAA CCATGAGACA	240
GTTGGGGGAC GGCANTATGG GAGTGTGCTT ATGGGCAAGA GTAATGAATC CGGGGNNGCTG	300
GTGGCCATCA AAAGGNTGAA GAGAAAGTTC TATTCTGGG GTGATGGCAT GAACTTNNGG	360
GGAGTTTAAG TTTCTGNAGG AACTTTATTC NGGCCATGTT ATTTAAATNG AAAGANGTTT	420
TTCNCCCCAA ATGACCCCTCT TTATTTTATA TTGGATTTTT GG	462

(2) INFORMATION FOR SEQ ID NO:1541:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

GGCACGAGCC GGACTCTTTT CCCTCTACTG AGATTCTACT GTGTGAAATA TGAGTTGGCG	60
AGGAAGATCG ACCTATCGGC CTAGACCAAG ACGCTACGTA GAGCCTCCTG AAATNATTGG	120
NCCTATGCGG CCCGAGCAGT TCAGTGATGA AGTGGAACCA GCAACACCTG AAGAAGGGGA	180
ACCAGCAACT CAACGTCAGG ATCCTGCAGC TGCTCAGGAG GGAGAGGATG AGGGAGCATH	240
TNCAGGTCAA GGGCCGAAGC CTGAAGCTGA TAGCCAGGAA CAGGGTCACC CACAGACTGG	300
GTGTNAGTNT NAAGATGGTC CTGATGGCA GGAGATGGAC CCGCCAAATC CAGAGGAGGT	360
GAAAACGNCT GAAGAAGGTG AAAAGCATTAC ACAGTTTAA AAGAAGNCAC GTTGNAATGA	420
TGCAGGTTGT TCTATGTTGG GAATTGTTTC CTTTNAATTT NTCCCATCAA AGGTTTACA	480
GCCTTTNTGC AAAG	494

(2) INFORMATION FOR SEQ ID NO:1542:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

GGCAGAGGNG ACTTGGAGAG ACACCCTACC CCCCGATTGC CGTTTGTGA CGTGGCAACA	60
GGGTCCTAG GTCAGGGATT AGGTACTGCA TGTGGAATGG CTTATACTGG CAAGTACCTT	120
GATANGCCA GCTACCGGGT GTTCTGCCTT ATGGGNGATG GCGAATCCTC AGAAGGNTCT	180
GTNTGGGAGG CTTTGCTTT TGCCCTCCCAC TACAACCTGG ACAATCTCGT GGCGGTCTTC	240
GACGTGAACC GNTTGGGGAC AAAGTGGCCC TGCACCCCTT GTGGCATGGC GCAGACATCT	300
TACCAGAATT GCTGTGAAGC CTTTGCGGTT GGAATAATTN ANTTANTGGA TGGNCCATGA	360
NTGTTGGAGG CCTT	374

(2) INFORMATION FOR SEQ ID NO:1543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

GGACGAGGTT TGCAGGACAG GCTCTCACCA TCCTGGGAAG TACTGGACCA GTGCTTGT	60
TTGAAAAGAT TTTNTTCAAA TTCTGCAAAG ACTATGCTCT TTCATACCTC TCCCTGCGAG	120
CTTGTATTGG ACTGTGGACC GCTTCCCTGT GTATTGCTCT TGTGGCAACT GATGCCAGTT	180
CCCTTGTCTG CTACATTACC CGTTTCACTG AAGAACGATT TGCCTCCCTA ATTTGCATTA	240
TTTCATCTA TGAAGCAATA GAAAAACTGA TTCACCTGGC AGAGACCTAC CCCATCCACA	300
TGCACAGCCA GCTGGACCAC CTTAGCCTCT ATTACTGCAG GTGTACTCTG CCAGAGAAC	360
CAAACANTCA CACCCCTCCAG TACTGGAAGG ACCACAAACAT CGTGACAGCA GAAGTCCACT	420
GGGTTAACNT GANTGTTCAT GTAAGTTGG GNGTGCCCCAG TTGTCNTAGG CNTGT	475

(2) INFORMATION FOR SEQ ID NO:1544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

CTACCTGCCA ACTTTNCCCA TGGGCCTTCA ATTAGTACAT TGGAATAGGA GTNCGGATGC	60
TGGGGCAAGG NAAAGAGAGC TANGAAGGGT CCTNCTGAGG TTTTCTCAAA CAATGATGAA	120
GGCCTTATTA ACAAAAAGTT ACCCAAAGAA CTTCTGTTAA GAATATTTNC CTTCTTGGAT	180
ATAGTAAC TT TNTNCCGATG TGCACAGATT TCCAAGGCTT GGAACATCTT AGCCCTGGAT	240
GGAAGCAACT GGCAAAGAAC AGATCTTTT AACTTCAAA CAGATGTAGA GGGTCGAGTG	300
GTGGAAAATA TCTCGTAGCT GATGCGGTGG ATTNCCTGAG GTAGCTCAGN TTTNCTAAGG	360
CTTGCATTGN NTGTTGGG	378

(2) INFORMATION FOR SEQ ID NO:1545:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

GGCACAGGTG GATGGGCATC TNAGTGGTTG TCGTCTTTT CTCTTCCTTT CACCTCTTT	60
NAGTTTTAT TGTGACTACT GCGATACATA CCTCACCCAT GGACTCTCCA TCTGTGAAGA	120
AAGACACACT GCAGGGGAAG GGAAACACAA AGAGGAATGT GCAAAGACTA TTNATNCAGA	180
AATGGGATGG GAAGAGCAGG CTTCAGAGCC TGATTGGACA AAACAACGGC TGGCATTCA	240
ACAAGGGAAA GGTNACCTCC TGACTNCCAT TCTNCTGGTN CCTTCCTCCT GGCAAGGGC	300
GGATGGTTAC CACCTTNC	318

(2) INFORMATION FOR SEQ ID NO:1546:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

AGGTGGAAAT GGCCCTAGAA GAATCATGGG AGCACAGTAA AGAAGTAAGT NAAGCCGAGC	60
CTNGGGGTGG TTCCTCGGG AATTCAAGGC CCCCAGAAGA AAGTGGCCAG GAAATGATGG	120
TGGAAAAAGA GGAAATAAGA AAATCCAAAT CTGTGATCGN ACCCTCAGGT GCACCTAAGA	180
AAGAACACGT AAATGTAGTA TTCATTGGCC ATGTAGACGC TGGCANGTCA ACCATCGGAG	240
GNACAGATGA TGTTTTGAA CTGGGAATGG TTGACANAAG GATCACTNNG	290

(2) INFORMATION FOR SEQ ID NO:1547:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

GGCACGAGAG GAAGGCTCAC TCTGCTCCGT CTCCATCGAG AAGGCAGTGC CTGAGNGACA	60
GAGGCTTATA CAAGTTGTGTA GCCAAGATTG ACGCTGGCCA GGCAGGTGC TCCTGCCAAG	120
TCACTGTGGA TGAATGCTCC AGCCAGTGAA GGAACACCAA GGCCCCAGAG ATGAAATCCC	180
GGAGNCCAA GAGCTCTCTT CCTCCCGTGC TAGGAAGTGA GAAGTGATGC GACTGTGAAA	240
AAAGAAACCT GCCCCCAAGA CACCTCCGAA GCAGCAATGC CCCCTTCAGA TCATCCAGTT	300
CCCTGAGGAC CAGAAGGTTA CGCGNCAGNG NAGTCAGTGG AGTTTTTNG GCAAAGTGGAA	360
CAGGGCATTG AGNCCATT	378

(2) INFORMATION FOR SEQ ID NO:1548:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

GGCANGAGGG AATCAACTCC TGAGCTTTCT GCAGAACCCA CACCAAAAGC TCTNGNAAAC	60
AGTCCCAAGG AACCTGGTGT ACCTACANCT AAGNCTCCTG CAGCGACTAA ACCTGAAATG	120
AACTACANCA GCTAAAGACA AGACAAACAGN ANGAGGACTT ACGTACTACA CCTGAANCTA	180
CAACTGCTGG CACCTAAGGT GNCAAAAGCG G	211

(2) INFORMATION FOR SEQ ID NO:1549:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

GGCACGAGCA AGCCCTCCTT ACCATAGTAT GATGGGTGAT GATGAAGATG CGTGTAGGGA	60
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CACCGAGACC ACTGAAGCCA TGGGCCAGA CATCCTAGCC AAGAAATTAG CTGCTGCTGA	120
AGGCTTGGAG CCAAAGTACC GGATTCAGGG ACAAGAAAG CAGTGGGAGA GGAGGATAGT	180
GAACCTCTCA CCTGAAGAAC GAGAAAAAAA GCGACAATT GAAATGAGGA AGGAAGCTTC	240
ACTACAATGA AGGACTTCAA TATTCAAAC TAGCCAGACA ATTAATTTC AAAAGACCTA	300
CATGNTGGTG GTTGAAGTTG NAGAAATGTT TAGAGANTGC AGATGGNGGA AAGCCTTGAA	360
TTACGGGAGG NTTCAATTCC AGGTTCT	387

(2) INFORMATION FOR SEQ ID NO:1550:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

GGCACGAGCT ACCCCAGCAG CACCAATGTG GAGACCGTCA ACGATGGTGN TGAGTCGGCC	60
ATGTTCAAGC AGCTGTTCCA GAAGTGGTCA GTAAAGGACC AGACCATGGG CCTGGGGAAA	120
ACGTTCAGCA TTGGTAAAAT TGCTAAAGTT TTCCAGGATA AATTTGNATG TGACTCTGCT	180
ACACACCAAG CCAGAGGTAG CTGCCAGGG AAAGAATGGT CGATGGATGG CAACGGGAAA	240
AGTTGAGGTC TGGGAGGAAT TNGAGGAACC TGGGNNGCTGG GTCCCTGTGG GAGTTATTCA	300
ATGGTNTGGG CTTTCTTTN ATGGGNGGGA G	331

(2) INFORMATION FOR SEQ ID NO:1551:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

GGCAGAGCAA CCCGGTGCCT AAACCTCTACA GATCTGTAAT TGAAGATGTA ATTGAAGGAG	60
TTCGGAATCT ATTTGCTGAA GAAGGTATAG AGGAACAAGT TTTAAAAGAC TTGAAGCAGC	120
TCTGGGAAAC CAAGGTTTG CAGTCTAAAG CAACAGAAGA CTTCTTNAGA AATAGCATCC	180
AATCACCTCT GTTTACTCTT CAGTTGCCGC ACAGCTTGCA CCAAACATTG CAATCGTCAA	240
CAGCATCATT AGTTATTCCCT GCTGGTAGGA ACTCTTCCCA AGTTTTACCA CGGNGGAACT	300
GGGGCATTTC AAATTCCATG GCAAATTAC NTTTNCCCG GTTNTNCCCT TCCNGTACCC	360

GCAGGTNTTG NCCTTCCGG CTGTTTTGG GTCACTTTT NAAGGGCAAT NTCCCATT	420
GGGTGCCAGG GTTTTGGGG GGGGCCGGGT TTTTTNGGG TNCCATTGG GGNAG	475

(2) INFORMATION FOR SEQ ID NO:1552:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

GGCANAGGGA ATGCTTTNA TCCAGTTGCC AAAGATTCCA GTTTATGTGG GCCGTTAAAG	60
TACTTCTATA GAGGCCTTGT ACCTAATAGC AACTAATGGA ACCCCAGAAC TTCAGAATCC	120
AGAGAAAC TTCCCCAATGA TTTCGGGAT TTCTTAAATC GATGTTGGG AAATGGATGT	180
GGAAAAAAGG GGTCAGCCA AAGGAATTAT TACAGCATCC TTTCCTGAAA CTGGCAAAC	240
CGTTATCTAG CTTGACACCA CTNNNTNCATG GGCAGCTTAA AGNAAGCAAT GGAAGAGTTA	300
ACCGTTNAAC ATCCACTG	318

(2) INFORMATION FOR SEQ ID NO:1553:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

GGCACGAGCN CGGTGGTACG CTCNAGGNCG CGAGCCNACC GAGCGGACGC CAGTGGATGA	60
CCCGCGGCGG GGGAGGAGGN GATANCATCA GCAAAATGCC AGACGTCAAG GAGAGTNTNC	120
CCCCGAAATA TCCTGGCGAC TCAAAGGGCA GGTCTGTAA GCCCGAAACC TCAGGACCCC	180
CCCAGGAAGA CAAGAGCGGC TCCGAGGACC CCCCTCCCTT TTTTCTGTC ACAGGTCTGA	240
CAGAAACCGT TAATGAAGTT TCCAAGCTGA GCAACAAGAT TGGGATGAAT TGTGATTACT	300
ACATGGGAAG AGAAGGTTTT ACCTCCAAGC AGTCTGGAA GGCAAGGTTTC AAGGAGACAG	360
TGCACAATGC CTTTTGGGG ACCATNTTAA AGGGCAANTN TCAGCAAATT CCCCTTGANT	420
TCAGNTGTGC TCTTTGAACT TTTGAAAGG AATTTAAGG GGTTTTT	467

(2) INFORMATION FOR SEQ ID NO:1554:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

TCCTGAAACA CCACGGNGC AGTTCAACCA AGGTCAATTGA CTTTGGGTCC AGCTGTTTCG	60
AGTACCAAGAA GCTCTACACA TATATCCAGT CTCGGTTCTA CAGAGCTCCA GAAATCATCT	120
TAGGAAGCCG CTACAGCACA CCAATTGACA TATGGNGTTT TGGCTGCATC CTTGCAGAAC	180
TTTTAACAGG ACAGCCTCTC TTCCCTGGAG AGGATGAAGG AGACCAGTTG GCCTGCATGA	240
TGGAGCTTCT AGGGATGCCA CCACCAAAAC TTCTGGAGCA ATCCAAACGT GCCAAGTACT	300
TTATTNAATT CCAAGGGCAT ACCCCGGTTA CTGGTCCTGT GNACTACCCA GGCAGNTAGG	360
GAGGGTTGTG NTTGTGGGG GTCGNTCACG TAGGGGTTAA AAAGCAGGGT NCCCCAGGCA	420
GCAAAGATTG GGGACAGCAT TGNAAGGGTG TGGTGGCTAT TTGTTTATAG GGTTTTTGAGA	480
AAGGT	485

(2) INFORMATION FOR SEQ ID NO:1555:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

AGCGGCACGA GGNCTCCTNT TGGCAGANTT GGCCAGTNTT CCCCAGTGAC AGCCTGGNTC	60
TTTGGATTCA AGCTGCCTGG TCAGACTGCA NGTTCATCTG TACAAAGAAG GAAGCAACAG	120
TGCCAGGTTC CAGCGTGCCT TCCAAGTTCC ACATTCTGTG TGGCAGACTC CCAACGCCAG	180
AGCAAAGGCA GGCCCCTGGC AGGGGGACTC TGNAGGAAAG TGGAACTNCC AGGAGACACT	240
GCCTGNAAT TGTTCCTAAA GTTCAAAGGG AGCCAAACGG TGTNACGAGC TTCCCTCTTT	300
NGCCGTNCCC CTNTTNAAGA AGCCAGCCAT GGCCCTGAGT GATTGT	346

(2) INFORMATION FOR SEQ ID NO:1556:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 188 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

GAGTCACTGG CATTACGAA CTCAGCTTAT GCAAAATNTC AGTCACAGGT AGTCCAGGTA	60
TGCAGAGAAG NNGAAGAAAA ATCTTAGATA CGTCATGGC ATATGTCGG GGAGAACAGA	120
ACTTAGCNGG ACTGGCGGCC CCGTGGGAGN ACAGCCTCA TCCTTNAGCA CCANTGGGA	180
GCTGGNGG	188

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

GGCAGAGCTC ACCTCCAGTT CACATGTTAA AGTCCTCACCC CAGCAAGA CAGTNTTGGA	60
GGTGGGGCCT TTGGGAAGGG GAGCAGGTTT AGAGAACATC CTGGGGGACC CTCACGAATG	120
AGATGAGTGC CCTGATGGGN AAGAGACACC GGGAGCCTCC TCTCCAGGTA GTCACACACG	180
GGGACNGTGC ACATGAGCAA GAGGCTGCTG TGCCGTAAAG CTTGGGGGT GGTCTTCCA	240
ACNGGTAACT GGGNTGCTGT GGTCACCTGG GAGGCTGTGT TTTCCCAACT GNNCAGTAGC	300
TTGGGNGGA	309

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

GGCACGAGCA ACAGACTCAA TAGAAAGACT CCCAGTGTAT AACAAAGCTG CCTGGAAGCA	60
TTACAACACC AACCAACGAGG CTGACGACTG GTGCGTCCCC AGCAGAGAAC CCAAAGACAT	120
GACGACGTTG CGCAGTGCCT AGNACACACT TGGGAACATC GGAAAATCC AAATGTGGCT	180
TTTGTATTAA ATTTGGAAGG CTTAACCTCT NCAAGCTCTT GAAGGTTATN AAGAGGGATT	240
GATTAGTGCC ATGGATTCCA GGTCTTGAG ATTAAAAGGG CACGGAACGT NCCCTTCCA	300
AGGTTACTGG CATTTTTAA CAAGTTGGAA GNTTGTGGG CAATTCTTNC ATTGNG	356

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

GGCACGAGGG AAAGCACCC GAGAACACAG GAAAGAAAGA ATGCAGCACT GGTTACCAGG	60
ATGAAAGCCC AGAGGCCAGA GGAATGCTTA AACACATCA TTGTAGTGCT GGATCCAGTG	120
CTCTTACAGA TGGNAAGGTG GGGGCCAGCT CCTAGGAGCA CTGNAGACCA TGGAGTGCCG	180
CTGTGTGATT GAGGCAGCAGC TGTGCCTTGC AGTGTCACTT GGAGGAGAAG GGCTGGGCCG	240
TCTGAGGACA GNGAGGACTG GGTGGAGGAG CCAACAGTAC TGGTGTGCT CGGGCAGAG	300
GCATTTGTNT CCATGATCGA CAATGGAAAG CAAGGAAGNC TNGACAGCAT TATGAAAGGG	360
AAGGAAACGN TTCAGGGTTT TTAACTGNCN TCACAGCAA GNCAGCAAGG AAAGTTTTT	420
CACTGGTGAT TNTGGTCAG GGNAATGTTT CATTGGTCAG ATTCTCCCCA GAAGGGNAA	480
CAGGGGCAAT TAACCAGCCC AG	502

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

GGCACGGCTC ACACCGGCCT GTCTGAGCA AGGGTTGCT GCTGCTCCTC TGGCTCTCCT	60
TTGCTGAGAC CTGNAGTCAC CGGTTCGCCT TTGATGTNCT CACTCGTCTT GGTTGTGTTT	120
TCATAGCCCT TGGCAACTTG CTTCTGGGAT ATTCAAGTTTC AGGGTGTAA GGNGTTACGT	180
TATTGAAGAT AAGAGTTCT TTTCTGTAA CTTGTTCTAA TTTGGGTGGG TAATAAGAAC	240
AGAGGCCTTC AGAGAAGTAT TTACTCTGAC GTCTTAAAG CTTTTAAGG CCCACGGCCA	300
GATTCTTTA ATACACTTTG GGCATCCTCT GTCTGAAAA TTAGGAAATT GTATAATGTC	360
CTCGCTAACCA TACTTCAGG TTAACCTGTT TATGGTTCTG ATGTATTTAC ATGAAATTG	420
GGTAACACTA AATATAGTGA ATGTTTCTT ACAGACAGAA CCTCCACTCA ATACACCAGA	480
AAGCAGAGAG TATCTTGCAG NANT	504

(2) INFORMATION FOR SEQ ID NO:1561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

GGCANAGNAA	AAAAAATTCA	AGACCAAGAC	CAAGAGCTGG	CCACTGTGCT	GTTGCAATCG	60
GCANTCGATT	GTATTTTGG	AGTGGAAAGAG	ATGGCTACAA	AAAAGCATGA	ATAGTCAAGT	120
TTGCTGCANG	NTCTTGTA	TCTTGNTACT	GNGANACCAC	CGGNACCATC	TCAAGTACAG	180
CTGATCAAAG	CCACTACCAA	CTCCTTGAT	GTCAAGTGGG	ATGAAGTGTGTC	TACAGTTGNG	240
GGCTATCTT	TGCAGTTGAG	TACAGACTTG	NCATACCAAG	CTGGCATCAT	CNAGATT	300
TCAGCAGCAC	CAATTNTGCA	AGGAGTTCA	GNTGGGACCN			340

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

AAGAGAAAGG	AGGCTCTCAG	TAAAATGACC	CAAATCATCC	ATGAGACAGA	CCTGTTAATG	60
AACACCATGC	TCATAGAAGA	GCTGCANGAC	TGGGAGCGGC	GGCACAAATC	GCCTGCATCG	120
GGGGTCCACT	CCACAATGGG	CTCGACCAGC	TTCAGAACTG	CTTTACACTA	TTGGCAGAAA	180
GTCTTTCCA	ACTGAGAAGG	CAATTGGAGA	AACTAGAGGA	GCAATCTTAC	CAAAATGNAC	240
ATATGGAAGG	TGATCCCATT	CCAATGCAAA	GAACTCACAT	NGTTAGNAAG	AGTCACCTTC	300
TTGNTTN						307

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

GGCANANCTG	CTTCGGGGCA	TAGACAGCTT	ATTCTNTGCC	CCNATGGACT	TCCGGGNCT	60
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CCCTGGGAAA CTACCACAAA GAGGAGAACCA AGGAGCACCA GCTGGGNAA CAACACCCTC	120
TCCAGGCCACC TCCAGATCGA CAAGATGACC GACAACAAGA CAGGAGAGGT GCTGATCTCC	180
GAGAAATGTG GTGGCATCCA TTGCAACCAG CGGAGGGGGA GCTTCGAGGG TGATTGAAA	240
GGTACCCAGG ATGGAGGAGA AGGAGGCCT TGGTACCCAT TNCAGAAGGN CCACGGGACA	300
GTTCCTCACA AAGAANTTCC NNCCCCGGTT TGG	333

(2) INFORMATION FOR SEQ ID NO:1564:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

GGCAGAGGNA CCAGCGCGCC CCATTACACCT TGGCTGTNGT NGTTNCACAT GACCCAGGCT	60
GGCCAGTNGT CAGGTTGCAC CGCCCTTTGG TTCCCGAGCA TGCTGTTTN TTTNAGCCTT	120
CTNTCCAACC TTAACCAAAT CGGCAGCAGC CACCTNGAAC CGNCCACACA TTCCTGGCCA	180
ATNAGCTCAG CTGTTTATT ACCAAATGTT TTCACAACAA CTACAGCAGC AGCTTCGGT	240
TAACAAAAAA GCAGGAAAAA TCCACAAACAC CNNGTTGGC AACCAANTAA ATCCAAGGGA	300
ACATNTGGNA AAACCTTTT	319

(2) INFORMATION FOR SEQ ID NO:1565:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

ACGGAAACAA TCTGAAGGTG AAGAGAACAC ATTAACAGGG GNCGTGTAAA ACCAGTCCTN	60
CCACGTAANT NNACCAAAGA AACAGCTGCC TTCTATTCCC AAAAATGCTT TGCCCA	116

(2) INFORMATION FOR SEQ ID NO:1566:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

GCCCTGGAAG ACGATCCCNA GTTCAACGCA GGTTGTGGGT CTNTNTTGAA CACAAATGGT	60
GAGGTTNAAA TGGATGCTAG TATCATGGAT GGAAANACC TGTCTGCAGT AGCAGTGTCC	120
GCAGTCCAGT GTATAGCAA TCCCATTAAA CTTGCTCGGC TTGTNATGGA AAAGACACCT	180
CATTGTTTC TGNACTGACC AAGGCGCAGC AGTTTGAG CAGCTAATGG GGGTTCCAGA	240
GATTCTGGA GAAAAACTGG TGACAGAGNA GAAACAAAAA GCGCCTGGAA AAAAGAGGAG	300
GCATGAAAAA GGTGCTTCAG AAAACAGGTT TGTTCAANAA AACTTTGGGG AACCNTGGGG	360
TGNTTGTNG TCTTGGGAN	379

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

GGCACGAGAG CCTCCTCAAC TGGAGGCGAG TTTNTTCCTT CACGGGNCG GTTCCCCGCG	60
NCCCGGNACG NNCACCGAGC GGGGGCCATC CGGGAAAGCTG ATGATCATCT TTGGAGGGGG	120
AAATAAGGGC ATCGCGGATG AAGCTGGCAC GTNTACAACA CGGCTACGAA TCANTGGTNT	180
CTGCCAGCTG TTAGAGGAGA TATCCCTCCA GGCTGTGNTG CCCATGGATT TGTCTGTGAA	240
TGGTACCAAG AATATTAGTA TTTGGGGAA TGGTTGAATA TGGGAGNTTA CAGCAATGGA	300
GTATATATGA AGTTACCAAG CAAGTGCCTT GGTTATTGGG AAAAAAAGTG AAACCCCCAT	360
NCCCCCTNCN TTNTGGTTTT AACNCCCTTG TCC	393

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

GGCACGAGGG AAGAACACA GTAATGANTT TAANATGACG TCATTCTGT TAATCCAACA	60
CCTGCNACCT TNTTNACTGT NTGANGCGGT ACAGCGGGGA TGAAGGGCTT CATGAACCTCA	120
AAATACAGCA AAGCACAAACG GAACACTGCC TTAAGANCTT TAACCTCACC GAATACCGTC	180

AGTACTGAGC CGAACCTTC CATTCAAATC TACCAGCAGC TCTTGAAAAT TGCCGAGGGT	240
GCGTTACAGC CGNTGATAGT TTNTTCCCAT GTTGGGAAAT NNNGGGCTTT CCNGG	295

(2) INFORMATION FOR SEQ ID NO:1569:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

GGNACAGGTC GGCATTATTT AAATGAAATT GGACAGTATG ACAAGGATAT GGNTTTNGG	60
GGAAGAGAAA ATTTGGAACT TTNACTAAGG ATCTGGATGT TTGGAGGCCA ACTTTTATA	120
ATCCCCTGCN CTCGAGTAGG ACATATCACT AGGAANAAA CTGGGAAANC CTTCTACAAT	180
CATCAGTGCC TATGAACACAA TNAACTGNCC TAAGATCTGG TGGCACGTTT GGTTGGATGG	240
ATTATNAGGG GAGCCAGTTT TTTNTTTCGG AAAGTCTGGT CTGGAAATAT GTNACCTNCG	300
GGAAANTT	308

(2) INFORMATION FOR SEQ ID NO:1570:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

GGCAGACCGG CACGAGGNNA ANCTGGGTGC TGGAAATGGA AACCTGCAGT NCCTNGACAC	60
ATGCAGAAAG CCAGAGTGGAA AACTAGCAGA GTTCTTCACA TCATGGNTTT NNAANGAGGG	120
CAAAAAACTTC TAAATNCCAG TTATTACAGC TGGTAG	156

(2) INFORMATION FOR SEQ ID NO:1571:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

CGCCAGACGG CCATGTCCGA AACCTACGAT TTTTTNTTTA ATTCCCTTGTT TATTGGAAAT	60
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GCAGGANCTG GNCAAATTN GCTTACTTC	TCANTTTATT GAAAAAAAAT TCAAAGATGA	120
CTCAAATCAT ACAATAGGAG TGGAAATTG	GTTCAAAGAT AATNAAATGT NGGTGGTAAA	180
TATGTAAAGT TACAAATATG GGATACAGCA	GGNCAAGACC GATTCAAGTC CGTGNNGGAG	240
NAAGTTATTA CCGAGGCCGCG GCCG		264

(2) INFORMATION FOR SEQ ID NO:1572:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

TATTTGGTCA AGATACTCAC TTGTAATTAT NCCAAAANT	TGGAGTCTGT TTCCNGTTAA	60
TTCNTTTTG GGGCAGCAG GAGCCTCTCA CCTTTNGGT	ATTTGGAGAT ATAACCAAGA	120
NCTAAAAGCT AAAGCACACA AATGAAAAGA NTTCCGTGATC	ACCTGANCAA TCTAGATGTG	180
GACAAAACCA TTGGGGACCT AGTTTATTAT TTGGTTATTG	ATAAAGCAAA GCTAACTGTN	240
TGTTTAGAAA GGCAGTGTNA ACTGGTAGCT AGTCCTTGG	ATTCCAATAG AAAATGNCA	300
GCAAAACTTT TAATAAACAG TTCTCTNTAN CATGG		335

(2) INFORMATION FOR SEQ ID NO:1573:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

TTTTTANCTT CGGGCTCTNA ATTTTNGCGA GTAAAANTGG	CTAAGTGACT ATGGTGGAAA	60
TGGTTTCGGA AGGACGTNTT AGAATGATGT	TGAAAACATAT NACCCATG	108

(2) INFORMATION FOR SEQ ID NO:1574:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

GGNAGGAGGT GTCGACTCCC TCAAAGCCAT GACCAGGCGA ANCAATACGG ANAAGTTNCT	60
AATCTCCTTN AGGGTGTAAAT GAATGTCCTG GAAGCACTTC CACAAGTATA TGGGGATTCC	120
CCAGATCCGG CAGCTTCCG AAAGNNNTGAA GGCTGCACAG ACTGANTTAG GACAGCAAAT	180
CCTGGCAGAT TTTGAAAGAA GCGTTTCCTT CCCAGGGCA CCAAGNGNCC AGGTGGACCC	240
AGCAATGTTT TTACGAGATG CATGTTCTGG TTGCTAAATA TTCTGGATTTC CCAGGGTTCA	300
ANCNGGNATC CTTCAANAAG TTTNTTAAA	329

(2) INFORMATION FOR SEQ ID NO:1575:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

AGCTGCCAAA AGGGCATCCT GGAAGCCCCA TGGAGGACGG AGTAANATGG ATCGGGAAAT	60
TTCCATTGTT GTNCTTAATT TTNAATGAAA ATANGTTTG GTATTTGGAG GAAAATNTGG	120
CAACCCATGG NTCCCAGGAT CCAGGCAGTA TTAACCTACA GGATGAAACT TTCTTGAGA	180
GCAATAAAAT GCATGCAATC AATGGGAAAA CTCTATGCCA ACCTTAGGGG TCTTACCATG	240
TACCAAGGTG AACGANTGGC CTGGTACATG CTGGCCATGG GCCAAGAATG TGGATCTACA	300
CACCNNTCCAT TTTCATGCAAG AGAGTTCCC TCTATCGGAA TGGCGGGGAA CTACCGGGGC	360
AGTTGTGGGT GGTCNTTTC CCCNNGGANT TTNAAGG	397

(2) INFORMATION FOR SEQ ID NO:1576:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

AGCCCAGGGN AGCCCAGCCA GACGCCTCCG GTAGTGTAAA TAAGGACAAT GCCTGCTGGC	60
CCACATGAAC GGGGGGATGT AGACGGCAGC GGCGCCAGTC GTNCCTGGCA CCATGGACGA	120
TGCCACANTC CTGAAGGAAG AAGGGTTACA TCGTAGGCAT CAATCTTGGC AAGGNTTCCT	180
ACGCAAATT CAAATCTGCC TACTCTGAAG CGCCTCAAGT TCAATGTGGC TGTCAAGATC	240
ATCGACCGCA AGAAANCACC TACTGANTTT TTGGGAGAGA TTCCCTCCCT CGGGAGGATG	300

GGNCATCCTG GGCAACTNTN CAAACCAA 328

(2) INFORMATION FOR SEQ ID NO:1577:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

AATAAAGATG CTTCANACTG CAAAGAATTG	60
GTGAAAGAG GAGAAATTGG TGCATAGCTA	
TCCGTATGAC TGGAGGACCA AGAAACCTGT GGTTATTCTGT	120
GCCAGCAAGC AGTGGTTTAT	
AAACATCACG GATATTAAGA CTGCAGCCAA GGAATTGTTA AAAAAGGTGA AATTATTCC	180
TGGATCAGCA CTGAATGGCA TGGTTGAAAT NATGGACAGG CGGCCATATT GGTGTATATC	240
AAGGCAAAGA GTTTGGGTG TTCCAATTCC TGTGTTTCAT CCATAAGACC AAGGATGGAA	300
TACTTGATN CAACAGGTTG GTTGGNCCCT GATGCCTTGG GAATATGTGC CCAGGTCCAG	360
GTNATTGATG GGACATCTGG GNTTGNTAG GCAGGAACCTT TCC	403

(2) INFORMATION FOR SEQ ID NO:1578:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

CGGCNTNTNT NTGCTCCGTC GCAGGACGCA GGGTCGGGC CTAGGGTAGG CTCTCCTGAA	60
TCGACAGGCG CCGGACCTCT NACAATGCAG ATCTTCGTGA AAGACTCTGA ACTGGTAAGA	120
ACCATCACCC TCGAGGTTGA AGCCCAGTGA ACACCATCGA GAATGTCAAG GCAAAGATCC	180
AAGATAAAGG AAGGCATCCC TCCTGACCAG CAGAGGCTGA TCTTGCTGG NNAAACAGCT	240
NGGNAAGATN GG	252

(2) INFORMATION FOR SEQ ID NO:1579:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

TNTNCCCATC TTCCACATCC CTGGNCGTAC CTTCCCTGTT GANATCCTCT TCAGCAAGAC	60
CCCACAGGAG GNTTACGTGG AGGCTGCAGT GAAAGCAGTC CTTGCAGGTG CCACCTNTGC	120
GGGGGCCCT GGGAGACATC CTTATCTTTC ATGCCTGGNC AAGAGGACAT TGAAGGTGAC	180
CTNAGACCAG ATTNTGGAG CATCTGGNAG GGAACTNNGA GAACGNGNCC TGCCCTNGGG	240
TGTGNTGGNC CATCTAATT NNAGTTGNNT TTTGAANCTT CCAGGNAAA ATTTTCCAG	300
AAGGGTTCCA ATTGGGGGTT CGGGAAGTTG CATGGTTGGC CAACNATATT GCCCGGNGAA	360
GGTTTTTNA ATTGTTGAN GGGATCAAGN T	391

(2) INFORMATION FOR SEQ ID NO:1580:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

GGCACGAGTA AAGTTAACCA TTACTATGAA CCCAAGCTTA TTATAGATCT TTCCAATTGG	60
AAAGAACAAA GCAAAGAAAA ATCTGATAAG AAAGGCAAAT CAAAATGTGA AAGGTAATGG	120
NTTGGTTAAA GCCCAGATAG CGCTAGAGGG AAGCATCACA GCAACTGGCT GGNAAAAGNA	180
AAGGGAAAAG NAATCAGGGA TTTGAATTTT GAATTCTTT ATTGCAGGAA CTATTNCAGC	240
TTAGTTCCC AGNCATGAGC CTACTGATGT TGTTGATAAAA ATTNAATGG ACTTGGAAATA	300
GCTCAGTGTGTT CCCAACTNNG AATTTGAAAA GGTTTGATA TCCAAGGTTTC CGTAAGNCCA	360
GGGAAAANCC GGG	373

(2) INFORMATION FOR SEQ ID NO:1581:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

GATTNAACAA CGCNTTACTG CTCGCTGGGT TCATCCCGCC NATGGNCGTG TCTATAACAT	60
TGGAATTCAA CCCTCCAAA NCTGTGGGGC ATTGGTGACC TGGACTNGGG GNCCCTCTGC	120
ATTGCAGC	128

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

GGCAGAGCTC GTCCTNTTNC CCAGGGACAA GTGAGGTCGA TGAAATCTTT AAAATTNCC	60
AAGTTTAGG GACTCCCCAA AAAAGTGACT GGCCAGAAGG ATACCAGCTG GGCATCCTCT	120
ATGAANCTTC CGTTTCCCC AGTGTGTTCC TATAANCTTA AAAACTCTTA TTCCCAATGC	180
CATAATGAGG CTATTCAAGCT CATGACCGAA ATGTTGAATT GGGGTCCAAA GAAACGGACC	240
GACAGCAAAG CCCAGGCATT GAAACACCCCT NTTTNCCAAG TTGGTNCAGG TNTTAGGCC	300
TTGGTTCAAT CCATCTGGGA TNCAAAACAT CTTTAATTAA GCAGTNGCAA CCCTTAGATT	360
CAAAGCCCTC TTTAGTTNG GGTTNGGNCT TAGG	394

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

GGCACGAGTG GACTAGGACT GGCCCCGGCA AAAAACAAAGT NTTATAGCTG CCCAGTGTCC	60
TCTGAGTGGA TGCTGGTGAT TCTGGTATGG AGCCCAGATG TAAGGCAGCA GGTGGTCCAG	120
AAGGCACCAG AAGAGGTCTC CTGTCAAAGT CAGGGCCAGA GAAGAAGGCA CAGGGNNCCT	180
ACTGCACGAG AACTTCACT TGCAACGAGC AACCCATGAT GAGGAGGGAG GATT CCTGGG	240
GGCATTGAGT CCCCAGACA CAAGGACCN GNACCTTCTT GCTTGGGAAA GTGGANTTCC	300
TTCAGAATTC CGAGATGATG CCATTTNGG AGGAAGNTGA CATGAGGGAC CCAAAACTTT	360
NTTGCTTTGG AAAGTGNATT	380

(2) INFORMATION FOR SEQ ID NO:1584:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

GAGCTCGTGC GGNTTNANTT AATTCTNCTG TTTCGTGAAC TCGCAGTGGA ACAGGAATCT	60
CTGTTGANAG CTTTNNNGCTG TGCCCTGCAG TTTTNAGGCA ACATTCNCCTC ACGGATTGAA	120
GATTCCCAGT CTATTGTTTG GGTGCATGCT TTCCCAGAAC TNTTTTGTC TTGCTTAAAT	180
CATCCGGACA AAAAAATTNT TGCCTACTNT NCAATGATT TGTTTACATC CCTTAATCAT	240
GAAAGATTGA AAGANCTNGT GGAGGAACCT NAATATTGCA ATTNATGTCA TAGATGCTTA	300
CCAAAAACAT CCNGAATCAG ATGGCCGTTTC CTTGAT	336

(2) INFORMATION FOR SEQ ID NO:1585:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

GGCACGAGCT TTGCACCNAG CCTGTGCTAA TGGACATACA GATGTTGTAC TTTTCCTAAT	60
TGAGCAACAA TGCAAAATAA ATGTCCGGGA TAGTGAAC AACATCCCCAT TGATTAAGGC	120
AGTACAGTGT CAAAATGAGG ATTGTGCTAC TATTCTTCTA AACTTTGGTG CAGACCCAGA	180
TCTGAGGGAT ATTGTTTATA ATACTGTNCT TCACTATGCT GTTTGTGGTC AAAGTTTGTC	240
ATTAGTTGAA AAACTGCTTG AATACGGAAG CTGGATCTTG AAGCGGAAAA ATAAGGGATG	300
GGTATACTCC ACTATTAGTT GCCGTTTATT TAACATTATN CAAAATGGT AAAATTCTT	360
CTNGNGGAAG GGGGNTGATG TGAATGCTTT CAGN	394

(2) INFORMATION FOR SEQ ID NO:1586:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

GGCACGAGGG NCTCTTCAGC TCAGCCCTCC ACAAAAGTGTG AGCCTGAAGG ACCACCCTGA	60
ATTGCCCTTG TAGGACCCAG AACAGCTACC AGCAGAAATCA GATTCTNATG GACCAACTGG	120
TATTCAAAGA GACAATCTGG GAATGAATGC GTTCTGGCAG AACCCCTGGG AACCAAGGGAG	180

NCCTGGNCAG TGAATTATCT TATTCATCAC CGCTGTCCTG CTTCTGAATC TTATTTGCCA	240
TCGTGTTGG TTTACTCACT TCCACAGAAA ACACTTCAGT GTGNAAGCGG GTNAAAGAGG	300
AGTNAACCTG GACTTNGCTG GGGGACTGAG AN	332

(2) INFORMATION FOR SEQ ID NO:1587:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

GGCAGAGCGG CACGAGAGAA CCAGAAGGCT GGGCTGGGCC CTCGCTTCTN GCCCATCACC	60
CCTCTCCAAC AAGCTGCTCC CGGAGTGGGT CCCCCCTTCA GCCAGGNNNCC AGCTCCCCAA	120
CTACCCCCAG GACCCCCCTGG CGCCCCCAAG CCACCACCTG CTTCCCAGCC CAGTCTGGTC	180
TCCACTGTGG CCCCTGGCTC CGGCCTGGTT CCCACGGCAC AGCNCGGGC ACCGTTCCAT	240
GGCAGGCACT TTGGNCCAG GAGGGGTGAG CGGCCCTTTC CCAGNCCAGT TGGAAGNCCC	300
CAGTCCTTGG GTTGGGGAAG CAATTNAATT TTTCCAATAA AGTTTTTTTG GNCTTGGGAG	360
CGGGGGTTNC TTGGANTTGG GNAAAGGGAA AACCCAAAAT TTG	403

(2) INFORMATION FOR SEQ ID NO:1588:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

GGCACGAGAA TGAGCTCGTC GGCTGAAAGG GAACATCCGA GTAATTGCTC GTGTCCGGNC	60
AGTNACCAA GAGGATGGGG AAGGACCTGA GGCCACCAAT GCTGTAACCT TCGATGCCGA	120
CGACGACTCC ATCATCCACC TGCTGCACAA GGGNAAGCCT GTNTCCTTCG AGCTGGACAA	180
GGTCTTCTCC CCACAGGCCT CGCAGCAGGA CGTGTCCAG GAGGTGCAGG CCCTGGTCAC	240
CTCTTGCATT GATGGCTTCA ATGTCTGCAT CTTTGCCTAC GGCCAGACGG GCGCCGGCAA	300
GACGTACANG ATGGAGGGGA CCNTGNNAAC CCCAGGTTTT CAACCAGNGG GCCNTGCAGT	360
NGTNTTATTC CGAGGTGNCA GGAGAAGGCG TTTTATTTGG GAGTTACACC TTCACCTTCA	420
GGNTTGNNGN GNNTTACAT TGAGGTTCTNT CAGGGACTTN TTAGGGGAAG AGCCNTCAGG	480

GAAAAATGGA GTTCGGTTNT GC 502

(2) INFORMATION FOR SEQ ID NO:1589:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

GGCACGAGCC CCGGTGTTCA CTCAGGAGGA GAGATAACAAG ATGGTGCAGG CCATCAAATG	60
GGTGGACGAG GTGGTGCCAG CGGCTCCCTA CGTCACTACA CTAGAGACCC TGGACAAATA	120
CAACTGTGAA CTTCTGTGTT CACGGCAATG ACATCACCCCT GACTGTAGAT GGCGGGGACA	180
CCTATGAGGA AGTAAAGCAG GCTGGGAGGT ACAGAGAACATG CAAGCGCACG CAAGGGGTGT	240
CCACCACAGA CCTCGTGGC CGCATGCTGC TGGTNAACCA AAGCCCNCA CAGCAGCCAG	300
GAGATGTCCT CTGAGTACCG GGAGTTGGC AGACATTTCG GCAAGTGCCT GGTGGCGGT	360
AACCCCTGGGA CCGGGGTNTT CCCATTNCTG NCAGACTTTT CAGNAGNTNC TTCCATTGN	420
TTNTGGGAA GGAGCCCCAG CCAGGGAGAC ATTNNNTATG TNGTTGGTGN CTTTGGACCT	480
TTTCCACNTG GGGCTGTGGA TTTC	504

(2) INFORMATION FOR SEQ ID NO:1590:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

GGCAGACCTG CACNCCTGAT CCATAATGCT NACGCCAAA AAAGCTCCTT GGGTCTNANA	60
GGCCTCCAAA GCCTACTCCA AGGTTTCACC NNTNTTNCC TGAAGTNANC CTGCTTCGGN	120
AGNATAGACA GCTTATTCTN TGCCCCCATG GACTTCCGGG GNTTCCNTGG GAAACTACCA	180
CAAAGAAGGA GAACCAGGAG CACCAGCTGG GGGAGCAACA CCCTCTCCAG CCACCTCCAG	240
ATCGACAAGA TGACCGACAA CAAGACAGGN GAGGTGCTGA TTTCCNGAA ATGTGNGTGG	300
CATCCATTNC AACCAAGGGT GGGGGAGCTT TCGAGGGGTG ATTTGAAAG GTACCCCAGN	360
TTGG	364

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

GGCAGAGTGA ACTTCTTCCT GTTGGTNTCC CCCCGCCGCT GTGGGGCCGT CGAGACCCGN	60
CTGGNCGCTG AGATCCTGTG CCAGGGCAAG AAGTTCTACT TTGTGCGCAC CAAGGTGGAC	120
GAGGACCTGG CGGCCANGGC AACCNAGNG GCCGTCGGGC TTCAAAAGG CCGCTGTTCC	180
TGCAGGAAAT CCGAGACCAC TGTGCCGAGC GGCTGCGAGA AGGCCGGCGT GGCTGACCCCT	240
CGCATCTTCC TGGTGTCCAA CCTCTTNGCC GGTTCCGNTA ACGACTTTCC CACGCTGGTG	300
TCCAACCTGGG AAGCATGACC TGNCCTCCNA ACGGTGGCCA AGNTGGTCTG GT	352

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

GGCAGAGGNT GGTCATACC GACGGGAAA GGCGACCTGT GGTGATGTCG ACGTGCTCAT	60
CACTCACCCA GATGGCCGGT CCCACCGGGT NATCTTCAGC CGCCTCCTTG ACAGTTTCG	120
GCAGGNAAGG GTTCCTACA GATGANTTGG TGAGCCANNA GGAGAATGGT CAGCAACAGA	180
AGTACTTGGG GGTNTGCCGG CTCCCAGGGC CAGGGCGGCG GCACCGGCAC CTGGTACATC	240
ATCGTGGTGC CCTATAGCGA ATTTGCCTGT GCGCCTGCTT CTACTTGCAC CGGCTCTGCA	300
CACTTNCAAC CGNTCCATGC NNAGCCCTGG CCAAAACCAA GGCAATGANTT CTGTTCAGAA	360
CATGCCCTTC AGCAATGNTT GGGTTCCGGA AACAAACCATG GGTGNAAAGT TGGGGCCTGG	420
NCNA	424

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

GGCAGAGAGA ACTTCTGANC GTTGGTAGTN TGGGGATCCT GGCTTTNTNC TTCTTCACCC	60
ACCGTATCAG GATCGTCCAG GATACAGCAC CACCCCTCAA TTATTACTGG GTTCCATATAC	120
TGACGGTGAA TCGTTGGCTC CTACTTGNAT TGCACACGGT TTCTTCAGCG TCTATGGCAT	180
GTNTGTGGAC AGCTGTCCT CTGCTTCTTG GAGGACCTGG AGAGGAATGA CGGCTCGGCC	240
AGAACGTTN ACTTGCATGT CTTCCACCCCT CAAGAAACTN TTGAAACAAG ACCAACAAAGA	300
AGGNAGGGAG TTCCTGAAGG CCCCGTGNTC CCCAACTTTT CAAGGAGTTT TCATGNCGCA	360
GGTTGNTTCA	370

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

GGCAGAGTGC CTGATCGAAG GCAGCNCGGC CAAGCTCACT TGCCGCATTT NGGCTTTCCC	60
GGACCCATTC ATCCGCTGGA GTAAGGNCGG CAAGGAGCTA CGTAACGGTC CCAAGTANCG	120
CTACGTNTTC AAGGACCCTG AACGTGGTGG CACTGGTGGT GCGCGAACGG CAAGCTGGCA	180
GACCTGGGCC AGTACAGCAT CAACGTTCAC CAACCCCTTC GGCCAGTGCT TCCGACTTCG	240
GNCGCGGCAT CCTCGTGGGA AGTCCCCGAC GGAGGATTTC AAAAGGGGAC CCGACAACAC	300
TAAGGCGCGC AAAGGCACCA CCGTNAACGN TTGATTGGG AGATTCTGG GGAGAGNCTG	360
CGCCCCGACG TAGGNTNGGA CCAAGGACGG GGGAGGGACA TTGAGG	406

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

GGCACGAGCT GGGGTGCCTN ATGCNATCAT GCTGTGTGTG CGCCAAATCT GCGCTGTNAT	60
CCTGGAGTCC CCACCCANAG GAAGCCACTA TCCCCTACCA TCCNAGCCTC TCCCTAGGTA	120
CTGTTCTTCT CTCTGCCAAC CAGGGCTTCT NTGTCCAGGG TCAGTATGGG GCTGTGAACC	180

CCAGCTGAAG GTCACCAAGC TCCAGCAGCT CTGNAAGCNA TGC GGTTCCC CTTTGGGNAC	240
ACCCAGCGTG GTGCCAGGGA CTGNGATCCC GGCACACAGA CCAGCTTCAC AGGAGTTCC	300
TGGGTTCCCA ACGATTGAA TTGGTTGTNT GGATT CGGGN CGGCCAGGG NAGCAAAGNT	360
TCAANGGAG	369

(2) INFORMATION FOR SEQ ID NO:1596:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

ACAGAACGGC CACGGNTTCA CCTGCCAGG CACCTGCCCA AAACCATTCA AAAGAACGGTC	60
GGGGAGCCTG TGAAACCTTC TNATCCCTTT CCAGGGCAAG CCCCGGCCTC AGGTGAACCT	120
GGNACCAAAG AGGGCAGCC CCTGGNAGGT GAAGGTAGGT GNAGCATCCG CAACAGCCCC	180
ACAGANACCA TCCTGTTNCA TCCGGGTCG	209

(2) INFORMATION FOR SEQ ID NO:1597:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

CCTTTGTCCG TNTGAATTAC CAGCACCGTA TGTCCCTGA ATTGCCCGC CTTTGACCC	60
CCCACATTAA CCAGGATCTG GAGAATCATC CATCTGTTCT TAAGTATGAG AAAGATTAAG	120
GCCAAGTNCA ATTCCCTGCA GAGCTTGCG AACTGGGAAT GAGAAGAAAG CATAAGAATT	180
TCAGGGNATG ATTNNATC TTTTTNAAA GCTTACGATT AAGAAAGTGC CACGTTTCC	240
AATTGCTCCC TNCTGGGNT TCTTGGGACC ACTGNNTTC CTTCCCTTC TGCCAAGGAG	300
CCGNTTGCT TGTGATTG	318

(2) INFORMATION FOR SEQ ID NO:1598:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

CTAGTGNNTC	CCCCGGGCCT	GCAGGAATTC	GNAGAGCAC	ACCTTTCCNT	NTCCTTTTG	60
GTGATGAAGG	GCCCGATTAA	GGCCCTGCTG	CGGTGGCCCT	TNANCCAGAA	GGTAACCTTA	120
ATNCTGCTCG	ACCAGAATAA	CCGGGAAGCA	CGTAATTNAG	NGCTTCAGG	CCCGAGGTGA	180
ACTTCATCCT	GTTTAAAAG	GCCAGTTAAA	CGNCATGTAA	CATNGCAAGG	NG	232

(2) INFORMATION FOR SEQ ID NO:1599:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

GGNAGAGGTG	ACCCTCTGGA	ACCTGCNAGG	AGCCGGCTCT	CCAGGCTGCC	CGGCTNANAA	60
GTACCTAAAG	CAGGTAGACT	TCANCCGCTA	TAACTTCTTC	CTGTTGGTCT	CCCCCGGCCG	120
CTGTGGGGCC	GTCAAAACCC	GNCTGGGCCG	NTGAGAATCC	TGTGCCAGG	GCCAAGAAGT	180
TCTNACTTTG	TGCGCACCAA	GGTGGACGAG	GACCTGGCGG	CCACGGGCAC	CTNGTGGNCC	240
GTGGGGTTN	NAAAAAGGCC	G				261

(2) INFORMATION FOR SEQ ID NO:1600:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

CCCGGCTGCA	GANTCGAGAG	CCGGACACCG	AGTCGAGNTT	TTNAGGACAT	GTTANTAGAC	60
ATCAAGGCTT	CACCGNTTTC	TGCACCAGGC	CGTGGTGTAT	TNACGCAGAA	TGTNACGTGG	120
GATCCTGAGT	CTTCCGAATG	GGCGGACGAA	AGACATGGTC	ATCATGCCGG	TACTGGTGAG	180
GGACGTCGGC	CAAGTCTCAG	GGGAGGGAAG	TCGAATGGAG	GGGGGAGTGT	GGAGTCAGTG	240
CAGTGGAGTA	CATGTNTTCA	GGACAGGGAC	GCAGGGATCT	GCAGTGGTGG	GCAGCAGAGC	300
GAGAGGTGTG	TGGTGCATGG	CGAGGCAGAA	GTGGATTCTG	AAGCAGAGTC	GAGCAGGAGT	360
CCGGGTCACT	GTACATGNCG	CCATGGCGAG	ACGTGCGTGC	CACAAGCCCA	GCTGCCNTAG	420

CTCTCGTGGG GTGTGAAGGG GANTGGCGCA GGGTGTNCTG AGGCAGAAGC TGGTCTGAAG	480
GACCTGTCTG AGGCACAATT CGGTGTGTCT CAAGAGTCTC AAGGTNGNTT NGTT	534

(2) INFORMATION FOR SEQ ID NO:1601:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

GGCACGAGCT CACCATNTCC ATNAACGTGN TCTACAACTA CCTGGAGGCC AACCCCAAGG	60
TGCCCTGGGA CGATCTCCGN TACCTTTTG GTGAAATNAT GTATGGNGGC CACATCACAG	120
ATGACTGGGA ACCGTCGGCT GTGCAGGACC TACCTGGNTG AATACANCCG GACGGNGATG	180
CTGGAGGGAG ACGTNCTGNT GGCCCCCGGC TTTGCAAAT	219

(2) INFORMATION FOR SEQ ID NO:1602:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:

ACCAAAGTCC AGCACANACC CTCGGGNCTC ATCANGGCCA GGTAAGCTGA TCCACCTTGN	60
GATCAAGCCG GCCATCCGGA ACCAG	85

(2) INFORMATION FOR SEQ ID NO:1603:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

GGCAGAGGTG TGGCGAGGTG GTCCGGGACC ACATCATCAG GGCCCTGGGN CAGGCCTTCC	60
ACCCCTNCTN CTTCACGTGT GTAACCTGCG CNNGGTGCAT TGGGGATGAG AGCTTTGCC	120
TGGGCAGCCA GAACGAAGGT GTACTGCCTG GACGACTTCT ACAGGNTATT CGCCNCCGTT	180
TGCAGCATCT GTGAAAATC CCATGCATCC CTCGGGGATG GGGAAAGATG CCTTCAAAAT	240

CGGAATGCAT GGGAAAGAAA CTTNCATGNA AAATTGCTNA CAGGTGTGAA GGNCTGCAAG	300
ATCCTCCNGT CTGT	314

(2) INFORMATION FOR SEQ ID NO:1604:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

GGCACGAGGG TACNCCATTG CGGCCATGTN TGTNATGCGG CCGGAGCAGA TCATGAAAGT	60
CCATCATCCC AGTGGTCATG GCTGGNATCA GANNCCATCT ACGGCCTGGT GGTGGCAGTC	120
CTCATCGNA ACTACNCTGA ATGAACGTAC ATCAGCNTCT ACAAGAGCTT CCTCCAGCTG	180
GGNGCCGGCC TGAAGCGTGG GCCTGAAGCG GCCTGGCAGC CGGCTTGTC ATCGGCATNG	240
TGGGGGAACG CTNGCGTGC GGNNGCACCNC CAG	273

(2) INFORMATION FOR SEQ ID NO:1605:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

GGCACGAGAG GTCATCGGGA CCCTGGAGGA GGTCCACATG CCACAGAAATG GGAATCAACC	60
ACNCTGGCAT CACTGCCCTG GCCCAGGCTT TCGCTGTCAA CCCCCCTGCTG CGGGTCATCA	120
ACCTGAATGA CAACACCTTC ACTGAGAAGG GCGCCGTGGC CATGGCCGAG AACCTTGNA	180
GACCTTGCGG CAGGTGGAGG TGATTAATT TGGGGACTGC CTGGTTGCGC TCCAAGGGTG	240
CAGTTGCCAT TGCAGATGCC ATCCGCGGCG GCCTTGCCCA AGTTAAAGGA GCTGAACCTG	300
TCATTTCTGT GAAATCAAGA GGGTTGNTGC CCTGGNTGTT TGTTGAGGCC ATGGCAGACA	360
AAGTTNAGTT GGAGAAGTTG GACNTGAATT GGCAACANCC T	401

(2) INFORMATION FOR SEQ ID NO:1606:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

GGCACGAGGT TTGATGAGGG CCGGCTGACA GATGGAAAAG GGAAGACCAT TGATTGCAAG	60
GACGCCATCT TCATCATGAC CTCCAATGTG GCCAGCGACG AGATCGCACA GCACCGCGCTG	120
CAGCTGTAGG CAGGAAGCTT TGGAGATGAG CCGTAACCGT ATTGGCCGAA AACCTGNGGG	180
GATGTCCAGA TAAGTGACAA GATCACCATC TCAAAGAACT TCAAGGNGAA TNTGATTGC	240
CCTATCCTGG AAAGCTTCAC TTCCGGAAGG GATGAGTTT TNGGGACGGG TNCAATGGAG	300
GTCGTCTNAC TTT	313

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

AACAACAGGC TGAACAAACCG CGCCAGTTTC AAGGGCTGCA CGGCCTTGCA CTATGCTGTT	60
CTTGCTGATG ACTACCGCAC TGTCAAGGAG CTGCTTGATG GAGGAGCCAA CCCCTGAG	120
AGGAATGAAN GNGGACACAC ACCCTTGGAT TATGCCGAG AAAGGGGNAA GTGATGAAGC	180
TTCTGAGGAC TTCTNAAGCC AAGTACCAAG AGAACGAGCG GAAGNTGNAG GCTGAGGAGC	240
GGCGCCGCTT CCCCTGGAG CAGCGACTTA AAGGNGCACA TCATTNGGCC AGGAGAGCGC	300
CATCGNCACA GTGGGTGCTT GCGNTTCCGG AGTAAGNGAG AATGGCT	347

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

GGCACGAGAG AAGATGCTGC GTATCCAGAA GGAGCACCGC GNCNAACTTC CCACGCTCCA	60
AGCACCTGAC AGGCGAGTGC AAGGACCTCA TCTACCACAT GCTGCAGCCN GACGTCAACC	120
GGCGGCTCCA CATCGACGAG ATCCTCAGCC ACTGCTGGNA TGCAGCCAA GGCACGGGGA	180
TCTCCCTCTG TGGCCATCAA CAAGGAGGGG GAGAGTTCCC GGGGAATGGA ACCCTTGTGG	240

ACCCCGAAC CTGGCTCTGA CAAGAAAGTCT GCCACCAAGC TGGAGCCTGA GGGAGAGGCA	300
CAGNNCCAGG CACAGTCTNA GNACAAAACC CGAGGGGACA GCAATGCAA TN	352

(2) INFORMATION FOR SEQ ID NO:1609:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

GGCACGAGCC AGGTGCCGGT TGCTGCCAA GGGGTGCAGG GACAGATGAG GGAGGGCACT	60
GCCCTTCAGGN ACGACATATG GGGGCCACCA TCGCTTGTT GGTGGGGACA GGGTCCCCCT	120
TTTTTTTTTT TTNAANATGG GNTNTT	146

(2) INFORMATION FOR SEQ ID NO:1610:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

GGCAGAGCTT TGATTAACCTT CCGGGAGTTT GTCTCTGGC TAAGTGCTGC ATGCCATGGG	60
GACCTCACAG AGAACGCTCAA ACTCCTGTAC AAAATGCACG TCTTGCCTGA GCCATCCTCT	120
GATCAAGATG AACCAAGATTG TGCTTTGAA AGCAACTCAG TACTTCTTG AAGATATTAC	180
CCCAGAATGT ACACATGTTG TTGGNATTGG ATAGCAGAAG CAAACAGGGT GCAGATGATG	240
GCTGTGTTAC GGTGAGCCTA AAGCCAGACA AAGGGAAGAG AGCAATTCCC ANGAAANTCG	300
TAATTATTTG NGACTGTGGA CTCCAGAAAA TAATCTAAGT CAAGNTGCAA AGGTTTACCC	360
AANTAAATTC AGGGCATTTC ATTGNACCTT GTTAAGACAT GGTATANCNG GTTCAGCGA	419

(2) INFORMATION FOR SEQ ID NO:1611:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

GGCANGAGGT GACCTCCGTG GGCTGGTCTG AGCGGGGGAA CCTNGTGGCG GTGGGCACAC	60
ACAAGGGCTT CGTGCAGATC TGGGACGCAN CCGCAGGNAA GAAGCTGTCC ATGTTGGAGG	120
GCCACACGGC AGCGTCGGGG CGCTGGCCTG GGAATGCTGA GCAGCTNTCG TCCGGGAAGC	180
CGCGACCGCA TGATCCTGCA NAGGGACATC CGNACCCGN CACTGCAGTC GGAGCGGCCG	240
CTTCANGGCC ACCGNCAGGA TGTGTGCGGG CTCAAGTGGT	280

(2) INFORMATION FOR SEQ ID NO:1612:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

NTGGTTNCCC CGGGCTGCAG TANTGGGCAG AGTGAAGGT GCCTGNGGNG CAGCAGCAC	60
TGCTTTCCG TGGCCAGCTC CTGGAGGATG ACAAGCACCT CTNTGACTAC TGCATTGGC	120
CCAATGCCTC TATCAATGTC ATCATGCAGC CCTTGGNGAA GATGGCGCTA AAGGAGGCC	180
ACCAGCCGCA GACCCAGCCC CTGTGGCACC AGCTGGACT GGTCTAGCT AAACACTTG	240
AACCACAGGA TGCCAAGGCC GTGCTGCAGC TGCTAAGGCA GGAGCACGAG GAGCGCCTGC	300
AGAAGNTTAA GCCTGGAGCA CCTGGAGCAG CTGGNCCAG TACCTNCTGG CAGAGGAGCC	360
TCACGTGGGA GCCCANTTNG	380

(2) INFORMATION FOR SEQ ID NO:1613:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

GGCACGAGGG GTTCTGAAA GCGGGNCTGT CTGGGGAGTT TNGACCCCGG CACATGGTCA	60
GCTCCATCGT GGGGCACCTG GAAATTCCAG GNTCCCTCAG CAGAGGCCA ACCAGAAGAA	120
GTACTTTNTG GGGGAGGGAGG CCCTGTACAA GCAGGAGGCC CTGCAGCTGC ACTCCCTTT	180
CGAGCGTGGC CTGATCACAG GGTGGATGA CGTGGAGAGA CTNTGGAAGC ACCTNTTTGA	240
GTGGGAGCTA AGGCGTGAAN CCAGCGACCA GNCCCTGNTT TGCAACGGAG CCCTCCCTGG	300
G	301

(2) INFORMATION FOR SEQ ID NO:1614:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

GGCACGAGCG GCGGCTGCAC GCTGTGGCCC GGCNCCAGCG CTGTAGGCCT GTGGCAAGAC	60
CTTCCGCTAC CGCTCCAACC TGCTGGAGCA CCAGGAACTG CACCTGGCG AGCGCGCCTA	120
CCGCTGTGAA GCACTGCGGG CAAGGGCTTC TTCTACCTGA GCTCCGTGCT GCGCCACCAG	180
CGCGCCCATG AAGCCGCCGN GGNCCGAGCT NNCGNTGCC C	221

(2) INFORMATION FOR SEQ ID NO:1615:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

GGCACGAGGG AAACCTGCAC GACAACCTGT NGGACCTNCG TGCCCAGGTG GCAGCCAACC	60
AGAAGGGCAT CCAGCTGGTG GGGGAGCTCA TTGGGCAGTA CGGCCTGGAA CGTGGTGCAG	120
GCCTGACATG GGCCATATTG AGGNAAACGC TGCAGCTGGA CCGTGCNAG ACATGTTGCG	180
TGCCTTTGT AACCTTCCCG GCAGGNNCCG NGG	213

(2) INFORMATION FOR SEQ ID NO:1616:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

GGCACGAGGT CAATCTCACG GGGTTGAAGA AGCGGGACCG CTGCGNAAGG CCTGGCCTT	60
GCGGAGGAGG TGATGGATGA CATCCTGGAC TCCGCGGACC AACCCCTGAC GGGCCGAAAG	120
TGGTGGATGG GCGCGGAGGA ACTCTGGCAG ACGCTGGCCT GCTGTATGGA GGTGGCGAAC	180
GCTGTGGCG CCTCCAACCC TGAGCGCCTA TGTCTCCCAC CTCCCCGTCC ATCAGGAGNC	240

TTCTTGCAAC GGCCTGCAGC ATTATGCTGT NCTNGGCCGC GGACANTGGG GGCGCCGNCT	300
CCGTTCAACC TGG	313

(2) INFORMATION FOR SEQ ID NO:1617:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

GGCACGAGGN AAGAGTGTAA GCCCTGCCTG AAACAGACCT GCATGNAGTN CTACG	55
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(2) INFORMATION FOR SEQ ID NO:1618:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

AACGGCCTNC ACNGACGGNA TCGGNTTNGC CATGCCCGG NGTTTGGCCC AGGACAGGGC	60
CCACGTGGTC GTNAGCAGCC GGAAGCAGCA GAATNTGGAC CAGGCGGTGG CCACGCTGCA	120
GGGGGAGGGGG CTGAGCGTGAC ACGGGCACTG TTTCATNNNTG GGGAAAGGCGG AGGNACCGGG	180
AAGCGGCTNG TGGCCATGGC TGTGAAAGTT TCATGGAGGT ATCGATATCC TAGTCTCCAA	240
TGCTGCTGTG CAACCCTTT TTTGGAAGNC TAATGGGATG TNNACCGNAG GAGGTNTTGG	300
GGACAAGATT TTTGGGACAT T	321

(2) INFORMATION FOR SEQ ID NO:1619:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

AGGTACACAG ACACACGTTA TTACATATGT GCACATGCAT GCATATGCAA ATATGCACAG	60
TACACAGACT GCACAGAGCT CCACAGACAT ACACATTGCAC CTTCGGGTTT AAGCCCTGAG	120
CAAATTGACA TCCC GTGTCT TGTTCTCCAC AGTGTCTCCA GTGCCAAGCA TGGGGCTGGG	180

TGTGGTAAAT GTTTNTNGAG TCAGTGAATG CATGGNTGGC TCGAACCGTG TCTTGACTCA	240
GCAACACCGG GNCCAGTGGG GTCTGGAGGT GAGGTCAGG AGACAGTCAG CCCTCTGCTT	300
TTGCTGGAGA CTGGGAACA CCTTTAGGGA CATTTCAGAG GAAGGACAGT TGCAGGNACA	360
ACTTTGGTCT AGCAAATCAC AAGNCTGGGT TGAGGNCTCA GGATTCCTT GTACCGTGTT	420
NCTTTCCAA TTTGCCAGA GNTAG	445

(2) INFORMATION FOR SEQ ID NO:1620:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

GGCACGAGCC AAGGGTGAGC GCCATGGCTC AGCAGCCGAA CGACTTCTGG CAGCTCAGAA	60
CCCGCTCTCC CAGGCTGATC GCCCTCATCA GCTGTTGCA GATGCACCTC CTCCACCCCTC	120
TGCTCCCAAT CCTGTGGTAT CATCATTGGG GTCTGGGCTT CCTCCACCAG GCATGCCTCC	180
TCCTGGCTCC TTCCCACCCC CAGTGCCACC TNCTGGAGCC CTCCCCACCTG GGNATACCCN	240
CAGCCATGNC CCCAACAACT ATGGCTNCTG GGGCTGNAGG ACATGGCCCC CCATNGGCAG	300
GNACCCCCAGG GTAGGACATT CTGGTNAATG GGCATTNANA ANTTNAACNA TTTNCAACGG	360
GTGGGATNNC CCCNTTCAGG GGTNTTTAA ATGGAAATTG GAAAAAAATG GGGCTTTAAG	420
GTTTGGGGA ATNCCAAGGT TGGGACCCCCA GTTTGGGGG GNNAATNAAT GGTC	474

(2) INFORMATION FOR SEQ ID NO:1621:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

AAGCTGGCT TACAGGATGG AAAAGAATAT TTATTCCAGG CCAAGGATGA GGCAGAGATG	60
AGCTCGTGGC TACGGGTGGT GAATGCAGCC ATTGCCACAG CGTCTTCTGC CTCTGGAGAG	120
CCTGAAGAGC CGGTGGTGGC CAGCACNCGN NGGGTCATGA CCCGGGNCAT GACCATGCCN	180
NCAGTGTAC CCGTCGGGGC TGAGGGGCCT GTTGTGCTCC GCAGCAAAGA CGGCAGAGAA	240
CGAGAGCGAG AAAACGCTT CAGCTTCTT TAAGGAAGAA CAATAGTTNG GGGCAAGTTC	300

CAGGNCAATT CCTTCCTTNN GTTCAGGAAA NTT 333

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

GCTGCGCTCC TCCGAACCTG CCTGCACGCA GCCTGGGTTC CAGGATCTGG AGGTCGTGCC	60
CCCAAAACCA CAGCCGAGGC CTACCACGNG GGCATGTGCA GCCGGGAACG GTCGGGTTAC	120
AGCGAACGCCT TCATGCAGGG CCAGTTGCGG GTGGTGGTGG CCACGGTGGC CTTTNGGATG	180
GGGCTGGACC GGTCAGATGT GCGGGGTGTN CTGCATCTGG GGGTTGCCCC CAAGNTTCGA	240
GAGCTACGTN CANGCCGTGG CGGTGACCG	269

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

CATGCCCTCC CCGGNTATGA GGCGGGCCGT GCTGGAGACC AAACAGAGCC TTGAGGCTGC	60
GGGGCACACG TGGTTCCCTT CTTGCCAACG AACATACCCC ATGCTCTGGA GACCCTGTCA	120
ACAGTGGGCT CTTCAGTGAA TGGTGGCCAC ACTTGCCTAC AGAACTTCAA AGGTGATTTC	180
GTGGACCCCT GCCTGGGGGN ACCTGGTCTC AATTCTGNAA GCTTCCCCAA GGCTTAAAGG	240
TATGCTGGCC TTCCTGGTTG AAGCTNCTGC TGCCANGGCT GTCCAGTTN NCTCAGCAAC	300
AT	302

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

GGCANAGGGA GGCTCAGTCT GTAAGTGAAG CAGGGCGNTC TCCCCGATAT CTGCATCGGA	60
CGGCCCTCT AGTGGAAACC GAGAGTNAAG CGGCCTGGAT TCCGCGATGA ACAGATTCTT	120
TTGTGTCGCT GGGAACACTG GAGGGTTGTC GTTAATGTCC TTCACCTCCA CGTCCACATG	180
GGAAAACCTG CAGCGGCTT TCCACGATCA CCTCCAGGNG GATGCTGCAC TCCGCGCTCC	240
GCCCGCACAG CTCCTCGCGG TCGATCCGAG AATTACACAA CAAAATGCCA TTCTGGCAGA	300
TTTACCTCCA GAAGGTCCCC GGGGNCTTTT GGGATTCCAA TTGGAACAGN GNNGGGCANC	360
A	361

(2) INFORMATION FOR SEQ ID NO:1625:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

GGCACGAGGA AGGAACATCAC TCTGGGGGCC TCACAGGCCA CCACGGACGA GGTAGCTGCC	60
TTCTTCGTGG CTGANCTGGG TGCCATAGTG AGGAAGCACT TTTNCTTCT NAAGTGCCTG	120
CCACGAGTCC GGCCCTTNA TGCTGTCAAG TGCAACAGCA GCCCAGGTGT GCTGAAGGTT	180
CTGGCCCAGC TGGGGCTGGG CTTAGCTGT GCCAACAAAGA TTGCTTCCGT NATCAACTCA	240
GCCTTGGACC TGTACTTCCC ANAAGGGCTG TGGGGCTGGG ACATCTTGG CTTGAGCTTG	300
GGCGGGTTAC TNACGTGNAC CTNGGCCTNT NACTGGTGGG CAGTCAGCA TTCATTGCCA	360
AAGAAAGGGA GGTTCTTGNT TAGACCAGGN CTNGGNAGGG GAGGAGGAAA ATGGTTCCAN	420
CTTCCAAAGA CCATCGTTGT ACCACCTTGG ATGGAGGGC GTGTATTNGG ATCTTCAAA	480
CTTCNAGTCC CTGGT	495

(2) INFORMATION FOR SEQ ID NO:1626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

GGCACGAGGC CAGCAGTGGC TGGAAGCCAC TGGCGTACTC TGACACCGAC GAATTTNACC	60
CAGTTGCAGG AGGCACAATG AGCCAGCATT TACCTTGTT CGCCGCACAG CCCGGCATCT	120

GGATGGCAGA AAAACTGTCA GAATTACCCCT CCGCCTGGAG CGTGGGCAT TACGTTGAGT	180
TAACCGGAGA GGTTGATTGCG CCATTACTGG CCCGCGCGGT GGTTGCCGGA CTAGCGCAAC	240
AGATACGCTG CGGATGCGTT TTAACCGAAG GATTAACGGC GAAGTCTTGG CAGTGGGTGCG	300
ATGATGCGCT GNACGTTNCG AACTNGCCAG AAATTNATCG ACCTACGGAA CCAACATTTG	360
ATCCGCACGG TACTN	375

(2) INFORMATION FOR SEQ ID NO:1627:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

GGCACGAGAA AGAGATGACC CCAGGGAACA TCCTGACCAAG GCCGGNTTCC TGGATGGCTG	60
TNTTCAATGC CATGCCAACC ATCTGCTTCG GAATTTNAGT GCCACGTCAG CAGTGTGCC	120
GTNTTCAACA GCATGGCAGC AGCCTGAAGT GAAGACCTGG GGTGGTAGTG GTGACAGCTG	180
CCATGGTCAT AGCCCTCGCT GTCTACATGG GGTGCAGGCA TCTTGNGGT TCCTGACCTT	240
TGGNAGCTGC TGTGGGTCTT GACGTGGCTC CTGGTGCTAT CCCTCGGAGG TACATGGNCG	300
TGGCCGTTGC CCGAGNCTTT CAGCATCCTG AGCGTNGCTC ANTCNT	347

(2) INFORMATION FOR SEQ ID NO:1628:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

GGCACGAGGC GCCGGTAAAA TCGACCACAA AGGCATAGT ACCGTCAGGC TGGCGAATCA	60
GGTTCGACTG CTTCACATCC CCCGTTGAAC GACGCGTTN TTGCACCCAT GCGTTATCTG	120
GCGCATGCAG TTTGTTTCA TCACGGCTGA AGGTGATGGT GTATTTAAAG TTCATCTCTT	180
TACCCGGCTC CGGCAGCTGA TCCGGCGTCC AGTAAGCGAC GATGTTATCG TTGGTTTCAT	240
CGTTGGTTGG AATTTCCACC AGCTCAACGC TGCCTTACC CCACCTCCCT TTCGGAGTCA	300
CCCATGCGGT TGGGACGGAG NATCGTAAAC GATCATCGAG ATCTTTCAA GCGGGAGAAA	360
ATCACGACCC GNGTTGCAAC AGACCCAAAG NCTTGNGGGG TTTTNCCAT GGGAGNAAGT	420

TGTTT 425

(2) INFORMATION FOR SEQ ID NO:1629:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:

GGCACGAGCT TTGCTCCCAC CCCACCCCCA ACCCACAAACC CCTGCCTCTG CCCATCAGCC	60
TGGCCTTGAT GAGGAGCGGG AAGGCCTCCT GCACCCCTGGA GACCGTGTGG GAAGACAAGC	120
ACAAGTATGA GGAGGCCGAG CGGCGCTTCT ACGAACACGA GGCCACACAG GCGGCCGCCT	180
CCGCCCAGCA GCTGCCAGCC GAGGGGCCAG CCATGAATGG GCCCGGCCAG GACGACCCTN	240
AGGACGCTGA TGAGGCGGAA GCCCCTNACG GCGGCAGCAG GCGTNGATCC CAGGAAGAGC	300
CAGGACAGCA GGAAGCCCCT NCAGAAAAAG NAGGAAGCGT TCCCCCAAGA GCGGGTTNGG	360
CCCCGNGGGA CCTGGCCTTN TTGGCTTTT GGCGAA	397

(2) INFORMATION FOR SEQ ID NO:1630:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

GGCACGAGGC GGCTGTCGCT NAGCCCCTG CGGGGCGGGG AGGCCGGGCC ANACGCCTCA	60
CCCACAGTNA CCACACCCAC GGTGACCACG CCCTCACTAC CCGCAGAGGT GGGCTTCCCG	120
CACTCGACCG AGGTGGACGA GTCCCTGTNG GTNTCCCTTN AGCAGGTNNNT GCCGCCATCC	180
GCCCCCACCA GTAAAGCTGG GCTGAGCCTC CNGCTGCNTG GCCCCCGGGC GCGGCNTCG	240
GTTTCCCCAC ACGATGTGGA CCTNTGCCTG GTGTNACCCT GTNAATTNA AGCATCGCAA	300
GGTGGTGCCA ATGGCACGNC AACCTGNTTT CCCCCGGNAG CTTCGNAATG AANAGCANTN	360
CCCGGTTCAC AGGAACGGGG CAGGTGGGCT GGGGGCCGAG NAGACGCCAC CCACATTGG	420
TTCAGCAATT CCCTGCCAA CCTGTTGAN TTGGATCCNG TTGCCCTNGN CCCGGTTGCG	480
GNANANTTAG ACGGAGACAA A	501

(2) INFORMATION FOR SEQ ID NO:1631:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

GGGGCAAGAG TATNCCCTCA TGGGNCAAA TTGGCACCCC TTTGGGTTGG NCTTNCAAAG	60
GGTTTCCAGG GGCCCAGGGT CCCTATTTAC TNTGGGTGTG GGGAGCANAC AGAGGCTTG	120
GGCAAGGGGN CCATCGTGGG AGGGCCCCTT TAACCGGGGC CTNCTTTTT ATTNTTNGGG	180
TTCAAAANTT GGGGGGGGGC TAATTCCGG GGGT	214

(2) INFORMATION FOR SEQ ID NO:1632:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

GGCAGAGNCA TACCAAGAAG ACGGTGATGA TCAAAACCAT CGAGAACACG GGATGGGGAG	60
GTCGTNAGTN AAGGCCACAC AGCAGCAGCA TGAAGTCTCC TAAAGACAGA AACCCCTCTGC	120
NACCAGAAC CGTTCCCTCAC CCCTGTTCCCT CACTGGCTCC CTGAAGCCAG CNTTCTTCCA	180
TCCCAGGGAC ACCACACCCA GCCTTCANTC CTCCCCTNAN AGCCTCTGAA CCCCTCCTNA	240
TTGGGCCATC CCTNGTGGTC CCCAACAGCG ACATAGCCA TCCTTGNTTG GTTCACGGGG	300
CATGGTCCCG GNCACCTTG NGGGNNCCTA GTTGTAAAGC TTTTGGGTGT TTGGGA	356

(2) INFORMATION FOR SEQ ID NO:1633:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

GGCAGAGGGA ACAACTCCAT GTTTTTNTAA AGGCCTAGAG AACATATATC CAGTGCCTTT	60
CCTTTTGCC TTTGTATTCA TCATTTGGC AAATTACTGG AAGATGACGG TTCTGGCAA	120
AAGGCTGGTT TTNTTTTGG GTCACATTTT CTTGCTTCTC TGCGTTAGAA ATCTTGGATT	180

AGATGATGGA CATGGTGAAG ATCTCAGCAA CCTCATTACAC TAGAAGATCA TGTGGATTGG	240
GANTCATACA ATGGGGAAC AAATGGAAAA GAGTACTTT GNAAATAGTG GCTGGNGAC	300
CACTGTGGAC CACAGANTGT TCAAGACACG TGCTGCCNT AACTGTTAC TN	352

(2) INFORMATION FOR SEQ ID NO:1634:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

GGCACGAGCT GGCCCCGTGT TCAAGGGCGT CTGTAAGCAG TTCTCACGCT CACAGGGCCA	60
TGGCTTCATC ACCCCCCGAGA ACGGGTCCGA GGACATCTTC GTACATGTTT NTGACATCGA	120
GGGGGAGTAC GTGCCANTGG AGGGCGACGA GGTGACCTAC AAGATGTGCC CTATCCCTCC	180
CAAGAACCAAG AAGTTCCAGG CCGTGGAGGT GGTGCTCANT CAGCTGGCCC CCCACACTCC	240
CCACGNAGAC GTGGTTCTGG CCAGGTCGTG GGCTCCTAGG CTGAGTGGTT CACAGGCCAG	300
CTGGCCGNGG GTTGGGNGAG CCACACAGGG TGAACGGNCA GCAGCCGGCT CCATGCCCA	360
CTGCCTNGNT GATGAGT	377

(2) INFORMATION FOR SEQ ID NO:1635:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

GGCACGAGGN AGAATCTTGC CTAGAGCTTG CGGAGTCCAG CNAGGCCCT NCTGAAGGGC	60
CCCAAACAC CGGCCACTTC TCCCCCGTCC ATCTAACCAAG CTGGGCCCT GCGCCCACCT	120
GGCCTCCACG TTCCCTCTCC TCTAACCCAC ACCCCTGGCC ATGGCTAACT ACTATAAAAGT	180
GCTGGGNGTG CAGGCCAGCG CTTCCCCGGA GGACATCAAG AAAGCCTACC GCAAGCTGGC	240
CCTTCGTTGG CACCCCGACA AGAACCCCTGA CAATAAGGAG GAGGCGGAGG AAGAAGTTCA	300
AGCTTGGTGT TTTGAGGCCT ATTAAGGTTT CTGTTNTGGA CTTCCAAGGA AACGNTTCCT	360
TGTTATGACC GTGTTGGTT GTAAACAGTT GGGGGGTTTG TTTGGCGGGG GCCAGGAANG	420
GTNTTACCAA AGGCCCTTTT GGGAAACGGG TTANAANTTT CGTAAACCTT TNNGGG	476

(2) INFORMATION FOR SEQ ID NO:1636:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

TGCCTACTCT AAGCGCCTCA AGTTCAATGT GGCTGTNAAG ATCATCGACC GCAAGAAAAC	60
ACCTACTGAC TTTNTGGAGA GATTCCCTCC TCGGGAGATG GACATCCTGG CAACTNTCAA	120
CCACGGCTCC ATCATCAAGA CTTACGAGAA TCTTGAGAA CCTCTGAACG GACGGATCTA	180
CATCATCATG GAGCTTGGCG TCCAGGGCGA CCTCCTCGAG TTCATCAAGT GCCAGGGAAG	240
CCCTGCATGA GGACGTGGCA CGCAAGATGT TCCGACAGCT CTCCTCCGNC GTTCAAGTAC	300
TGNACGACC TGGGACATTG TTCACCGGGG ACCTTCAAGT TGCGNAGAAC CTTTTCTTG	360
GACAAGGANT TTCAACNTCA AGTTGTCTGA CTTTGGTTT TTCCAGGGGT TGCCTNGGGG	420
ACAGAATTGG GGGTNT	436

(2) INFORMATION FOR SEQ ID NO:1637:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

CGCACTGTCA AGGAGCTGCT TGATGGAGGA GCCAACCCCC TGCAGAGGAA TGAAATGTGA	60
CACACACCCCT TGGATTATNC CCGANAAGGG GAAGTNATGA AGCTTCTAAG GACTTCTGAA	120
GCCAAGTACC AAGAGAAGCA GCGGAAGTTN GAGGCTGAGG AGCGGCGCCG CTTCCCCCTG	180
GAGCAGCGAC TAAAGGAGCA CATCATTGGC CAGGAGAGCG CCATGCCAC ANTGGGTGCT	240
GCGATCCGGA GGAAGGAGAA TGGCTGGTAC GATGGAAGGA ACACCCCTCTG GTCTTCCTC	300
TTTCTTGGG GATTCAATTCT GGAATTAGGG AAAAACAGA GCTGGGCCAA GCCAGACAGC	360
CAATTNTTTN GCACAAGGNT GCTAAAAAG GGNTTNATT CAGGTTGG	408

(2) INFORMATION FOR SEQ ID NO:1638:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 458 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

ATAATGTNAC GTCAGCCGTA GAAGGCATCA ACAGAATGAC CAGAGCTCTC ATGGACTCGC	60
TTGGGCCTGA GTGGCGCCTG AAGCTGCCCT CAATCCCCTT GGTGCCTGTT TCAGCTCAGA	120
AGAGGTGGAA TTCCTTGCT TCGGAGAACC ACAAAAGAGAT GGCTAAAAGC AAATCAAAG	180
AAACCACAGC TACAAAGAAC AGAGTGCCTT CTGCTGGGA TGTGGAGAAA GCCAGAGTTC	240
TGAAGGAAGG AAGGCAATGA GCTTGTAAAG AAGGGAAACC ATAAGAAAGC TATTGAGGAA	300
GTACAGTGGA AAGCCTCTTG TGTAGTTAAC CTGGGATTCT TGCCACGTTA CAGGCAACAG	360
AGGCACTTG TTATTTGGT CCCTGAAGGC AGTAACACAG AAGNCAGTGA NGGACTGCAC	420
ANAGGCCCTG AAGGTNGGNT TGGAAAGACC TTTAAGGG	458

(2) INFORMATION FOR SEQ ID NO:1639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

CCCGAGGNAT TATTCGATAA AGATAAGCTT ACATTATGAA GAGCAGCATA TTACAGCCGT	60
ATGGTCTACT TGCNCAGTAA AATTTGAAGA GCATTGGAAG CCTGTTGATG TAGAGGTCGA	120
GTTTAGATGC AAGTTCCAAG GAGCGAAAGG TGGATGGGTA GGTTATATAG GGATATAGCA	180
CAGAGATATA TAGCAAAGAG ATACTTTGA GCCAATGTTT GTGGAAGCGG TATTCGCAAT	240
ATTTTAAGTA GCTCGTTACA GTCCGGTGCG TTTTTGGTTT TTTGNAATG CCNNNTTCCA	300
AAGCCTTTG GGTTTCCAA AGGNTTTNG GT	332

(2) INFORMATION FOR SEQ ID NO:1640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

CAACCCTTGG ACGTNAGCNC TGAAGGCTAC AACANCTGGN TCTTCATGTC CACCCACTTC	60
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TGGAATGAAA ACCCACAGGG CGTGTGGTAC CCTGGGCCTA GAGAACAAAGG GCTTACTATT	120
TNAACACGGG GACGTTGTAC CGCTAACACG CTGCTGCTCC TATGGGAACG GCCGAGGACA	180
TGANAGGCC GGCCCTTACAG GCCCCCCAGG TGAACCAGCA NCGGTNNNTT GCAACGGGAC	240
ACAGAGGGGC TTNTCCCAAGG	260

(2) INFORMATION FOR SEQ ID NO:1641:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

TCCTCACCAA TNTAACCNNTT NTCCANTTGC TGCAACACCG TGCCCCGGTA ACCAGAGCAC	60
CGCCCCCACC TGAGCCCTAA GGNTGAAGTA GAGCCCCAGC NACAACCAGA GCCCACACCA	120
NTTAAGGGAG GAAATAAACGC CACCACCGNC ACCACTGCTT CCTNACCCCG NTAACTCCTC	180
CTCCTAAGAT TGGTGTCTGT GAGCCCCGGGA AGCTGACTGT GGGCATCANT GGTTTGAA	240
CGCATCGNTC GCCTGGTTCC TGNGAGGTTG CNTGGNGAA GGGTGTAAAG GTGGTGGTTG	300
TGAAATGATT CCTTCATTG GACCCGGATT ACNGGTGTAC NGTTAAGTT TGGTTTCCAC	360
CCAGGGCCGT TACAAGGGAG TTTGGGATT CAGGATTGGN CAATTGGTN TGGGCAACCT	420
GGGTTTTTTT TTTCCCNNTGN AANGG	445

(2) INFORMATION FOR SEQ ID NO:1642:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

GGCAGAGTGT AAAACCAGAA AATATANTAA TAAAGGATGT CCTGAAATTA GGGGACTTTG	60
GCTCCTGCCG GAGTGTCTAT TCCAAGCAGC CGTACACGGG AATACATCTC CACCCGCTGG	120
TACCGGGCCC CGAGTGTCTC CTCACTGAAT GGGTTCTACA CGTACAAGAT GGACCTGTGG	180
AGCGCCGGCT GTGTGTTCTA CGAGATCGCC AGTNTGCAGC CCCTCTTCC TGGAGTNAAA	240
TGAAACTGGA CCAAATCTGC AAAAATCCAC GATGTNCATC GGCACACCCG NTTCAGAAGA	300
TCCTGCACCA AGTTCCAAAC AGTTCGAGGA GCTATGGAAT TTTGGATTT TCCTTTGAA	360

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

GGCACGAGCC AGTTTCTGT TGCCCTTACC AATTCTGGAG CTGTTTATAC CTGGGGCAAA	60
GGCGATTATC ACAGGTTGGG CCATGGATCA GATGACCATG TTCGAAGGCC TCGGCAGGTC	120
CAAGGGTTGC AGGGGAAGAA AGTNATCGCC ATCGCCAATG GCTCCCTGCA CTGTGTGTGN	180
TGCACAGAGG ATGGTGNGGT TTATACATGG GGCGACAATG AATGAGGGAC AANTGGGAGG	240
ACGGAACCAC CATTGCCATA CAGAAGGCCT CGGTTGGTAG CTGCCCTTNC AGGGTNAAGA	300
AAGGTNAAAC CGTGTGGNCC TGTGGGTTCA GCACATNACC CTTCG	345

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

ANGCAACGGA CAGGCCCTG GAACGAAAGG CATNCCGNG CCAAGGTGGC TCCCCTAGAG	60
GTNACAAGTC TTAGGCATTN CGGTCGGGAA ACGCTACCTG CCTGGAGNTC ACT	113

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

CCCNNGGGAT CCCCCGGCCC TGCAGGANTT CGGCANAGTT CTGGTTGGTA CAAACCCACG	60
GTTTTTGAGG CACCACTGTT TAATGCTAGG NTTGAAAGA CCTNGCTNGC ATAATGGNCT	120
TAAAATTGGG CCTT	134

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

GGAAGCCCCA GCGCATTNCT TTTCNCTCTG CTACTCTGGT TCCCAGATAT AACTGGNGAA	60
ATAGTGATGA CGCATTNGCA GTCACCCTGT CTGTTCGCT AGGTGAAAGA GTCACCCCTCT	120
CCTGCGGGGC CAGTGAAGAG TATTAGCACT AACTTAGCCT GGTACCAGCA GGAAACCTGG	180
CCAGGCTCCC CGANCTCCTG CATCTATGCT GCATCCACCA GGGNNCACTG GNCATCCCAG	240
CCAGGTTNCA GTGGCAGTGG GTTTGGGGA CAANTGCAC TCTTCACCAAG CAGCAGCCTG	300
CAGTTTNGAA GNTTTGGGG GTCTNATTAC TGT	333

(2) INFORMATION FOR SEQ ID NO:1663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

TCCCAGATCC AGGANTTAA GGGAGGGTTT NAACATGNNTT AACCAAGTNAC CTTGATGGTT	60
TCATTAANAA GGGGGGACCT GGGACGGAAA ATGTTGGCTT CGTNGGGGT AAGAACCCCC	120
	120

(2) INFORMATION FOR SEQ ID NO:1664:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

CATGGGGTTT TNCCTTGGC CACATATATG CGAATTTTTT ANGAGAAGGT GATATTTGG	60
ACATCANGGG AANTGGTTAC TNTTCCAAAA GGGTTGCC CACANTTTT ACC	113

(2) INFORMATION FOR SEQ ID NO:1665:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

GGCANAGCCG NCGGTTCCNA GGATGCCAGC GCCATGCTGA GGCGCTTCCT GGGCCGTGAA	60
CCCCAAGCAG GACGCCTTCC TCCTGAGCAA GGGGCTGCAG GTCGGGGCT GCAAGCCGNA	120
GNCCGCAGTN TGNCTGAGGC CTGGTNACTG CGAACTGCC AGTNTGGCCT GCGCTCCCFC	180
CGCCCTGGTG CCTTAGCCCC CGGNACAGGT ATGGGGTNAG GCTNTGGCA CATGNCTGGA	240
GAACCTGGCA	249

(2) INFORMATION FOR SEQ ID NO:1666:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

AAGAGGCCAA NGTACAGTGG TNGGTGGATA ACGACCTGCA NTCGGGNAAC TCCAAGGAGT	60
GTCACAGGCA GACACAAGCC AGCACCNACA GACTCAGTAA CA	102

(2) INFORMATION FOR SEQ ID NO:1667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

NGGGGGTNGG TGACCCNCGG CTGCTGCAGG GAATCTGCNG ANCTTGCAGN CCATGGGGC	60
GCACCTGGTC CGGCGCTACC TGGGCGAATG CCTCGGTGGA GCGCGACCCCTGCAGATGC	120
CAACCTTCCC GTTCAGACTT ACGGCTTCCC CGAACGGCAA GGAGCGCGAG ATGGTGGCCA	180
CACAGGCAGG AGGATGATGG ACgtGCCATT NAGGGCTCCA GCTGGGGGA CTAATTGCGG	240
CCCACCAACCT TCATTCCGGN TGCTTCAAGT GGCAAGTTTT GGACAGTTTT TCCCCAAATT	300
TNCTTGGGCC TTGNAAAACA NGGAGCNGGG CAGGA	335

(2) INFORMATION FOR SEQ ID NO:1668:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

GGCAGAGNCA CAGATGTCTC AGACGGCCTG TCCATCCGCC TCGGGNCAGC CCTGAAAATC	60
TACGAGCACC ACATCAAGGT GCTTCAGCAA GGCCACTTTG AAGGATGAAT GACCCCNATG	120
GCTTCTTAAG GCTGAGCGCC CAGCCTGCAC CCCTGCCCA GCCCATTCCG GCCCCCATCT	180
NCACCCAAGA ATCCCCCAGA GTCCAGGAGC TGGACGNNGA CACCCTNCAG CCCTCATGAA	240
CAGAATTCCA AGGAGAGGGC ACCCTTTGT GCCTTATCTT TGGCCCTTGT GTCTGTTCA	300
CACACATNTG CTTCCTTCAG CACGTCGGTG TGGGGAGGGG ATTGCTTCNT AAAACCCAG	360
TGGNTGNACC TTCCCCACCC ATTCCAGGAC ATTTAGGAAA AAAAAATGNA ATTTGGGGGG	420
TTTTANTTTC CCAGTTCTTT T	441

(2) INFORMATION FOR SEQ ID NO:1669:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

GGCAGAGGCC GGTGCAGGTC CAGCCCTTGG AGCTGCCCAT GGTCACCACC ATCCAGGTGA	60
TGGTGTCCAG CCAGTTGAGT GGCCGGAGGT GTTGGTCACT GGATTCCTG CCAGCCTCAG	120
GCTNAGCTGN AGGTGGAAGC TGCTGGNACA AGCTCAGAGA ATCTNCTTG GNCAAGACTA	180
GGNAACGGTG GTNGNCGGAT GTGGNACGTT CCGGGAAAGCT AACTGCCAGG GAAGTNTTCA	240
TGCTGGGGTT TGCTAGGGAA TGGAGTGGGC TCANCGTCTG TNCCCAAATC GGCCAGTTTC	300
ACAGTGCCCA CTGGGTGGG GCAGCAATT CCTCTGAAGA GTTTTNTCCG TATGTGAAAT	360
GGGGAGTTCC AAAAGGNTGA GTTCAGTTGN AACCATTTCC CGTTCGGTNA NTGGTG	416

(2) INFORMATION FOR SEQ ID NO:1670:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

NAGCCGCATC CTCAGGGCAG GGGGAAAAT CCTAACTTTC AACCAGGTGG CCCTGGNACT	60
CCCCTGAAGG CCTGTGGCAC TGTCTGTT TGCGGGTGC CGCGAAGGCG CGCAAAGCCT	120
GTGANGGGC ATTTGGGNNA AGGCCCCAG GAAGCCCCGG CACAGCCACA CCAAACCCATA	180
NCGTCNG	187

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

GGCAGAGTAT GATGATGTNA AGAGTATGGA GACCAAGGTT CAGTTCTTAA AGAATTAAA	60
CCTGGGAAGG AGCCATGATC TGGTCTATTG ACATGGATGA CTTCACTGGC AAATCCTGCA	120
ACCAGGGANC CTTACCCTCT TGTCCAAGCA GTCAAGAGAA GCCTTGGCTC CCTGTGAAAG	180
GATTAACCTA CAGAGAACGCA GGCAAGATGA CCTTGCTGCC TGGGGCCTGC TCTCTNCCA	240
GGNAATTCTN CATGTGGGAT TCCCCTGGC CAGGCCGGCC TTTGGGATCT TCTCTTNCCA	300
AGCCTTCCTC GGACTTCCTC TTAGATTCAT AGATTGGAC CGGTTTGTT 360	360
GTGTTGGANT NGTTGNCCCTG GAGTTACATT AAAAAAAATT CATTGGNTC CAAAAAAA	420
AAAAAAAATT CGGGGGGGGG CCCGTAACCA ANTGGGCC	458

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

GGCANAGGNA CAAGCCCAGC AACACCAAGG TGGNACAAGA AAGTTGAGCC CAAATNTTGT	60
GAACAAAACT CACACATGCC CACCGTGCCC CAGCACCTGA ANCTCCTGGG GGGAACCGTG	120
NAGTTTCCTC GTTCCCCCA AAACCCAAGG ACACCCCTCAT GAATCTCNNG GNACCCCTGA	180
GGTCACATGC NTGGTGGTGG ACGTGAGCCA GATGGACCCT GAGGTCAAGT TCAACTGGTA	240
CGTGGNACGG CGTGGTAGGT GCATTAATGC CAAGTACAAA GNCGCGGNGA GGGGGNGTNT	300

300

(2) INFORMATION FOR SEQ ID NO:1673:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

GGCAGAGGTT CGCTGCACCG ACCGNCCCTC AAGGACCTGC TCTNAGGTTTC AAAAGCAAAC	60
CTAACGTGNC ACACTGACCG GCCTGAAAAA TGCTCAGGT GTNACCTTCA CCTGGAACGC	120
CCTTCAAGTG GGAAAGAGCG CTGTTCAAGG ACCACCTGAA GNCNTGAACC TCTNTGNGCT	180
GCTAACAGCN TGTGCCAGTG TNCCCTGCCGG GGCTGTGCCG NAGCCATGGG AACCATGGGA	240
AAGACCTTGN ANTTGCAGTG CTGCCTTACC CCGAANTCCA AGAACCCCCN TAAACCGNCA	300
CCCTTTCAA AATTCCGGAA ACACATTCC GGGCCCGAGG TTCCAACTTG TTGNGCGTCG	360
NCGTTNGGAG GGAGTT	376

(2) INFORMATION FOR SEQ ID NO:1674:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:

GGCANGAGCC CTGGCGCACCA CGNCNGCGTN AAGGGTGAGC ATCCCGCTGT CGATCCTGGAA	60
GCCCCCGCAC CGGTACCACA TCCACCGGGCG NAAAGAGCTT TGACGCCCTCT NAACACACTG	120
GGCCCTGCCCG CGGCAC TGCTGGGCTG GGAACATTTT TCCTCCGAAG TNTGAGAAAA	180
GCTCAGCCCC CAGGAACCTG GACCTCTGGT CTNCTGTTTT CCGCTGAGGG CCCAGCAACA	240
GAAAGNTGTC CGGCAACANC AAGCCTTTT AAACCGGGCT TNAACAATTG ANATTGTTNC	300
CCCCGAACCC GACTTGTAA TT	322

(2) INFORMATION FOR SEQ ID NO:1675:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

GGCAGAGCNA AGGTGGACAA GAAAGTTAAG CCCAAATNTT GTAACAAAAC TAACACATGC	60
CCACCGTGGC CAGCACCTNA AACTCCTGGG GGGAACCGTA AGTATTCCCTC TTCCCCCAA	120
AACCCAAGGG ACACCCCTGCA TGAATCTCCC GGNACCCCTG AAGAGTTCAC ATGCGNGGTG	180
GTGGGACGTG AAGCCACGGT GTACCCCTGTG GTCAAGTTCC AACTNGGTNA CGTGGGACGG	240
CGTGGTGGTG CNTNAAT	257

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

GGCANAGTGC ATCACCAAGT TGGAGACCTT TATCCAGGAG CACCTGAGGG TCATTGGGC	60
TGTGGGGATC GGCATTGCCT GTNTGCAGTN CTTTGGCATG ATCTTCACGT GNCTGCCTGT	120
ACGGAAGTCT CAAGCTGGAG CACTACTGAA CCCTGCCCTG GGCCTTNGCT GCTGCTGCAC	180
CCAACTACTG AGCTGTAGAA CCACTGTAGT NACCAGGNGG TCTGGGNCTT CCCTGAATNG	240
	240

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

CCTAGCACCT NGTGGATCCC CCGGGCCTGC AGGANNTCGG CAGAGNATTG GGTGACCTTA	60
AGTNTACAGA NCAC TGATTC CCCATCCTAT CCAGAGATTA GTTTTAGTTG CAGCATGGAA	120
CAATTACAGG ACTTGGTGGG GAAACTAAA GATGCTTCGG AAAAGCCTGG NAAAGAGCAA	180
CTNCANTTGT AAAC TTGGGG NAAGTTAAAN NATCCGCCCG AGTGCCAGAG GGAAAACCAG	240
AAAGNCCTTG CCTTCAGCTG GAACCACCGT TTGTGCGNAG CTGGGATGTN CCTTTTCAGT	300
AGGAAAAGAA TTTTCCCTTT TGANTTTATA ACCATTCATC AATTTGAAC ATTTNAAAAA	360

GNGTAAAAAG GGTTAAGAGG GGAAAGATTA TTGCCAGTT TTTGNATTG GTTTAGTGG	420
TAAAATGTNC CATTN	435

(2) INFORMATION FOR SEQ ID NO:1678:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

GGCACAGTGA AATACATTT GGAAGANAGT TTTTNATCTT AGAGATTGGT GAACAAGTGT	60
AAGGGTGTNA GAAACTCACA GGAATACAAA TTNCCCTGTA TGTTTGTTGG GTTTTTTTT	120
TNCCCCNTCA AGATGTTNC TATTC	146

(2) INFORMATION FOR SEQ ID NO:1679:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

GGCAGAGGTG CCTGATAACGA CTACCAGGCA GCCGACGACA CANAGATCTC CTTAACCCCC	60
GAGAACCTCA TCACGGCAT CGAGGTGATC GACGAAGGCT GGTGGCGTGG CTATGGGCCG	120
GATGGCATTG TGGCATGTNC CCTGCCAACT ACGTGGAGCT CATTGAGTGA AGGCTGAAGG	180
GCACATCTTG CCCTTGCCCC TCTNCAGACA TGGCTCCTT ATTGCTGGAA GAGGAGGCCT	240
GGGAAGTTGA CATTCAAGCAC TCTTCCAGGA ATAGGACCCC CANTGAAGGA TGAGGCCTCA	300
GGGCTCCCTC CGGNTTGGN AGATTCAAGCC TGTNAACCC AAATGCAGCA ATTGGCCTGG	360
TGATTTCCTA NAATTCNTT CCTGGNAACC CCCGAACCTT TCCCCAAAAAA TTTGGTTTT	420
NGCCCCTTAA NAGTTTTT GGGCCCAAGC	450

(2) INFORMATION FOR SEQ ID NO:1680:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

ANTCTGGGCC ACGGGANAGA CAAGCTGGAA CCTGCATTTG NAACCCTNGC TTCAGNGAAT	60
ACCACCATTG TTTGCAACTG CATTGGACGG CAGCAACTGG GGGGCAAGTA ACAACGGGNA	120
GATTNACCNT TGNTTGCACT CCCANGGTTC AAAGGTC	157

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

GGCACGAGCA CCAGCNACTC TNCCAGCTCA AGGNACCCAC CTGCNAGTAC AGGGCAGCCC	60
AATCTGGTCC CTCTNAACGG CCAGGACCTC CGCAGAGGGC CCTGCTGGCA CGAGGCACTA	120
AGTCTCAGGG GCCAGCCAAG CCCCCACCCC CAAGGAAGCC ACTGCNTGCN GACCCCCAGG	180
GCCGGTGCC ATCGGGTGAC CTGCCCGGCC CAGGGGCTGG AATCCCGCCC CTAGTGGTAC	240
CCTCCANACC AGCGTCACCG NCTCCAACAG TGTTCCCTCGC TCTTACCTCT GAACCTCTTC	300
CGGGAGGTTT CCGGTTGCCT TCCAAAGCCG GGACTTTAGG GGTTCAAAG AAGGCGGGGT	360
GTTGCCCTTT TGGGNAGTCC CCCTAACCAT TGANTTAAAG GGGNAAAAA AANTTGGGGG	420
TGTTTTNAAGATTTGGGGG AAACGCCAAG GGGTTTTT	458

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

GGCACGAGCA CAGGGGAGCT GCTGGCGAG TACAAGGCC ATAAGAACCA GGAATACAAG	60
CTGGACTGCT GCCTGANCAA GCNTAACACA CATGTGGTCA GCTGTTCTAA GGACGGGAAG	120
GTGTTCTTCT GGGACCTGGT GGAGGGTGCG CTGGCTCTGG CCCTGCCTGT GGGTTCCGGT	180
GTGGTGCAGT CGCTGGCTA CCACCCAACA NAGCCCTGCC TGCTGACCGC CATGGGAAGG	240
CAGCGTCCAG TGCTGGCGAG NGGAGGCCTA TGAAGGCAGA GGATGGAGCA GGCTGAAGCC	300
AAGGGACCCA CCAACAGGAC CAAGGACCGA GACACAGACA TGGAAGGACT TCAGTTACCN	360

CTTATTTTA GAGACGTAGT TGACCCAAAA ATTAGGGGNG GGGGTTNGGT TTTNCAAATT	420
NATTAATTAG AGGGGGGGGT AAGACCTTCC TGGGNCCCCA AA	462

(2) INFORMATION FOR SEQ ID NO:1683:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

GGCACGAGGA ATCCTGACAG GGACAGGCAG GCACAAGGCA CAAAACCTGG GAAATCTNAG	60
CCACAGAGAA TGCTGTTTG CTGCGGCAA GGCGCCTCGT NAGTCCTGGG GCCTGTTGC	120
TCTTGGCCCG GGNGCCAGGG CCAGTTCTG GCACCCCTAG GAGAATGAAT AGGGCTCAGT	180
GTGGTGGCTC CGCTGAAGCT TCAGAGCCCC CTTNTGCCT GCCTGGGAGT GNGCCGTTAA	240
GGAGTGCAGAA CCAAGGACCT GCCGGTGNNG TGGGCTGTCC CTGCAGGAGC TCTTNAGTT	300
TGCACTGGGA GGGGCANGTT CANCCCCAGC CCCATGGTTC CCTGTTCCCTG NAACAACCCC	360
GAGTGGTTTT TCCTTGNCTT CCAGGCTTTN GGTTAAGGT TGGGCTTCAA AACCATGGG	420
GAATTCANT TTTNGCCCTT NCCCGGCTTA AGGTTTTTA AACTCCTTTT GGGATNCCTT	480
AAAGGTTGGG TT	492

(2) INFORMATION FOR SEQ ID NO:1684:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

CAGCACANCC TGTGGCAGGC CCGTAAGTTT TCCTNTTCCC CGCAAAACCA AAGGACACCC	60
TCATAATCTC CCGGGACCCT TAAGGTAACG TNANNNGTGG TGGACGTAAG CCAGAAAAAC	120
CCCAAGGTNC AGTTCAACTG GTCACGTGGN CGGCGT	156

(2) INFORMATION FOR SEQ ID NO:1685:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

GGCANAGGGC CAAGGNGAAG NTCCCGCGCT ACTACANGAA CATCGGNCTG GGCTTCAA 58

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

GGCACGAGCC CAAATTCAAC ACATTCCACT CATAAGTGTT CTGTACTCTT CAAAAATATT 60
CATTAAAGTC AAAGAGAGGC TGAGGAACTA TTTCAAACTC AGGAGACTTG GAAACTAAAT 120
GCAGTGTGTG ATCTTGGATT GGATTTAGA TTAGTAGGAA ACATGACTGT AAAAAAGTGN 180
CTGAAAATA NCTGGTATTA TTGGGACATC AATGTTAAAT TTCATGAATT TAATATATAT 240
TGGTTATGTA AGTTAAATGT NCTTGTNCTG AGCTGNAAT TAAGTTGAN CCTATTAGGG 300
GGGCAAAGCT GTCTAAANCT CCCCAAATAG TTCCTGCAA ANGGTTTCC AGTGGGGTN 360
ACCACACATT GGGAGAGGNG 380

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

GACGCCCTCA GGCCCACGT GACTTCATCC TCTTTTCAGA GGCCAGTCAA CGACATGAAC 60
ATCGCAAGCG GCTGCCCT CTTCTGCCCT GTNTCCAAGA TGGAGGCAA GAATTCTAC 120
GTGCGGGACG ATGCCATCTT CATCAAGGCC ATTNTGGACC TGACAGGGCT CTAACTGCTC 180
CCTACTGGTG TTTGGGGTT GGGGGCAGCC AGGCACAGCC GGCTCACGGA GGGGCCACCA 240
CGCTGGGCCA GGGTCTCACT GTACAAGTGG GCAGGGGCCG CGCTTGGCG CTTGGGAAGG 300
GTNTCGGCCT GCAGCCAAGT TCACTGTCCA CGGGGGGAAG GAGCCACCAAG CCAGTTCTC 360
AGATTCAGA GACTNCGGAG GGGTTNGGC AGACGGTTT AGNCAAGGGG TTTTGTGGCA 420
TTNGCCGAGG GTTTTCGGG GTGNNTTCCA G 451

(2) INFORMATION FOR SEQ ID NO:1688:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

TTNTTTCCTC ACCNTCCACC AAGGCCCAT NGNTTTCCG CCTGGGGCCC TGTTCCAGA	60
AGCACCTCCA ANAGTGACAG GGCCCCTGGG CTGCTTGGTC AAGGACTACT TCCCCGGAAC	120
CGNTNACGTT TCGTGGAACT TAAGGCGATC TGAACCAAAG GTNTGCACAT TTNCGGTTG	180
TCCTANAGTA CT	192

(2) INFORMATION FOR SEQ ID NO:1689:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

GGNAGAAAGG NGCGCACGCC CNATGGCCAG TACATCTNCA GGCTGGAGCC GAACGTGGAG	60
GAACTCNGCC CGCTTCCTTA ACCTGCCTGC CCGAAAGCCC CTNACCTACC AAACGNANN	120
AGCTCATCGC CCGAAAAAT CCGAGGTGGA GNAAGATGCG GCGGGCGGAG GTTTCTCCCC	180
GGGNTAGAGG AACAGCCCC AGGTGGATG GGAAGCCCC CAGGGCTCGA AGAGGGTNTG	240
CTTGGGNGGG GCATTGGGG AGAAAGGGGG TGCACCGACC TNCCCCACGC AACCTTGNGG	300
CANCGGTTGG G	311

(2) INFORMATION FOR SEQ ID NO:1690:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

CAGCCCCGAN ACCCACAGGT NTATAACCCTG CCCCCATCCG GGAATGACCT GACCAAGANC	60
CAGGTTNAGCT TGACCTGCTT GGTCAAAGGT TTCTNTCCNA NCAACATCGC CGTGGAAAGTG	120

GGAAGANCAA TGGGCCAGCC GGAGANCAAC TACAAGACCA CGCTTCCGGT GCCTGGANTC	180
CGAACGGCTN CTTCTTCCTN TNACAGCAAG CTNCACCGTG GGACAAGAGC AGGTGGGCAG	240
CAGGGGNAAC GTTTTCTAAA TGNTTCCGTG AATGGCATGA GGGTNTTTTG CACAACCAAT	300
TACAAGGCNG AAGAAGCCTN T	321

(2) INFORMATION FOR SEQ ID NO:1691:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

GGCACGAGCA AGATCACGTC TCCC GTGCTC ATNATCCACG GCACGGAGGA CGAGGTGATC	60
GANTTCTCGC ACNGGNTGGC GCTCTACGAG NTCGNCCCCA AGGCGGTGGA GCCCTGTGNG	120
GTGGAGNGCG CCGGGCACAA CGACATCNAG CTCTACAGCC AGTACCTGGA GCGCCTGNTT	180
CGCTTNATC TTCCCAGGAG CTNGCCCAGC CAGCGCCGC	219

(2) INFORMATION FOR SEQ ID NO:1692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

TCCCCGGCNG CCCCTACTGG AAAGTAAGGA GCCCCCTCTGC NTGGCCAGCC GCCCCGTCCG	60
GAAGGNCGGT GGGGGGGTCA GCCCCCNC CCNATCTGGA AGGTNAGGGG	120
CACTTNTNCC GGGCCGCCGC TACTGGNAAA GTGAAGGAGC CCTTNTGCC GGCCAGGACC	180
CCGTTGGAA GGTGTGCCA GCGGNTCATT GGGGATGGGG CATGATGACA ATGGCGGTTT	240
TTGGAATAGA AAGGNGGGAA GGGTGGGGAA AAAATTNAGG AATNGGGTGG TTTNTTGGTT	300
TTTTTGATA GAAGTAGACN TGGGA	325

(2) INFORMATION FOR SEQ ID NO:1693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

ACCCCAAATG TCCTCATCAT CCCGTAAAAN CTGAGGTACT TCGTAAAGGA TGT CCT NGGC	60
TGTTTCTGTT TAAACCTGG GCGCCTTACC AAAGGGCAGG TGGGAAGGNA CCTTCGCCCG	120
ANTNTACCTT AGGAAGGCCG GCAGCGGACG GGNGCAGAAA GGCAGAGCCC ATGCATTGCT	180
GTGCAGGTCTG TNAGGTATCT GAGGGCTTCT TTTNCTCTGC TGTTCTCTGC TGTTGGGN	240
CCTAAAAGT NTTTAGNCCA AGAG	264

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

GCCTGTTGGA GGAGGAGAGA GCTTTNTGGC ATGANCCACA GTTTCTTGAT GGNGGGCATC	60
AACCTTTGGT GAGGGTTNTN TTGGGCCTGA AATTGTTGGC CATGGTGGGT GGGTTTAAGG	120
TGGCTNTGCT GATAAGGGCC TCCGTTCTG GGTTAAGTGA NAAGAGAAAA AAGGAGTTAT	180
TGAAGTNGAC GTTGATAATA GGTTAANGT GAATCATGAA TGNAGGAATT GGAGNATTG	240
TGGTTGGAAA AGGGGAAGGT TTTTNCGGTA ATG	273

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

ANACTACGTG GGCAGCCCCA TCACCTGCAC CTGCTTCACC CGGGATGGGC AGTGCACCCT	60
GGTGTCCAGC CTGGACTCCA CATTGCGGCT CCTGGACAAA GACACAGGGG AGCTGCTGGG	120
CGAGTACAAG GGCCATAAGA ACCAGGAATA CAAGCTGGAC TGCTGCCTGG ACCNAGCNTG	180
ACACACATGT GGTCAGCTGT TCTAAGGACG GGAAGGTGTT CTTCTGGAC CTGGTGGAGG	240
GTGCGCTGGC TTCTGGNCCT GNCTGTGGGT TTCCGGTGTG GNTGCAATNG NTGGAC	296

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

TCCCGGGGGN CAAGGNAGGN CAGTTCCAGC CGAAACCGNA NGAACCAGGA AGGTCACGCT	60
GGAAATGCTC TTTCTAGCC GGACTACGTG GGTGTACTCC ATCAACAACG TTCTCATGTN	120
TCTTTCAGGA AAGACCCCCC ACCTGTATT TCATAGCATC CTTGGCCTGC TGGAACGGAA	180
AGAGACCAGT GCAGGAAACC CCATCGCTCA CATTAGCCCC CACCGCCTAC TGGCAAGGAA	240
GAACATGGTT TCCACCAAGA TCCAGGACAC CAAAGGCTGC CGGGCGTGCT TGTGTGGCGG	300
AGGGTGCAGAG TTCTNGGGGN CCGTTNCTGT NCGGTGCATT TGAGACGTCC GTTGTCCCTGT	360
TNAGTGGTAC CAGCCATGAA CAATTCTTGT T	391

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

AAGCCCACCT TTTTNGCTGT TCGGGTCCNT GACTCCATAG AANCGGTAGG TGCCGCAGGA	60
TTAATGGNCC TGNNTCCAGAA TCTTGTGCT ACCGGCAATT AAC	103

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

GGCAGAGNCA AGGGCTCTTT NCCCGTGCCCT CTGTACGATT ACCAGGCAGC CNACGACACA	60
AAGATCTCCT TTAACCCCGA GAACCTCATC ACGGGCATCG AGGTGATCGA NGAGGCTGGA	120
ACACGTGGNT ATGGGCCGGA TGGCATTATT GGNATGTTCC CTGCCAACTA CGTGGATGCT	180
CATTNANTGA GGCTGAAGGG CACATNTTGC CCTTCCCCTC TAANACATGG TTTCCCTTATT	240

GCTGGAAGAG GAGGCCTGGG AAGTTGACAT TTCAGCACTC TTCCAGGAAT AGGNCCCCA	300
GGAAGGTTNA GGNCTCAGGG GTTCCCNCAG GGTTTGNAAG	340

(2) INFORMATION FOR SEQ ID NO:1699:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

GGCACGAGCC AGGATCACGC CATTNCACTC CAGCCTGGGT GATTNANTNA GACTCTGTTT	60
CAAAAAAAA AAAAAAAA CC	82

(2) INFORMATION FOR SEQ ID NO:1700:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

ANAGNCAACA GTTCCNAGTT NAGTGCTCAC CGGCGCATCC ACACTGGGGA GAGCCCATA	60
AAGTNTGCAG TGTGTGGAAA AATCTTCAAC AATAGCTCCC ACTTNAGTGC CCACCGAAAA	120
ACCCACACTG GTGAAAAGCC TTANAGGTGT TCTNACTGTG AAGAGAAGGC TTCACTTAGA	180
ANCTCTGNCC T	191

(2) INFORMATION FOR SEQ ID NO:1701:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

GGCAGAGCAC GCGTGGNTGG TATNTGTTG TGGCTGCTCC CATTCCCTATA ACCTCCGAGA	60
CCTTCACTCC TAGGAATGTC CCAAGGCCAA TTCCCTTGGC AGCAATGAGA AGAAATGCC	120
TTTTCAAAT AGCGACTTCT GCAAAACCCG CTGTTGTTG TGGGTGAGCA CTGCAGTNCC	180
CACCGCATGC CACAGCCAGC CTCCCTCCTG GCTCCTCTGC CACGGTGGCC TTCCCCAGCC	240

CTCACCCAGG CCCCGACTTT CCTCTNANAG GTTCCAGTT TCCTGGGGC CTNGGAAC	300
TTCCTGAGTT CCTTCCNAA NCCAACAGGT CCAG	334

(2) INFORMATION FOR SEQ ID NO:1702:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:

GGCAGAGCGG TGACAGCGNC TCCAGGGCCG AAGCCGCNGG GCNCCACTCG GGGGCTGN	60
CTGCGCGTTG GNAGACCGTG CTCCTNAGTC TGCGGTTCCC GANTNATCAG CNGCTGNTCC	120
CGGAAGTGGG GCCAGTGCTG CGAACCTCTC TATATGGATG TGCAAGCTAC AACTCCTNTG	180
GACCCCCGGG TGCTTGATGC CATGGTCCCT TACCTAAATC AACTACTATG GGAACCCACA	240
NTCCCGGACA CATGCTTATG GCTGGGAAGA GTGAGGNAGC CATGGAACGT GCTTGTNAG	300
CAAGTTAGCA TCTNTGATTG GGAGTTGATC CTCGTGAGAT TCANTTTAA TNAGTGGGTG	360
TTA	363

(2) INFORMATION FOR SEQ ID NO:1703:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

CCTCCCCAGG CCCCAAAGCA CCCCAAGGCT GGTATTCCTT GAGTNATAAGG TATTAATAAT	60
AAAAGCCTCA ATGCAGCTTC TCCATGTAGT TCCTCTCCTA CAAGCCAGGT GGATTCTGGT	120
CCTAACTAAA GAGATGGGAG TTCACCTGAG GGCAAGAAGT ACCCAGGATG CCCAAACAGC	180
CGCACAGGTG TCCTGTGCTT CCTGTGAGAC TTCCCTGGGG AAATATACAA ACTTAATATA	240
TTTTTAAATG TTTACGTCAT TTACACTGCT GCTTTCTAA TANTCTGNNT TTNATTACTT	300
GTAGTNAATC ATTTGTTGG GGTTCAAGC ACTGTCTTCC	340

(2) INFORMATION FOR SEQ ID NO:1704:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

GGCAGAGCNA ACGTTGGTGA GGACTNTCCA GTATTCAATG GCCTGTTAA GTTCTGTNAG	60
TTGTNTACTG GTGGTTCTGT GGCAAGTGCT GTGAAANTGN AATAAGCAGC AGACGGGACA	120
TGGNTGTGAA ATTGGGCTGG GGGCCTG	147

(2) INFORMATION FOR SEQ ID NO:1705:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

AGGCCCCCTG AAGCTGCAGC CCCCCCGAGA ANCTGGCCTG GAACTATGGC CGCCCCTNAN	60
CTTCCCTCCA CCCCGNATCC GGAAGAAGNC ATCCAGGAAA G	101

(2) INFORMATION FOR SEQ ID NO:1706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

GGCAGAGGGN ATGGAGGATC TCAACTGTNA ATCCACACTG TTCTCCAGGC CAGGGAAAGC	60
CTGGGAAGGT AAGCCTGGGA AGAGGCCCAA GCCCACAGTG GTTAATTGGC CCCATGGGCT	120
NCCAGACTGT NNACTNCCCC AGTTGAATC ACTGTGGTGC TCCAGCCTGG CTGTGATCTA	180
GTNAAGGGTG TTGTGGGGG CATCTNTGGG CCTTCAGGGG CCCCAGGTNA CTTCCCTGGGT	240
ATAACTTGNG TNACACGTGT T	261

(2) INFORMATION FOR SEQ ID NO:1707:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

GGCACGAGCG GAGATTGACC TGGGAGGCCA CGCCCCGTTG GATTCATGAC GGTGTGGCTG	60
CGGCCATCAT GAACAGCGAC TGCCTTGTGTT TCGACACAGC CATAGCACAT CTTTTGNCA	120
GATAATGGGA ACCTTGGGAA TCAATGTTAC TATTCTACA TGTTGTCCAT GNATGTGAAC	180
TTTCGTAAAC CTTCAAAATT ATTTGGGCAT AGTGCTCTAT GTTTGAATNA AAGGTTTTA	240
TAGATGTTT ATTCCA	256

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

TGTATTAAGT CTGCGCTAAC TAGGTTCCCA GGGCTTCTGT CCCTGGGACG TGGGGTCCCC	60
ACAGACCTGG AAATTCTCCG GCGTCTTCCT TTGCCCAGAG CAAATTGAGA CATCCCCGTG	120
AAGAGCCCGA GGGTCGCTTC CTTTTGGGTT TAAAGTCGTC CTGAGGCTGG TCTCGTCCCC	180
GGTCTTCTG CTATAGGTCA ATGTATACAC TTTCTGTTGA GTANTTTCC TGCTGTAAAA	240
CCTTGTCTG AT	252

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

GGNAGAGGNT AAGACGCCTC CNTNCTGCTT GTGNAACGTC CTAAGCGTAC CCNCTCTTCC	60
CAGCACCCAG GCCAGTATTA AAATCAATTG TNTCTATGAA AGGGAATCGA CTTCAATACC	120
TGCCATTAAC CCGTCCCCG AATTGAAAG AACTGAAATG NTGGACCTGT TCCCGTGGGA	180
ACCCTGGAAC CCAGTAGAGA AAAGCCCTTG GAGAATGCCA AANTGGGGCA AGTGNANAGA	240
TTTCATGATA TTGCNCCTGG GTTGGTGGTT NTTACTGG	278

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

CAGAAGAGTT AGTTTCCAGG CATCCATTTC CAGGTCTGG CCTGGNAATC AAAGTAATAT	60
GTGCCTGAAG AACCTTATAT CTGTAANGNN CTTTCCTGAA AACCAACAAT ATTTTAAAAA	120
TAGTAGCTGA TTTTCCTGC CANT	144

(2) INFORMATION FOR SEQ ID NO:1711:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

GTGCGNCATC CTAAGCACCA TCNATCGGGA AGCTGCTCAA GCCCAACGCC TCATTGGCCC	60
TCCACAAGCA CAGCAATGCA CTGGTGGACG TGCCTGCCCG CCGAAAGCCG ACAGCAGCAT	120
CATGAATGCT NCACCTTCAA ACCAGAAGCC AGATGTNAAT GTACGCGGAC ATCGGNGGC	180
ATGGGACATC CAGAAGCAGG TAGGTGCGGG AAGGCCGTGG AAGCTTCCCG CTTCACGCNA	240
TTTGGAAAGCT TTACAAGCAG ATTNGGANAT TGTTTTCNNC CCCGAGGG	288

(2) INFORMATION FOR SEQ ID NO:1712:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

ATCTCCNGC AGAAAGCTTT CTTTCTNAAA ATGGTGGTGG ATGCNGTAAT GATGCTCGAN	60
GATTTCCCTGN AGTTTAAAAT GATTGGAATC AGGAGGGTAC AGGGTGGNGC CTTGAGGGTT	120
TCTA	124

(2) INFORMATION FOR SEQ ID NO:1713:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

GNAAGACCAA GGCTCATGGA ATCCTCNAGC AAATGTGGGG AGCTTNCCTC CTCTATGTTT	60
CCATGANGAT GGGAAAGGNAC TGNGGGAAAA AGCCTTAACC AGCCCTNTAA GGTGAANAGC	120
TGTGGAAGGG GCCATTTCC CGAATAA	147

(2) INFORMATION FOR SEQ ID NO:1714:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

CTAAAGGACC TGCNCGTNTG GACCAGCCAG CTGAAGAGCA CCATCCAAAC GGCGGAGGCG	60
CTGCGGCTGC CCTACNAGCA GTGGAAGGCN CTCAATNANA TCAACGCGGG CNTNTGNAAG	120
GAGCTGACCT ACGAGGAGAT CAGGGACACC TACCCTAAGG AGTATGCCCT GCGGGAGCNG	180
NNCAAGTNCT ATTACCGNTA CCCCACCGGG AAGTCCT	217

(2) INFORMATION FOR SEQ ID NO:1715:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

GGCAGAGCTT AATGGCAGAA GCTCTGGAAA AGCTCTTNTT GCAAAAAATA AATGGGCTAC	60
CCACAGAAGA AACCGAGATC ATGATAGTCC AGGCAAAAGG AAGAGGACGT GGGAGGNAAG	120
AAACAGGGAC AGCAAAACCT GGCGTTCCA CGGTACCAAA CACAACTNAA GCATCGANTC	180
CTCCGCAGAC CCAGACCCCT CAGCCGAATC CTCCTCCTGT GCCAGGCCAC GGNTTCACCC	240
CTTCCCTGCG GTNNACCCCG GACCTNATCG TNCAGACCCC TGTAAATGAC ATGGGTGC	298

(2) INFORMATION FOR SEQ ID NO:1716:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:

GGAAGAGTGA CCGGCTGGTG GAGGTGCAGT GGGAACAGCA GGAGGCCCGA AGCCTCTGGT	60
ACCTGCCCCA AGGNCAAAA ACCTAANAGC AGCACANNCA TGGTA	105

(2) INFORMATION FOR SEQ ID NO:1717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:

CGCGGNTACT ACAACCAGAG CAAGGCCGGT TNTAAANACCA TCCAAATGAT GTATGGNTGC	60
AACGTGGGGT CGGACGGGAG NCTTCCTCCG CGGGTACCGT AGGNCGCCTT ACGAACGGCA	120
AGGTTTACAT CGCCCTGAAG AGGACCTGCG NTTCTTNGAC CGNGGNGGAA CATGGCAGT	180
TTCAAACCAC CAAGCACAAG TGGGAAGGNG GGCCCCT	217

(2) INFORMATION FOR SEQ ID NO:1718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

GNAAGACCAC CAAGGCCTCA AAATTAAACCT AAAGACCCAC TCCTTNCAAG TGGTGGTAAT	60
CTCCAANATC T	71

(2) INFORMATION FOR SEQ ID NO:1719:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

CGGGCAACCC TGAAGGCTGG TGGTGCCGGC AACCCAGTNC GGCTCCNTGA ATTGGGAAAA	60
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GGCGGGTNTA ANATCAANGA GAATCCGCAA AAGTACGGGG GCGCNGTCCA GGTGGCGGGG	120
GAATATGCTG CCCATTCCAC CGAGGGGGCC ATCACCATCG CTGGNGTGCC GCANTTTGTA	180
ACCGAGTGTT TCAGCNATTT CCCTGGTCAT GCTGGAGACG GTCTCCCCTT TTGAAAGGA	240
AGNGTCATGN CCTTCCGT	258

(2) INFORMATION FOR SEQ ID NO:1720:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

GGNAGANCNA GGTTACNAGG GCTGGCTGGC CGGCTACCAA ATGAATTNA AAACTGCAA	60
ATCCCGAGTG AACCCAAAGC AACTTCCAG TTGGCTACAA NACTGNATGA ATTCCAGCTT	120
CANACTGAAT GTGAAATGAA GGGGANAAA GTTTGGGGC TCCATTTACC AGAAAGTGAA	180
ACAAGAAGTT GGGAGACCGC TGTGNAATTG TTGCCCTGGG NCAGCAGGGN AACAGTTAAC	240
ACGGGCTTTG GGAAATAGCC AGCCCAAGTT ATCAGAATTG NACCCTGAAC GGCTGTTTT	300
TGNGGGTTA ANGTGNAACA AATT	324

(2) INFORMATION FOR SEQ ID NO:1721:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

AGATCAAGCA CTTTGGNATG CTTCGCCGCT GGGAAATGANA GCCAAAANTA CCTGTNAAAA	60
CAACGTCCAC CTGGTGTCCA AGGAGACAGC CAATTACCTG GTCATTTGGT GCAT'TGCNCCT	120
AGAGGTGGAG GAGAAATGTG CCACTCATGG AGCAGGTGGC CCACCAGAAC AATCGTTAAT	180
GCAATTAAAT CCTGGGAGCT GGCCAAGAGC CTTAAGGGTG GGACCCCCGG GNNCTGNTTC	240
CGGNAGTTT TCCACTAAGN TTTAG	265

(2) INFORMATION FOR SEQ ID NO:1722:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

GGNANANACG GAGATTAACC TGGGAAGGCC ACGCCCCGTT CCAATTNATG ACGGTGTGGC	60
TGCGGCCATG NATGAAACAG CAACTGCCTT GTTTCAANA CAGCCATAGC ACATCTTTT	120
GCCAGATNAA TGGGAAACCT TGGGAATGCA ATGTTAACTN ATTTCTANCA TGTNGTCCA	180
TGAATGTGAA CTTTGCGTGA AACCTTNCAA AAATTATTTG GGCCATAGTG CTNCTTATGT	240
TTAANAAAGG TTTTANTAG ATGTTTNTT CCCATATGTT CTTCA	285

(2) INFORMATION FOR SEQ ID NO:1723:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

GGAACAGGCC ATCTCCTTGG CNAAAAATTG CTTGGCCGGA NATNCGACCG CCGNNATCTC	60
CAAGAAGGGC CGTGGCTCCA ATCGAGCCGG GTAAAGCTGC TGTGC	105

(2) INFORMATION FOR SEQ ID NO:1724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

GGNANAGGNA GNAAGAAGGA GCTGAAGGCC CCCCGGCTCG GANCCAGCCC AAACAAGGAC	60
AAGGACGAAC CTTTCCCCC CAAAGCAGAA GGCGAGCGG NAGAAAGGAG CGCCCGGGTG	120
GCCAATTAAC GCCCGGGAGA GANTGNGNAG TNCCGTGAAA ATTCAAGAGG CCTTTAAGG	179

(2) INFORMATION FOR SEQ ID NO:1725:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

AACGACACCC TNAGGAAGAT CCTGGACCTA AAATTTAAG GGGGCCCCCC CAGGGCTAGC	60
NAGCCCTCTG GCCGCCTGCA GGCTNAACCA GTCCCTAAC AGGATGGACA ACAGCCAGCA	120
CCCCCAGCCT GCTGANAGCG NACAGAACTG GGTCTCAAAGGCTCTGGCC CAGAACCCCTC	180
CCACCACCCA CGGTTGCTGG TGAAAGNAAT TCTNTGAACC TGCAACTNTG GCCAGGAGGC	240
TGTGCTGNNTT CACTGTCCGT NAGGAGGGCC CCAACCGGGG CGG	283

(2) INFORMATION FOR SEQ ID NO:1726:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

GGCACGAGGG AACAAATGCCT TTCCCTGAGCC GGGCAGGGTG CCATTTCCCG TGCCTAANAA	60
AGTGCTGTGG CCGCAGCTGT GTAAGGCGCT CAANATGAAA TTNAAGGCCG AAGTGCAGAG	120
CAACCGGGGC CTGAACCAAG GAGAAACCTC GTGTTCTGG CGCAGAAACT NTTCAACAAAC	180
AGCAGCAGCC ACCTGGAAGG TATGACAGTG GCCTGTTCCG TNTCCTGGTC CCAGTTCCAA	240
CAGGGNGGNA CTTGCCGGGC TGGNAATTAN ACCTTTGGN CAGTGGTTTG AGGGGGTGAT	300
GGAGGTGTTG AAGANGCACC ANAAGCCCCA TGGAAATGATT GGGGCCTTCT AGGTTTTTG	360
AATTAGCCAA CAGGCCAGA ACTGNTNCTT AAACAAGTCC GGGGNACTTT TTGTTGGCT	420
TTAAGTGANT TCGAAATTTG GGGGN	446

(2) INFORMATION FOR SEQ ID NO:1727:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

GGCACGAGGG AACTGCCCT AAAACATCCT GCCCTTTNA AGGCAATTGG TGTNAAGCCT	60
CCTAGAGGAA TCCTGCTTTA CGGACCTCCT GGAACAGTAA AGACCCTGAA TTGCTCGAGC	120
TGTAGCAAAT GAAAATGGA GCCTTCTTCT TCTTGAATCA ATGGTCCTGA AGAATCATGA	180
AGNCAAATTG GCTGGTGAGT CTAAGAAGCA ACCTTCGTGA AAGCCTTGA NGGAGGCTGA	240

GAAAGGAATG CTCCTGCCCA TGCATCTTGC ATTGAATGAA GNTTAGATGC CATCGTNCCC	300
AAAAGAGGAG NAAAANTCAT GGTGNNGGTGG AGCGGTGCAT TGT	343

(2) INFORMATION FOR SEQ ID NO:1728:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

GCAGAGACCC CGACATCANG ATCTTGGA AGTGGAGCCC CGATGATGTG CAGATCNTGA	60
CTTCCCTGA NGGATTNCTT GAAGTGAGGA NAGTTGCCA GTCCCTG	107

(2) INFORMATION FOR SEQ ID NO:1729:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

GGCANAGATG AAAGTCCAC CAGTNTGTGC GGCTATNACG CTCCGAGAAA TAACCGCACC	60
ATCTCCTTNA TCCCACCCNA CGCGAAGTT CNAGCTCATG TCCTACCGTN TNAACACCCA	120
CGTAAAGCCT TTGAANATGG GATCGANTCG GTGAATCGAN AAAGCACTCC CACAGCCGCA	180
TCGAGTACAT GAATCAAGGG CGGCAAGGG GTTACCTGAA TGCGGGCCCA CTTNGGCCTG	240
NCTAAGTGTG GGAGGCCGAA GACAAGGGGG GGCAAGCCCC CGATTCACTG TCCAGTTCG	300
AGATNCCTN ATTN	314

(2) INFORMATION FOR SEQ ID NO:1730:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

GGCAGAGTNT ATACAAAAAA GCAGCTTTG GATAGNATGT GTATGAACCT TAGGTGGTCA	60
AGTCTCTAAA GAAATCTNCT TTGGAAGAAT TACAACCTGGT GCTCAAATG AACATTGAGAA	120

AAAGTNAACT NCAAAAGTGCC ATATGCCCCA AATTNTTCCA GTTTGGN

167

(2) INFORMATION FOR SEQ ID NO:1731:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

CTGGGAGGTG AATCAGTAAT GACCATGGNA TCAACCCCAC CGGAACCTAC NACGGGAAC	60
AGNGAACCTG NAGCTGGNCC GATTCTTTT TTACTANAAT GAAGGCCACA GGTGGNAAAT	120
TTNTNCCTGG TGCCNATCCT GGTGGATTCT NGAAACCTGG GAACCATGGC CTTTTTCGC	180
TCAAGGTCCCT TTTGGCCA	198

(2) INFORMATION FOR SEQ ID NO:1732:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

GGNACGAGGG AAGGTGTCTN AAAACTGGAG ACTGGGGCGC TGCCGAAAGG GGATTCTCCT	60
GAAGTGGAGA TGCAGTCAAA TGCCCTGGAA TGCAGCTAGA GGATGATTCT TTGTNCATAA	120
TCCCAGGCTA ATTNNAAATCC TGGCCTACCA GTTCCGTCCA AATGGTGCCA GCTTGAATT	180
GTCGGCCTCT GGGAGTCTTT NNTGGGGCAT GATNAGGACG TTTGCNACTT TNTCCTGGCC	240
AATTG	246

(2) INFORMATION FOR SEQ ID NO:1733:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

GGCACAGTGG TGGCTCATGC CTGCAGTCCC AGCCACTCAG GAGGCTTAGG CAGGAGAAC	60
ACCTAACCGG GAGGTGGNAG GCCGCGGTGA GTCGAGACCG GAAAACACTC TAGCCTGGGA	120

AAACAAGAGC GAAACTCCGC TCAAAAAAAA AAAAAAAA AAAAANNTNG GGGGGGNCCC	180
CNT	183

(2) INFORMATION FOR SEQ ID NO:1734:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

GGTAGTATTG CNGCGTACA GGTTGCCAGC TCGCGCTCC AGTNATAACC AAAGCCCAGC	60
ATTTAACGCT GGTTTTNAAT ATACGCAATG TTGTCGTACG TCCACGGTGC CGGAGCGGTG	120
TTGTTTTAA CCGCCGCGCC TTCCGCAGGC AGACCAAACG NGTCCNAGCC GATCGGCTGC	180
AGGACGTTTT TCCCCAGCAT ACGCTGGTAG CGGGCAATCA CGTNACCNAT GGTGTAGTTA	240
CGTACGTGGC CCATGTNTAG TCGACCAGAA GGNTTAGGGA NAGCATAGAC AGGCAGTAAT	300
AATTCTNTTT GATCTTCGTC TTTCGGTTAAC TTNAATGTG CGGTTTTAAT NCCCATGAAA	360
GT	362

(2) INFORMATION FOR SEQ ID NO:1735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

CACTTTATNA NCCGGGAAAT AATGCGGGCA ACGGTGTTA ATTATNTCGA TTGTNATTNC	60
AATCGGTGGC GGCGGCACAG TTGGTGTGGC GGCCTCAGTC CGGAACANTT TGAAANCAAG	120
ACCCTCGCTT AGGCCTGTNT TCCATATTAN GTGGGTAGGT TCAAAATGCC GTTTNTGGTG	180
	180

(2) INFORMATION FOR SEQ ID NO:1736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

GGCANAGGNA GAGAGAGAGA GAACTAGTCT CGAGCGGGAG TCCGGCGGGT TACAGCGGAG	60
GCCTAGGTGG CAGACAGGGG GCCCGGGCCG CTGCGTGTG TCCACCCAAA ATGGAGTTCC	120
TCCTGGGAA CCGTTNCAGC ACACCANTGG GGCAGTGCCT CGAAAAGGCA ACAATGGCT	180
CCCTGCAAAG TGAAGGNTTG GACGTTGAAA TATGGAGATC TGTGAACATC ATCCAATGAG	240
AACGGAGGNA AGGGCAAAG GATGCCATTG GAGCCCTGNA AGAACGGCT TCAACGGGA	300
ACCGATACTT ACAGAGAAGG TTGATGCTGG NATTTAANCA GTGNCTGGNA G	351

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

AGCACGAGGT GGACTCACAA TTCCAAATAT TACCAAGAAG GGAGCCATGT NAGACAGGAC	60
AGCATGGAGC CCAGCGACGC TCTGGGAATG AATGTGTCTA ACTGTCGGTG TGGGGACAGG	120
CTGAAGACCC TAGAGCAGAG GGCGCGGTAG CAGNCACGCA GAGCNCTGNG NNACATTGCA	180
CTGGTGGGGA CTCCAAACTA CATNGCACCC NAGGTCTNCC TCCGCAAAGG GTACACTCAA	240
CTTTNTGACT GGTGGAGTNT TGGAGTGATT CTTTCGAGA TGCTGGTGGG GGCA	294

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

GGCACGAGGG ANCANNCTCA ATAAGGTTGT NACACGACAC CCTNATCTNA AAGACTGCAT	60
GGTTTTGGCA NTGNCACATG TCGCAGCATG GTGGCCGTGA ANGGCATAGC GAACACCACA	120
GGGCAAGCTG G	131

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

GGCAGAGCCA ATNAGGGNTA TTTTNATNAT TCCCACAAAT CCACCACCAA CATTAGAAA	60
GCCAGANCTT TGGTCCGATG ATTCACCGA TTTTTTAAA AAGTGTGTTGG TGAAGAATCC	120
TGAGCAGAGA GCTACTGNAA CACAACCTTT ACAGCATCCT TTTATCANGG NTGCCAAC	180
CTGTATCAAT ATTAACAGAC CTGATCACAG AAGCTATGGN GATCAAAGCT AAAAGNNCAT	240
GNGGAACCAG CAACGGGANT TGGAAGGAGG AAG	273

(2) INFORMATION FOR SEQ ID NO:1740:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

GGCAGAGGGC GACCANAGGC ACTTTTCCCC ACAGACCGGC GGCAGTANGG CAAAGGCTGT	60
GGCGAGCNGT TCGCTGGAA GAAGTGCCTN CTGTGGTGGG CCANGCGCTG CTCGGAAGGG	120
CCTGTNTGCC CNCTGCTTG GCCATTGCTT GGGGT	155

(2) INFORMATION FOR SEQ ID NO:1741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:

GGCACAGGGN TCATCGGTGC AGGGGAGTT GGAGAAGTGT ACAAGGGCG TTTGAAACTN	60
CCNGCAAGA GGGAAATCTA CGTGGCCATC AAGACCTGA AGGCAGGGTN CTCGGAGAAG	120
CAGCGTCGGG ACTTTNTGAA GTNAAGGCGA GCATCATGGG CCAGTTCGAC CATCCTAANA	180
TCATTCGCCT GGNNGGTGTG GTCACCAAGA GTCGGCCTGT NCATGATCAT CACAGAGTTC	240
ATGGAGAATG GTGCATTGGG ATTCTTCCT CAGGCAAAT GACGGGCAGT TCACCGTGAT	300
CCAGCTTGTG GGTATGCTCA NGGGCATCGC TGCTGGCATG GAAGTACCTG GCTGNNATGA	360
ATTANGTGCA TCNGGGACCT GGG	383

(2) INFORMATION FOR SEQ ID NO:1742:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

GGTANAGGTT GTNCCGAGGT GACACAGTGT TGCTGAANGN AAAGAAGAGA CGAGAAGCTG	60
TTTGCATCGT CCTTNCTAAT GATACTTGTN CTGATGAGAA GTATTCGGNA TGNAATAGAA	120
GTTGTTCCGG GAATAACCTT CGTGGACGCC TGAGGGGTG TNATCAGCAT CCAGCCATGC	180
CCTGATGTGA AAGTACGGGA AACGTNATCC AGTGNTNGCC ATTGGTGACA CATTGGGAGG	240
GCATTACTNG GTAATCTCTT CGAGGGTATA CCTNAAAGG	279

(2) INFORMATION FOR SEQ ID NO:1743:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

GNAAGACCNA AGGCCAAGAC CATAATCGTG GCAGGCNTGG TGTNCCTGTT GGCGGGCCTT	60
ATGGTGATAG TGCCCGGTTT CCTGGAACGG CCCANAAAAT CATCCAAAAT TTCTANAATC	120
CGNTGGTGGC CTCCGGCCA GAAGCGGGAA ATGGGTGCTT CGTTCTACGT GGGNTGGGCC	180
GNTTCCGACC TT	192

(2) INFORMATION FOR SEQ ID NO:1744:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

TNGGGNTGCA GGAATTGGGN AGAGCGTGGG CAGCAAGGGT GGGTAAAGGA TCCAAANATG	60
GCTGGGCGAA AAATTGCTCT AAAAAGAATT NATTGGGTAG CTTTGCAGN GATAATANN	120
	120

(2) INFORMATION FOR SEQ ID NO:1745:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

GGCANAGGCG CGCCCGAAAN CCCGNGNTGA TCCGCCGCCG CTGCCTTGAG TCGACTCTG 59

(2) INFORMATION FOR SEQ ID NO:1746:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

GGCAGAGCCC GGGGTGGAGG AGCTGCTGAA CAAGGGCAG GACCCTCTGG CAGACAGGGG	60
TGAGAAGGAC ACAGCTAACAG GCCTCCAGCC CTTGGCGCCC CGGAACAAGA CCCGTGTGGT	120
CAGCTACCGG TGCCCCACAA CGCTGCGGTG CAGTNACGA CTACCGANAG AAGCGAGCCC	180
GCNTGGTCTT CGGGCCTNAG CTGGTGTGCG TGGGTCCCTGA GGAGCAGTTC ACAGTGTGTT	240
CCCTCTNAGC TGGCGGCC AAGCNTCCCC ATGCCCGCCG TGGGCTTCTG CCTGCTTGCT	300
GGGGCCTGAC TTCTTCACAG ACGTNATCAC CATCGAACG GNGGATCATG CCAGGNTGCA	360
ATTGCATTGG NTTACAATTG GNATTTAAGG TGAATTAACC GNAGGACCCC CAAGAGACGG	420
CCAAGTTTTT TTAANTGCCA ATTTTAGNN ATGCTAAAAA CCNTGNATCC CGGTNGGGGG	480
NCCTGGGTT	489

(2) INFORMATION FOR SEQ ID NO:1747:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

GGCAGAGTTT AATCATCCAG CGCACATTAA TTGAGCCTGG CTTTCAGCCT TCGTGTGTTGGT	60
GCAGTGTCAAG CCCCCGGCTT GAGTTCACCT CCTTGGCCCT GCACTCTNAG TGGCGGCTCG	120

TGGCCTTCGG CACCAGCCAT GGCTTGGCC TCTTGAAACC ACCAGCAGCG GCGGCAGGTC	180
TTTGTAAAGT GCACACTGCA CCCCAGTNAC CAGCTGGCCT TGGAGGGCCC ACTCTCCCGC	240
GTCAAGTCCC TCAAGAAGTC CTTGCGTCAT NATTCCGCCG GATGCGTCGG NGCCGGGTGT	300
CCAGCCGGAA GCGGCACCCG TTGGCCCCCC AGNAGAGGCA CAGNAGGGGA NTGCCAAGGT	360
TNAGCGGCCA GGCTTCCAGA ACATGGGAGT TTGNGGCTTT	400

(2) INFORMATION FOR SEQ ID NO:1748:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

GGAAGACCTG ACGGGCATTG TAAGCTGGGN ANATGCCTGT GNGGCCGAA ANAGGCCTGG	60
NGTGTACATN CTGGCCTCCA GCTATGCCTC CTGGAATCCA AAGCAAGGTG AACAAANCTC	120
CAGCCTCGTN TGGTGCCTCA AACCCAGGGG TCCCAGCCG AAAGAAACCT TTTTGGCAGC	180
CACCTGGCCT TAAAGNTNTG CCCCAGCCCA GGGNTNNNTG AGGCCCATCC TTTTCCTG	238

(2) INFORMATION FOR SEQ ID NO:1749:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

GGCAGAGNCA GCAGGCACAG TCTGCCATC TGCATCCATC TTGTTTGGGC TCCCTACCCCT	60
TAAAAAGTGC CTCAAATAAT ACCCTGGTGG CCATGGACTT CTCTGGCCAT GCTGGCGTG	120
TNATTGAAGA AACCCCCGGG AAGGCTCTGA AGTGTGGCCC TGGAGGAGGC CCAGGCCTGG	180
NAGGNAAGAA GACAAACAC CGCCTTCAGC CTGCCCATGC CAGCCTCCGG NAAGAGCCTC	240
AGTGGCAGCC ATCCACCGNA CCCAACCTTG GTTCCACGGG GCGGCATTTC CCGTGAAGGA	300
GAGCCAGGGT TNATTGGGA CAGCAGGGTT TNGTTAGACG GNCTGTTCCCT GGTNCGGGAA	360
GAGTCANGGG AACCCCCAGG GTTTGTCC	389

(2) INFORMATION FOR SEQ ID NO:1750:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

GGNAGAGCCN AGCTTAAGT TTTTTNTTTT TTTTTTTTTT TTTTTTTNAAA	60
AAAACCCCTT TTTTTTTN	79

(2) INFORMATION FOR SEQ ID NO:1751:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

CAACGNGNGN GGNCCAAGTA AGCAAGGGCG GGCAACTCCG GAGATNCAAC GGGGAGCTGT	60
ACGCCCGCT GCAGCATGTG AAGCCCCGTG CTGCCCGGGG GGGCGGCCGA ATCGGGCCCG	120
GNNTGCGCAA GGGGGACCAGC ATCCTGGAAG GTGAACCACG TGAATTGAA GGGGGCGACA	180
CACAAGCAGG TGGTGGGACC TNATTCGAGC AGGCNNNAAGAATTGAAT CCTTGAACAG	240
TTTTATCTGT ACCTCCTCAT GAGGCAGATT AACCTTAGAT CCCAGTGAAC GGATTCGTTN	300
NGGGACAATT NTTTTAACATG NTNTTACAAAC AGAAAAGCNA AGG	343

(2) INFORMATION FOR SEQ ID NO:1752:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

GGCANAGCTC GAGTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
TTTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTNNNC N	101

(2) INFORMATION FOR SEQ ID NO:1753:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

GGAAGANCCC TCTCCCAGTN TCCGAAAGGA AGAGTAATGA CCATTCCGTA CCAGCCCCATG	60
CNGGCNAG	68

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

GGCAGAGACT GGGAAAGGAAA GAACATGGCC TGTGTGCAGC GGACGCTTAT GAAATCTGGG	60
TGGGCTGGCA GTAGCCCGAA ATGATGGGCT CTTCTCTGGG GTATCCCAAC TGGTCCCTA	120
AGAAATCCAA GGTAGAACATCC TCGGNAACTT CTCGGATAAC CAGCTGCANG AGGGTCAAGA	180
ACGTGAATCG GGTTACAGAT GGGCACCAAC CGCGGGCGT CTTCAGGCAG GCATGNACTG	240
GNCTTACGGG AATGCCACGN CAGATCCTTT GAATCCCACC CCAGGCCTTN GCCCCTGNC	299

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

GGCANAGGTT TCCCGAAGTA AGTNCCCANA GAGCTGGCTG TGGAACGTTG AAGGACTTG	60
AANAGCCACC GAAAAATGGG AATCTNTACG AAGGCTCATG AAATATATTT TTAAAAGACT	120
CCATCACCAAC GTGGGAAGAA TTCTGNGCTG TGANGCATGT NGGGACAAGA AAGGGAATCT	180
NTNTGGCAAA CCCCTTCAAG GTTCACAGTT ATG	213

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

GGCAGAGTGA AAGTCACTGT GGATCGAGCT CACAGGGGC ACCCATGCCT GTTGTNAACA	60
GAGTCTNAAG CAGTCAGGGT GTTGGAAATT CTCTGTTGTT GTNATCAATT CCTGCTGAGG	120
GGTTTCTGGG GTTTTNTTTT TAATAAATGA ACTCCTTGTT AGCCTTGTT ACATAATCTT	180
CACTTTGGTT GTTGGTACCA AACAGAGCTC CCAGCCATCT CCTCCCTGTT CCTGAAAGAC	240
TAAAAATCCA CTTNCGGACT CTCCCTTCCT TCCTTCTTNA GCCCTCGAGG GTGCATATTA	300
GCTAATTAAG CAGGNCCAGA GNCAGAGAGG GGGGGTTCCA AAATGAANTC GGNTTTAAGG	360
GGCAAGTGNC CATTNATTGG GTTGGAAATTA ACGGTTATCC TTCATGGNCC GTAAATCCCA	420
GCATTTTG GGGGCCNGG CANGTGGGTC CCNAGGTTGG GGGTCGGGA CCAACNGGGC	480
CAAC	484

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

GGCAGAGCTT TGGAGAGAAG GGAACAGAAAG GTGACATCGG CTTCCCTGGG AATAACAGGC	60
GTAANTGGAG TCCACGGCCC TCCAGGGTCG CAGGGAGAGC TGGGGCGAAT TGGAACTGCC	120
TGGTGGCAA GGAAGATGAT GGCTGGCCGG GAAGCTCCGG GNTTNACCAG GTTTCCGGG	180
NACTCCGTGG GAATCCGCGG NNTTACACGG ATT	213

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

TTTTTTTTTT TTTTTTTTTT TTTTTTNAAA GGGGGGGGGG GGGGGNAATT TT	52
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(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

TCCGGNATGT GCCAAAGCTG GTTTCTGG GGAACGAACG CTCCCGAAGN NGANGTTCC	60
TTCCATCGTC GGGNGCCCCA AACACCAGGG CCGTGCATGG TGGGTCACTGG TNCCAGTAAG	120
GACTCCTGAC G	131

(2) INFORMATION FOR SEQ ID NO:1760:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

GGCAGAGGNA ACCATATAACA AGTTCTGCC GACCATTG ACGCAAGGTT GGAAAGTCCT	60
AAATTCAATC ACAATCTTCT GCCAAGTGNA ACTGGNACAT AAACCTGGAC TTGTCTCAA	120
AAACTCCCAC TTCTCCAAAA ACTCTTGTGA AAATCGCACA GTTTGGGCAC AGCCTNCCTG	180
AGTTTGAACA GTGGAGTTGA AACCTTCTCT ATCCCATGCA GAGGAAGCCT AAATNATGCA	240
AATAAATAAT TATCCAGCAC AGTGCCTNAA AGCTATTTCC TGTGAAGTCC CTTTCAGCTG	300
TGGGAAGAGG GATGGAAGGA TGGAAAGATGG GTNCATAACT GTGGGTGGGC CACAANCCCG	360
AGGGNATNNNT TTAACAGCAA TGGGGGGCGT GCTGAGTTCC CTAGGAAACT GGTGTTAGT	420
	420

(2) INFORMATION FOR SEQ ID NO:1761:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

GGCANAGTAA GAACAGGGTG ATTTTNAATC AGAGAAACTC TGGGAACGGG TAACTCGAGC	60
CATAAATGCC AAAGACCAAA CTGAAGCTAC CCAAGAGAAG TATGTTTGG ANGAAGCTCA	120
AAGACAAGCT GCCACGGATC GGAANACANA AANTGTNAGA GTGGTCTTTC AAATTATTTG	180
	180

(2) INFORMATION FOR SEQ ID NO:1762:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

GGCAGAGAGN ATGCTTCCTT TAAATACCAA TATTGACTT GCGTACTCAA ATGGAAAAGA	60
TGATGAACAG AACTTCATTC AAAATCTCAG TTTGTTCTC TGCACCTTTC TTAAGGAACA	120
TGNTCAACTT GATGAGGAAA AAAGGTTAAA TCTCAGGGAA ACTCTTATGG GAGGCCCTN	180
CATTATATGT TGTTGGGTAT CTGGAAGTGA GNAAGAAACT GGAAAATTCT TTGAAAATT	240
GTNCTTGGAA TGACTGGNAA TCCATNTAGG GCTGGCTGGA ACNCTATAGG AG	292

(2) INFORMATION FOR SEQ ID NO:1763:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

GGCAGAGNAG AAGTTTAAGA TCAAGCTCAT GAGTNANTTG GTCAGCAATG GCGTCCAGAT	60
ATACCANTTC CCAACGGATG ATGACACTAT TGCNANGTC AACGCTGCAA TGAAATGGNA	120
CAGTTGCCGT TTGCTGTTGT GGGAAAGTATG GTTGAGGTAA AAGTCGGAAA CAANTGGTCA	180
AAGCTCGCCA GTTACCCCTTG GGGTGTGTA CAAGTGGAAA ATGAAAACCA CTGTGAACCTT	240
TGTAAAAGCT GCGGGAAATG CTCCATTGTG ACAAAATATGG NGGTNCCTGC GNGAGNAANC	300
CCATACCAGG CACTATGAGG TTTTACAGGC GCTGCAANCT GGAGGAAATG GGGTTTACA	360
GTGTGGGCC AGNAAANCAA GCCATTCAATT TTTCAAGGGGA CNTTGNGGCC AAAG	414

(2) INFORMATION FOR SEQ ID NO:1764:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

AATGGCGGNA AATTNTTGAT TACAAGGNTA TTNAGCTTAG TTGGAAAGCA AGAAATTCA	60
ACTTTTATT GTTAGAGCN TCATAAAAGTT TTGTGAAAGA GNGAAGNATT TTTGGTTCCA	120
AGNTTATATG GTTNGGG	137

(2) INFORMATION FOR SEQ ID NO:1765:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

GGCAGANAAG TNTAAATGCA CATNANTGGC AGCTTATAGA GAACCACCTT GTAACCAGTA	60
TACAGGTACA ACTACAGCTC TTCAGAAATT GGAAGGTTTT GCTAGCCGGT TATTCATAG	120
ACACTCTAAA GGTACTGCNA CATGAATCAG AAAACAGCTC TGGNAAAATG AACAGCCTTT	180
CATTTCTTG AAACATACTG CCTTTATGGG AACAGATTCA ATGNAAAGAN TTTCTAGCCA	240
AAGCCAAAGA AGGACTTTT GAAAAAAATG GGGNGATTCC AACTCNGAAG TTAATGCCGG	300
ACTTGNAAG	309

(2) INFORMATION FOR SEQ ID NO:1766:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

GGCAGAGGGC ANCATCCACA ATAAAGAGAA GCCATTTAAG TNTCACTTAT GTAATAGGTG	60
TTTGGTCAA CAAACCANTT TAGACAGNCA CCTAAAGAAA CATGAGAATG GGAAACATGT	120
TCCGGTACAG CAACANCAGTC GACTCATTCT AAACNTGAA AGTACAGGTG NGAATTCTGG	180
TTGTACAAAG ATGAATGNTT ACTTTCACAG AAATTCCGAA ATTCATTGG GNAACANCAA	240
CCATGGGCAG CCAATCTCCC AGGTATTNTG GGTGGAGAGN ATGA	284

(2) INFORMATION FOR SEQ ID NO:1767:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

GGCAGAGCTC GTCNTNNGNN ATCAAAAGAA ATTTGGTTGC CACCCCCACA GTTCTACGAA	60
GGAGNAAGAC TTGCAAAC TT TGCCCTCTCTC TCTGACTTGC ACAAATTTG TTTGGGTCGT	120
GCATTAGAAG GACTGGTAAA CGTGGCTGCC GATCATCTNG TTAACTGCTG ATGGGATGGT	180
CCATCTTTA CCAGGTGATG AGCTATATT AGAAGATTCA NACTTTTG AAAATCTTAT	240
GTCTACTGAA AAAAAGACTG AGGAAATCAT GAAGGAAGGC AAGCAGTTTC ACCGGGNTAG	300
TGACATACCA TCGNCACCTT TATGGATATC CCCGNGGACT GTTCCAGCCA AAGTTTAAA	360
CCAGGTTTT CCNCANGAAC	380